

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 4, 2006, 12:46:10 ; Search time 44.4444 Seconds
(without alignments)
49.430 Million cell updates/sec

Title: US-10-700-632-1

Perfect score: 30

Sequence: 1 SYIYH 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

A_Geneseq_21:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	5	2	AAW27347
2	30	100.0	5	8	ADO32085
3	30	100.0	5	8	ADO91411
4	30	100.0	10	8	ADO32142
5	30	100.0	47	3	AAG36825
6	30	100.0	50	4	AAM85069
7	30	100.0	53	3	AAG36823
8	30	100.0	93	2	ADW97154
9	30	100.0	116	2	AAW22418
10	30	100.0	116	8	ADR40409
11	30	100.0	116	6	ADR40327
12	30	100.0	116	9	AEB21875
13	30	100.0	117	8	ADO32157
14	30	100.0	118	2	AAR79159
15	30	100.0	118	2	AAW27356
16	30	100.0	118	2	AAW27358
17	30	100.0	118	2	AAW27359
18	30	100.0	118	8	ADE25829
19	30	100.0	118	8	ADE25828
20	30	100.0	118	8	ADE25823
21	30	100.0	118	8	ADE25824
22	30	100.0	118	8	ADE25827
23	30	100.0	118	8	ADO32091
24	30	100.0	118	8	ADO32093

25	30	100.0	118	8	ADU77882	ADU77882 Humanized
26	30	100.0	118	8	ADU77875	ADU77875 Humanized
27	30	100.0	118	8	ADU77879	ADU77879 Humanized
28	30	100.0	118	8	ADU77883	ADU77883 Humanized
29	30	100.0	118	8	ADU77878	ADU77878 Humanized
30	30	100.0	118	8	ADU77867	ADU77867 Humanized
31	30	100.0	118	8	ADU77871	ADU77871 Humanized
32	30	100.0	118	8	ADU77874	ADU77874 Humanized
33	30	100.0	118	8	ADU77866	ADU77866 Mouse H c
34	30	100.0	118	8	ADU77870	ADU77870 Mouse H c
35	30	100.0	119	8	ADO91392	ADO91392 Amino aci
36	30	100.0	120	6	ABP59592	ABP59592 Monoclonal
37	30	100.0	120	6	ABP59987	ABP59987 Antibody
38	30	100.0	120	7	ADF69657	ADF69657 Humanised
39	30	100.0	120	7	ADF69652	ADF69652 Humanised
40	30	100.0	120	9	AEB03871	AEB03871 B-CLL pha
41	30	100.0	120	9	AEB03876	AEB03876 B-CLL pha
42	30	100.0	120	9	AEB21874	AEB21874 Human DC-
43	30	100.0	128	9	AEB21876	AEB21876 Human DC-
44	30	100.0	135	2	ADA89202	ADA89202 Human ant
45	30	100.0	135	2	AAR29016	AAR29016 pUC-RVh-1
46	30	100.0	135	2	AAR28669	AAR28669 p12-h2, 3
47	30	100.0	135	2	AAR29017	AAR29017 pUC-RVh-1
48	30	100.0	241	7	ADG30439	ADG30439 Human Bly
49	30	100.0	245	5	ABP46078	ABP46078 Human Bly
50	30	100.0	245	7	ADG96905	ADG96905 Single ch
51	30	100.0	245	8	ADG34308	ADG34308 Neurokini
52	30	100.0	258	5	ABP46079	ABP46079 Human Bly
53	30	100.0	258	7	ADG96906	ADG96906 Single ch
54	30	100.0	342	3	AAG40513	AAG40513 Arabidops
55	30	100.0	342	3	AAG22420	AAG22420 Arabidops
56	30	100.0	348	3	AAG22419	AAG22419 Arabidops
57	30	100.0	348	3	AAG40512	AAG40512 Arabidops
58	30	100.0	348	8	ADQ16287	ADQ16287 Thalecres
59	30	100.0	348	9	ABP46805	ABP46805 Stress to
60	30	100.0	546	9	AEB92076	AEB92076 Undefined
61	30	100.0	3210	4	ABP73958	ABP73958 Mycelia s
62	29	96.7	207	4	AAU17416	AAU17416 Novel sig
63	29	96.7	207	4	AAU36117	AAU36117 Human pol
64	29	96.7	207	4	ADB94124	ADB94124 Human nov
65	29	96.7	207	8	ADM24638	ADM24638 Human PRO
66	29	96.7	208	4	AAU19217	AAU19217 Human G p
67	29	96.7	243	5	ABP45395	ABP45395 Human Bly
68	29	96.7	243	7	ADG96222	ADG96222 Single ch
69	29	96.7	247	5	ABP45373	ABP45373 Human Bly
70	29	96.7	247	7	ADG96200	ADG96200 Single ch
71	29	96.7	327	8	ADR10158	ADR10158 Human pro
72	29	96.7	379	8	ADH62821	ADH62821 Lactobaci
73	29	96.7	383	8	ADH62822	ADH62822 Lactobaci
74	29	96.7	545	8	ADR15603	ADR15603 Streptoco
75	29	96.7	545	3	AAG51485	AAG51485 Arabidops
76	29	96.7	658	3	AAG51484	AAG51484 Arabidops
77	29	96.7	661	3	AAG51483	AAG51483 Arabidops
78	29	96.7	700	6	ADA50467	ADA50467 Human pro
79	29	96.7	1048	5	ABP85695	ABP85695 Larynx ca
80	29	96.7	1156	4	ABG30864	ABG30864 Human met
81	29	96.7	1186	5	AAU72895	AAU72895 Human met
82	29	96.7	1189	5	AAU74750	AAU74750 Human pro
83	29	96.7	1210	5	AAU85415	AAU85415 Human pro
84	29	96.7	1213	5	AAU77128	AAU77128 Human pro
85	29	96.7	1216	5	AAU77127	AAU77127 Human pro
86	29	96.7	1219	5	AAU77126	AAU77126 Human pro
87	29	96.7	1221	5	ABG76500	ABG76500 DNA encod
88	29	96.7	1222	5	AAU77125	AAU77125 Human pro
89	29	96.7	1223	5	ABG30863	ABG30863 Human met
90	29	96.7	1223	5	AAU79747	AAU79747 Human ADA
91	29	96.7	1223	6	ABP71574	ABP71574 Human agg
92	29	96.7	1226	6	ABP42736	ABP42736 Human ADA
93	29	96.7	1232	6	AAU77130	AAU77130 Human pro
94	29	96.7	1233	6	ABP71573	ABP71573 Human agg
95	29	96.7	1235	5	AAU77129	AAU77129 Human pro
96	29	96.7	1249	5	AAU77132	AAU77132 Human pro
97	29	96.7	1252	5	AAU77131	AAU77131 Human pro

98	29	96.7	1360	6	ABP71575	Human	agg	171	27	90.0	5	8	ADSS2435	Ades5435	Fab	targr
99	28	93.3	20	9	ADW93033	Tomato	ye	172	27	90.0	5	9	AEE28760	Ades2876	Human	CDR
100	28	93.3	21	9	ADW93026	Tomato	ye	173	27	90.0	8	5	AEE28537	Ades2853	scfv	anti
101	28	93.3	24	9	ADW93022	Tomato	ye	174	27	90.0	9	3	AA839811	Adm39811	Anti-H1L1	
102	28	93.3	26	9	ADW93029	Tomato	ye	175	27	90.0	10	8	ADM78096	Adm7809	Human	SJB
103	28	93.3	27	9	ADW93027	Tomato	ye	176	27	90.0	31	8	ADT40324	Adt40324	hSARS	vir
104	28	93.3	28	9	ADW93016	Tomato	ye	177	27	90.0	31	8	ADT59741	Adt59741	SARS	viru
105	28	93.3	30	9	ADW93023	Tomato	ye	178	27	90.0	31	8	ADT37854	Adt37854	hSARS	vir
106	28	93.3	30	9	ADW93030	Tomato	ye	179	27	90.0	31	8	ADY03418	Ady03418	SARS	coro
107	28	93.3	31	9	ADW93028	Tomato	ye	180	27	90.0	83	5	ADH32223	Adh32223	Novel	yea
108	28	93.3	34	9	ADW93019	Tomato	ye	181	27	90.0	97	2	AA857475	Aar57475	Human	HV3
109	28	93.3	34	9	ADW93010	Tomato	ye	182	27	90.0	97	2	AA892078	Aar92078	Human	HV3
110	28	93.3	34	9	ADW93031	Tomato	ye	183	27	90.0	97	5	ABG31425	Abg31425	Amino	aci
111	28	93.3	35	9	ADW93032	Tomato	ye	184	27	90.0	98	5	ABG78173	Abg78173	Human	Fv
112	28	93.3	35	9	ADW93024	Tomato	ye	185	27	90.0	98	5	ABG78174	Abg78174	Human	Fv
113	28	93.3	36	9	ADW93011	Tomato	ye	186	27	90.0	98	5	ABG91864	Abg91864	Human	ant
114	28	93.3	36	9	ADW93025	Tomato	ye	187	27	90.0	98	5	ABG91865	Abg91865	Human	ant
115	28	93.3	38	9	ADW93020	Tomato	ye	188	27	90.0	98	6	ABO27074	Abot7074	Human	ger
116	28	93.3	39	9	ADW93021	Tomato	ye	189	27	90.0	98	7	ADJ13220	Adj13220	Humanised	
117	28	93.3	42	9	ADW93012	Tomato	ye	190	27	90.0	98	7	ADF09902	Adf09902	Antibody	
118	28	93.3	43	9	ADW93014	Tomato	ye	191	27	90.0	98	7	ADF10010	Adfi10010	VEGF	anti
119	28	93.3	43	9	ADW93016	Anti-alpha		192	27	90.0	98	7	ADFI0010	Adfi0010	VEGF	anti
120	28	93.3	118	8	ADBE25825	Anti-alpha		193	27	90.0	98	7	ADJ80287	Adj80287	VH gene	1
121	28	93.3	118	8	ADBE25825	E. faeciu		194	27	90.0	98	7	ADY75292	Ady75292	Protein	e
122	28	93.3	226	5	ABP45956	Human	BLy	195	27	90.0	98	8	ADK68604	Adk68604	plant	ful
123	28	93.3	256	7	ADG96783	Single	ch	196	27	90.0	103	9	ADY60816	Ady60816	Hydrid	pr
124	28	93.3	278	8	ADX89128	Plant	ful	197	27	90.0	110	8	ADM78051	Adm78051	Human	SKB
125	28	93.3	280	6	ABU37733	Protein	e	198	27	90.0	116	5	ABBS7555	Abbs7555	HLA-DR- β	
126	28	93.3	288	6	ABR81034	N. gonorr		199	27	90.0	116	9	ADZ42018	Adz42018	Ig H	chai
127	28	93.3	288	6	ABU37245	Protein	e	200	27	90.0	117	1	AA880149	Aap80149	Biosynthe	
128	28	93.3	293	9	ADY50263	Human	DOT	201	27	90.0	117	1	AA880148	Aap80148	Biosynthe	
129	28	93.3	293	9	ADY50264	Drosophi		202	27	90.0	117	1	AA862295	Aab62295	Sequence	
130	28	93.3	307	6	ABU39005	Protein	e	203	27	90.0	117	1	AA862296	Aab62296	Human	mye
131	28	93.3	317	6	ABU30631	Protein	e	204	27	90.0	117	2	AA866334	Aar66334	Human	imm
132	28	93.3	330	4	ABG26073	Novel	hum	205	27	90.0	117	6	AA888716	Aar88716	Mouse	ant
133	28	93.3	333	6	ABM67136	Phototrab		206	27	90.0	117	6	ABO27265	Abot7265	ICAM-1	bi
134	28	93.3	347	8	ADQ16288	Pea	proba	207	27	90.0	117	8	ADS82880	Ades8280	Human	Myo
135	28	93.3	371	8	ADY25044	Plant	ful	208	27	90.0	117	8	ADSS2892	Ades2892	Human	Myo
136	28	93.3	393	8	AGA43592	Arabidops		209	27	90.0	117	8	ADY60815	Ady60815	Hydrid	pr
137	28	93.3	424	8	ADG22716	Cyanophag		210	27	90.0	117	9	ADZ42017	Adz42017	Ig H	chai
138	28	93.3	482	8	ADN23647	Bacteri		211	27	90.0	118	1	AA862293	Aab62293	Murine	mo
139	28	93.3	501	8	ADL04331	M. catarr		212	27	90.0	118	6	ADA89115	Ada89115	MS-Pro-2-	
140	28	93.3	517	8	ADY07414	Plant	ful	213	27	90.0	118	7	ADG74366	Adg74366	MSPRO	hea
141	28	93.3	519	8	ADN47071	Thermoco		214	27	90.0	118	9	ADW38822	Adw38822	T-cell	me
142	28	93.3	521	8	ADN18646	Bacteri		215	27	90.0	118	9	ADY60813	Ady60813	Mouse	pro
143	28	93.3	521	8	ADS41935	Bacteri		216	27	90.0	118	9	ADZ42019	Adz42019	Ig H	chai
144	28	93.3	527	4	AA896629	Putative		217	27	90.0	120	2	AAU02551	Aau02551	Human	Ab
145	28	93.3	537	3	AA643591	Arabidops		218	27	90.0	120	4	AAU02553	Aau02553	Anti-adip	
146	28	93.3	578	3	AA643590	Arabidops		219	27	90.0	120	6	ABU18719	Abj18719	Antibody	
147	28	93.3	635	4	ABB70972	Drosophi		220	27	90.0	120	6	ABU18673	Abj18673	Antibody	
148	28	93.3	659	2	AAV08486	C. albica		221	27	90.0	120	9	ADZ42020	Adz42020	Ig H	chai
149	28	93.3	659	2	AAV18034	Candida	R	222	27	90.0	120	9	AEB08795	Aeb08795	Antibody	
150	28	93.3	766	5	ABE72285	Rat	prote	223	27	90.0	121	9	AEB21871	Aeb21871	Human	DC-
151	28	93.3	842	5	ABE77172	Human	oxi	224	27	90.0	122	1	AA881365	Aap81365	Heavy	cha
152	28	93.3	871	6	ABU27484	Simian	im	225	27	90.0	122	1	AA862300	Aab62300	Chimeric	
153	28	93.3	1175	6	ABU29788	Protein	e	226	27	90.0	123	1	AA862302	Aab62302	Chimeric	
154	28	93.3	1179	7	ADC66499	E. faeciu		227	27	90.0	123	8	ADU57863	Adu57863	Light	var
155	28	93.3	1213	2	AA002628	Classical		228	27	90.0	125	8	ADV68818	Adv68818	Streptoco	
156	28	93.3	1537	2	ADY50259	Human	DOT	229	27	90.0	125	8	ADV60071	Adv60071	Streptoco	
157	28	93.3	1592	8	ADL35711	Human	ang	230	27	90.0	125	8	AA845609	Aar45609	Monoclon	
158	28	93.3	1592	8	ABM81597	Tumour-as		231	27	90.0	126	6	ADA89123	Ada89123	MS-Pro-54	
159	28	93.3	1662	7	ABG16838	Novel	hum	232	27	90.0	126	6	ADA89124	Ada89124	MS-Pro-55	
160	28	93.3	1765	4	ADB80341	Human	MDP	233	27	90.0	126	6	ADA89116	Ada89116	MS-Pro-11	
161	28	93.3	1817	3	AA818255	Plasmodiu		234	27	90.0	126	6	ADA89120	Ada89120	MS-Pro-26	
162	28	93.3	2237	4	ABBE4977	Drosophi		235	27	90.0	126	6	ADG74375	Adg74375	MSPRO	hea
163	28	93.3	2415	4	ABBS8710	Drosophi		236	27	90.0	126	7	ADG74371	Adg74371	MSPRO	hea
164	28	93.3	3898	2	AA806996	Protein	c	237	27	90.0	126	7	ADG74367	Adg74367	MSPRO	hea
165	28	93.3	3898	2	AA810473	Hog	chole	238	27	90.0	126	7	ADG74374	Adg74374	MSPRO	hea
166	28	93.3	3898	2	AA860543	55	kiloda	239	27	90.0	126	7	ADG74374	Adg74374	MSPRO	hea
167	28	93.3	3898	2	AA895232	Hog	chole	240	27	90.0	126	9	ADW38826	Adw38826	T-cell	me
168	28	93.3	3898	4	AA820382	Hog	chole	241	27	90.0	126	9	ADW38828	Adw38828	T-cell	me
169	27	90.0	5	8	AAE38089	Human	COU	242	27	90.0	126	9	ADW38828	Adw38828	T-cell	me
170	27	90.0	5	8	ADS92895	Human	Myo	243	27	90.0	127	6	ADA89122	Ada89122	MS-Pro-29	

244	27	90.0	127	6	ADA90118	AdA90118	Anti-Abet	317	27	90.0	354	6	ADB10642	AdB10642	Alloiococ
245	27	90.0	127	6	AAO31083	Aao31083	Human ant	416	27	90.0	416	3	AAB53347	Aab53347	Human col
246	27	90.0	127	6	ADG74373	AdG74373	MSPRO hea	319	27	90.0	451	8	ADR23348	Adr23348	Human CD7
247	27	90.0	127	9	ADM38827	AdM38827	T-cell me	320	27	90.0	451	8	ADR23350	Adr23350	Human CD7
248	27	90.0	227	5	ABP26396	AbP26396	Streptoco	321	27	90.0	468	4	AAU63120	Aau63120	Canine Ig
249	27	90.0	227	5	ABP29725	AbP29725	Streptoco	322	27	90.0	474	8	ADR31323	Adr31323	Aspergill
250	27	90.0	228	6	ABR01526	AbR01526	Human ant	323	27	90.0	501	8	ABD43281	Abd43281	Bacterial
251	27	90.0	230	6	ABR01514	AbR01514	Human ant	324	27	90.0	506	4	ABD64965	Abd64965	Drosophil
252	27	90.0	241	6	ADG91404	AdG91404	Anti-Abet	325	27	90.0	507	2	AAW21010	Aaw21010	H. pylori
253	27	90.0	241	6	ADG30414	AdG30414	Human GMB	326	27	90.0	506	8	ADG67684	Adg67684	Novel hum
254	27	90.0	242	3	AAV15127	AaV15127	Anti-muri	327	27	90.0	782	4	AAAB6720	Aab6720	ACNV DNA
255	27	90.0	243	5	ABP45936	AbP45936	Human Bly	328	27	90.0	1968	6	ABAB6721	Abab6721	L. dispar
256	27	90.0	243	5	ADG96763	AdG96763	Single ch	329	27	90.0	1968	6	ABG76435	Abg76435	Sindbis p
257	27	90.0	245	4	AAAB6719	AaB6719	Human leu	330	27	90.0	2861	2	AAW27227	Aaw27227	Human TRI
258	27	90.0	245	4	ABP45440	AbP45440	Human Bly	331	27	90.0	2861	4	ABG17024	Abg17024	Novel hum
259	27	90.0	245	5	ABP45908	AbP45908	Human Bly	332	27	90.0	2861	4	AAAG58192	Aag58192	Novel hum
260	27	90.0	245	5	ABP45891	AbP45891	Human Bly	333	27	90.0	2861	6	ABR41116	AbR41116	GTPase pr
261	27	90.0	245	5	ABP45939	AbP45939	Human Bly	334	27	90.0	2861	6	ABU70968	Abu70968	Human GTP
262	27	90.0	245	7	ADP18275	AdP18275	Anti-TL5	335	27	90.0	2861	7	ADB89736	AdB89736	Human adl
263	27	90.0	245	7	ADG96718	AdG96718	Single ch	336	27	90.0	2861	7	ADBE82532	Adbe82532	Human GTP
264	27	90.0	245	7	ADG96267	AdG96267	Single ch	337	27	90.0	2861	7	ADDB89085	Addb89085	Human pro
265	27	90.0	245	7	ADG96735	AdG96735	Single ch	338	27	90.0	2861	7	ADG14306	Adg14306	TAT288. 1
266	27	90.0	245	7	ADG96766	AdG96766	Single ch	339	27	90.0	2861	9	ADY70472	Ady70472	Human TRI
267	27	90.0	245	8	ADR28090	AdR28090	NPB polyp	340	27	90.0	2883	4	ABG06312	Abg06312	Human bet
268	27	90.0	246	8	ADR28058	AdR28058	NPB polyp	341	27	90.0	2980	4	ABG20756	Abg20756	Novel hum
269	27	90.0	246	5	ABP45718	AbP45718	Human Bly	342	27	90.0	3038	6	ABG17025	Abg17025	Novel hum
270	27	90.0	247	7	ADG96545	AdG96545	Single ch	343	27	90.0	3038	6	ABM32684	Abm32684	Human Tri
271	27	90.0	248	5	ABP45167	AbP45167	Human Bly	344	27	90.0	3038	6	ABCO7226	Abco7226	Human p53
272	27	90.0	248	5	ADG95994	AdG95994	Single ch	345	27	90.0	3060	9	ABG06311	Abg06311	Novel hum
273	27	90.0	249	1	AAp80154	Aap80154	Biosynthe	346	27	90.0	3103	9	ADV97839	Adv97839	Murine pr
274	27	90.0	249	5	ABP45279	AbP45279	Human Bly	347	27	90.0	3135	3	AAAS7474	Aas7474	P. faecip
275	27	90.0	249	5	ABP45288	AbP45288	Human Bly	348	27	90.0	3135	3	AAAB18223	Aab18223	Plasmodiu
276	27	90.0	249	7	ADG96106	AdG96106	Single ch	349	27	90.0	9914	8	AEBO0350	Aebo0350	SARS coro
277	27	90.0	249	7	ADG96115	AdG96115	Single ch	350	27	90.0	9915	8	AEBO40120	Aebo40120	hSARS vir
278	27	90.0	249	8	ADR23322	AdR23322	Human CD7	351	27	90.0	9915	8	ADT37650	Adt37650	hSARS vir
279	27	90.0	249	8	ADR23326	AdR23326	Human CD7	352	27	90.0	5	3	AAAB26978	Aab26978	Rat antib
280	27	90.0	249	8	ADR23324	AdR23324	Human CD7	353	27	90.0	5	3	ADRI5142	Adri5142	Mouse ant
281	27	90.0	249	8	ADS92878	AdS92878	Human Myo	354	27	90.0	5	9	ADX98322	Adx98322	Human ant
282	27	90.0	249	8	ADS92890	AdS92890	Human Myo	355	27	90.0	5	9	ADZ233009	Adz233009	Human CXC
283	27	90.0	250	5	ABP46082	AbP46082	Human Bly	356	27	90.0	6	2	AAW42309	Aaw42309	Blottingla
284	27	90.0	250	5	ABP46086	AbP46086	Human Bly	357	27	90.0	6	4	AAAB50794	Aab50794	Murine an
285	27	90.0	250	7	ADG96913	AdG96913	Single ch	358	27	90.0	6	4	AAAG5299	Aag5299	Anti-TL-1
286	27	90.0	250	7	ADG96909	AdG96909	Single ch	359	27	90.0	10	4	AAAB35293	Aab35293	Murine PS
287	27	90.0	251	5	ABP45990	AbP45990	Human Bly	360	27	90.0	10	8	ADP47142	Adp47142	Human pho
288	27	90.0	251	5	ADG96817	AdG96817	Single ch	361	27	90.0	10	9	AEBO3715	Aebo3715	Murine 1G
289	27	90.0	252	5	ABP45355	AbP45355	Human Bly	362	27	90.0	10	9	AEBO3719	Aebo3719	Murine 2F
290	27	90.0	252	7	ADG96182	AdG96182	Single ch	363	27	90.0	14	7	ADB12847	Adb12847	Human lep
291	27	90.0	253	5	ABP45925	AbP45925	Human Bly	364	27	90.0	18	5	ABP46953	Abp46953	Human Bly
292	27	90.0	253	5	ABP45884	AbP45884	Human Bly	365	27	90.0	18	7	ADG97780	Adg97780	scFV VHCD
293	27	90.0	253	5	ABP46087	AbP46087	Human Bly	366	27	90.0	30	4	AAAM15251	Aam15251	Peptide #
294	27	90.0	253	5	ABP46090	AbP46090	Human Bly	367	27	90.0	30	4	AAAB34240	Aab34240	Peptide #
295	27	90.0	253	5	ABP45940	AbP45940	Human Bly	368	27	90.0	30	4	AAAM27712	Aam27712	Peptide #
296	27	90.0	253	7	ADG96711	AdG96711	Single ch	369	27	90.0	30	4	ABAB29081	Abab29081	Peptide #
297	27	90.0	253	7	ADG96752	AdG96752	Single ch	370	27	90.0	30	4	ABBI19676	Abbi19676	Protein #
298	27	90.0	253	7	ADG96914	AdG96914	Single ch	371	27	90.0	30	4	AAAM67423	Aam67423	Human bra
299	27	90.0	253	7	ADG96917	AdG96917	Single ch	372	27	90.0	30	4	AAAM55035	Aam55035	Human dxn
300	27	90.0	253	7	ADG96767	AdG96767	Single ch	373	27	90.0	30	4	AAAG49080	Aag49080	Human liv
301	27	90.0	254	5	ABP45972	AbP45972	Human Bly	374	27	90.0	30	4	AAAM02995	Aam02995	Peptide #
302	27	90.0	254	5	ABP45950	AbP45950	Human Bly	375	27	90.0	30	5	ABG37046	Abg37046	Human pep
303	27	90.0	254	7	ADG96799	AdG96799	Single ch	376	27	90.0	35	4	ABBB63997	Abbb63997	Drosophil
304	27	90.0	254	7	ADG96777	AdG96777	Single ch	377	27	90.0	43	8	ADSO80148	Adso80148	Staphyloc
305	27	90.0	255	5	ABP45145	AbP45145	Human Bly	378	27	90.0	44	5	AAAM50881	Aam50881	Anti-Dovi
306	27	90.0	255	5	ABP44846	AbP44846	Human Bly	379	27	90.0	50	8	ADSO55542	Adso55542	Staphyloc
307	27	90.0	255	7	ADG95673	AdG95673	Single ch	380	27	90.0	52	3	AAAG59651	Aag59651	Arabidops
308	27	90.0	255	7	ADG95972	AdG95972	Single ch	381	27	90.0	57	3	AAAB25044	Aab25044	Plant SDF
309	27	90.0	255	5	ABP45556	AbP45556	Human Bly	382	27	90.0	57	3	AAAB25060	Aab25060	Plant SDF
310	27	90.0	259	7	ADG96383	AdG96383	Single ch	383	27	90.0	57	3	AAAB24914	Aab24914	Plant SDF
311	27	90.0	260	7	ADG30483	AdG30483	Human GMC	384	27	90.0	62	7	AAAG59172	Aag59172	Arabidops
312	27	90.0	292	5	ADSG64666	Adsg64666	Saccharom	385	27	90.0	65	3	AAAB24912	Aab24912	Plant SDF
313	27	90.0	336	9	ADY85547	Ady85547	Catalytic	386	27	90.0	65	3	AAAB25043	Aab25043	Plant SDF
314	27	90.0	338	6	ADCB7251	Adcb7251	Human GPC	387	27	90.0	65	3	AAAB24634	Aab24634	Plant SDF
315	27	90.0	346	6	ADB10646	Adb10646	Alloiococ	388	27	90.0	65	3	AAAB24984	Aab24984	Plant SDF
316	27	90.0	353	6	ADB10644	Adb10644	Alloiococ	389	27	90.0	65	3	AAAB24984	Aab24984	Plant SDF

390	25	86.7	65	3	AAB25059	Aab25059	Plant SDF	463	25	86.7	152	5	AAB53492	Abb53492	Lactococc
391	26	86.7	65	2	AAG58171	Aag58171	Arabidops	464	26	86.7	155	8	ADG65048	Adg65048	Novel hum
392	26	86.7	67	2	AAV60139	Aay60139	Human end	465	26	86.7	156	3	AAB18156	Aab18156	Plasmodiu
393	26	86.7	68	7	ABO60858	AbO60858	Klebsiell	466	26	86.7	156	4	ABG07726	Abg07726	Novel hum
394	26	86.7	69	4	ABB68612	Abb68612	Drosophil	467	26	86.7	156	4	ABG14412	Abg14412	Novel hum
395	26	86.7	69	8	ADT50196	Adt50196	S. pneumon	468	26	86.7	161	5	ABP39960	Abp39960	Staphyloc
396	26	86.7	70	4	AAO11210	Aao11210	Human pol	469	26	86.7	161	8	ADSO6296	Adso6296	Staphyloc
397	26	86.7	70	3	AAB24983	Aab24983	Plant SDF	470	26	86.7	169	3	AAG42313	Aag42313	Arabidops
398	26	86.7	74	3	AAB24633	Aab24633	Plant SDF	471	26	86.7	175	7	ADC95018	Adc95018	E. faeciu
399	26	86.7	74	3	AAO13055	Aao13055	Human pol	472	26	86.7	182	8	ADY08022	Ady08022	Plant ful
400	26	86.7	78	2	AAV12285	Aay12285	Human 5'	473	26	86.7	183	6	ABM69768	Abm69768	Phototrab
401	26	86.7	81	4	AAM88921	Aam88921	Human imm	474	26	86.7	183	6	ABM69669	Abm69669	Phototrab
402	26	86.7	82	3	AAG59170	Aag59170	Arabidops	475	26	86.7	197	8	ADX78169	Adx78169	Plant ful
403	26	86.7	83	3	AAB25058	Aab25058	Plant SDF	476	26	86.7	198	8	ADF69324	Adf69324	Human lun
404	26	86.7	83	3	AAB25042	Aab25042	Plant SDF	477	26	86.7	199	6	ABUS2314	Abus2314	Human GPC
405	26	86.7	83	3	AAB25062	Aab25062	Plant SDF	478	26	86.7	199	8	ADL23963	Adl23963	Human NOV
406	26	86.7	87	4	AAO05988	Aao05988	Human ORF	479	26	86.7	208	5	ABP41664	Abp41664	Human ova
407	26	86.7	87	4	ABM17118	Abm17118	Human pol	480	26	86.7	210	6	ABM71218	Abm71218	Staphyloc
408	26	86.7	92	3	AAG45009	Aag45009	Human ner	481	26	86.7	213	6	ADA34834	Ada34834	Actinobac
409	26	86.7	97	5	ABP01374	Abp01374	Zea mays	482	26	86.7	216	2	AAV36107	Aay36107	Extended
410	26	86.7	98	8	ADOS8510	Ado85810	Human ORF	483	26	86.7	216	8	ADP19415	Adp19415	Human sec
411	26	86.7	99	3	AAG00044	Aag00044	GNAP gene	484	26	86.7	218	8	ADX89180	Adx89180	Plant ful
412	26	86.7	100	3	AAB44219	Aab44219	Human sec	485	26	86.7	219	8	ADX87858	Adx87858	Plant ful
413	26	86.7	100	6	ABP75800	Abp75800	Human can	486	26	86.7	221	3	AAG20197	Aag20197	Arabidops
414	26	86.7	100	8	ABM80110	Abm80110	Human sec	487	26	86.7	221	7	ADC52536	Adc52536	Rice wild
415	26	86.7	101	5	ABP10644	Abp10644	Tumour-as	488	26	86.7	221	8	ADCS2538	Adc52538	Rice Thrt2
416	26	86.7	102	4	AAM81263	Aam81263	Human ORF	489	26	86.7	221	8	ADK71877	Adk71877	Human kin
417	26	86.7	102	4	AAU31883	Aau31883	Novel hum	490	26	86.7	221	8	ADN72565	Adn72565	Thale cre
418	26	86.7	102	8	ADX95475	Adx95475	Plant ful	491	26	86.7	221	8	ADN72509	Adn72509	Thale cre
419	26	86.7	105	8	ADX73508	Adx73508	Plant ful	492	26	86.7	222	4	AAE03757	Aae03757	Chimeric
420	26	86.7	105	9	ADVO9297	Advo9297	Bacteriop	493	26	86.7	225	8	ADX66737	Adx66737	Plant ful
421	26	86.7	107	4	AAM84320	Aam84320	Human imm	494	26	86.7	225	8	ADX89364	Adx89364	Plant ful
422	26	86.7	107	6	ABP75844	Abp75844	Human sec	495	26	86.7	228	3	AAG59099	Aag59099	Arabidops
423	26	86.7	109	4	AAV95742	Aam95742	Human rep	496	26	86.7	231	3	AAG55880	Aag55880	Arabidops
424	26	86.7	111	5	ABG93107	Abg93107	S. Cerevi	497	26	86.7	234	9	ABM97051	Abm97051	M. xanthu
425	26	86.7	113	4	AAG65352	Aag65352	Anti-IL-1	498	26	86.7	235	6	AAO31140	Aao31140	Human cmo
426	26	86.7	113	4	AAG65308	Aag65308	Anti-IL-1	499	26	86.7	235	9	ADY34213	Ady34213	TRAIL, rec
427	26	86.7	113	9	AEB03812	Aeb03812	Murine an	500	26	86.7	237	3	AAG59098	Aag59098	Arabidops
428	26	86.7	113	9	AEB03773	Aeb03773	Murine an	501	26	86.7	237	8	ADK79711	Adk79711	Plant ful
429	26	86.7	114	4	AAV50793	Aab50793	Murine an	502	26	86.7	238	2	AAK45443	Aar45443	Sequence
430	26	86.7	114	9	AEB03736	Aeb03736	Murine an	503	26	86.7	238	8	ADX68433	Adx68433	Plant ful
431	26	86.7	114	9	AEB03755	Aeb03755	Murine an	504	26	86.7	239	2	AAW15186	Aaw15186	Single-ch
432	26	86.7	114	9	AEB03746	Aeb03746	Murine an	505	26	86.7	241	5	ABP45937	Abp45937	Human Bly
433	26	86.7	115	2	AAV74062	Aay74062	Human pro	506	26	86.7	241	5	ABP45292	Abp45292	Human Bly
434	26	86.7	116	8	ADO32158	Ado32158	Mouse ant	507	26	86.7	241	7	ADG30477	Adg30477	Human GMB
435	26	86.7	116	8	ADR73590	Adt73590	Anti-AR a	508	26	86.7	241	7	ADG96764	Adg96764	Single ch
436	26	86.7	116	8	ADT74985	Aeb21870	Human DC-	509	26	86.7	241	7	ADG96119	Adg96119	Single ch
437	26	86.7	116	9	AEB21870	Aeb21870	Human DC-	510	26	86.7	243	8	ADY23082	Ady23082	Plant ful
438	26	86.7	117	8	ADH17836	Adh17836	Murine an	511	26	86.7	243	8	ADY07353	Ady07353	Plant ful
439	26	86.7	117	9	ADM11467	Adm11467	Murine an	512	26	86.7	244	8	ADSO9265	Adso9265	Human c-M
440	26	86.7	117	9	ADM11467	Adm11467	Murine an	513	26	86.7	244	8	ADSO9240	Adso9240	Human c-M
441	26	86.7	118	7	ADG73662	Adg73662	C. histcol	514	26	86.7	244	8	ADSO9243	Adso9243	Human c-M
442	26	86.7	118	9	ADV98411	Adv98411	Human ant	515	26	86.7	244	8	ADSO9242	Adso9242	Human c-M
443	26	86.7	119	8	ADV98411	Adv98411	Human ant	516	26	86.7	244	8	ADX75616	Adx75616	Plant ful
444	26	86.7	119	8	ADV98411	Adv98411	Human ant	517	26	86.7	244	8	ADY05279	Ady05279	Plant ful
445	26	86.7	120	2	AAK30767	Aar30767	Mouse ant	518	26	86.7	244	8	ADX96158	Adx96158	Plant ful
446	26	86.7	120	8	ADT75107	Adt75107	Heavy cha	519	26	86.7	245	8	ADSO9252	Adso9252	Human c-M
447	26	86.7	121	4	AAE03752	Aae03752	Heavy cha	520	26	86.7	245	8	ADSO9270	Adso9270	Human c-M
448	26	86.7	121	5	AEG76555	Abg76555	HCV EI an	521	26	86.7	245	8	ADY05933	Ady05933	Plant ful
449	26	86.7	121	9	AEB21866	Aeb21866	Human DC-	522	26	86.7	245	8	ADY77142	Ady77142	Plant ful
450	26	86.7	121	9	AEB21867	Aeb21867	Human DC-	523	26	86.7	245	8	ADK75922	Adk75922	Plant ful
451	26	86.7	123	3	AAAB26977	Aab26977	Rat antib	524	26	86.7	245	8	ADK75922	Adk75922	Plant ful
452	26	86.7	123	4	AAU02587	Aau02587	Anti-adip	525	26	86.7	245	8	ADY07352	Ady07352	Plant ful
453	26	86.7	123	7	ADPE06762	Adpe06762	DL3 heavy	526	26	86.7	245	8	ADK67905	Adk67905	Plant ful
454	26	86.7	125	3	AAG23879	Aag23879	Arabidops	527	26	86.7	245	8	ADK75537	Adk75537	Plant ful
455	26	86.7	125	3	AAG45008	Aag45008	Zea mays	528	26	86.7	246	8	ADL58066	Adl58066	Reg IV-sep
456	26	86.7	126	3	ADZ23007	Adz23007	Human CXC	529	26	86.7	246	8	ADY07656	Ady07656	Plant ful
457	26	86.7	134	2	AAV12340	Aay12340	Human 5'	530	26	86.7	246	8	ADX89202	Adx89202	Plant ful
458	26	86.7	136	2	AAV06579	Aay06579	Arabidops	531	26	86.7	246	8	ADK77592	Adk77592	Plant ful
459	26	86.7	136	4	AAU76694	Aau76694	Mouse hea	532	26	86.7	248	3	AAAG46650	Aag46650	Arabidops
460	26	86.7	136	4	AAAB35290	Aab35290	Murine PS	533	26	86.7	248	5	ABP44956	Abp44956	Human Bly
461	26	86.7	139	9	ADK98261	Adk98261	Human ant	534	26	86.7	248	7	ADG95783	Adg95783	Single ch
462	26	86.7	148	2	AAV37594	Aay37594	Protein i	535	26	86.7	248	8	ADL58073	Adl58073	Reg IV-sp

536	26	86.7	248	8	ADX88352	Adx88352 Plant ful	609	26	86.7	315	6	ABU19255	Abu19255 Protein e
537	26	86.7	249	3	AAQ46649	Aaq46649 Arabidops	610	26	86.7	315	8	ADN42170	Adn42170 Human nov
538	26	86.7	249	3	ABG23451	Abg23451 Novel hum	611	26	86.7	316	3	AAG55879	Aag55879 Arabidops
539	26	86.7	249	5	ABP45719	Abp45719 Human Bly	612	26	86.7	319	6	ABJ38261	Abj38261 Apoptosis
540	26	86.7	249	7	ADG96546	Adg96546 Single ch	613	26	86.7	320	3	AAG59097	Aag59097 Arabidops
541	26	86.7	249	7	ADG09264	Adg09264 Human c-M	614	26	86.7	321	5	AD116831	Ad116831 Human NOV
542	26	86.7	250	8	ADY10376	Ady10376 Plant ful	615	26	86.7	325	5	AAU93031	Aau93031 Arabidops
543	26	86.7	251	8	AD158043	Ad158043 Reg IV-ful	616	26	86.7	325	7	ADE37307	Ade37307 Plant yie
544	26	86.7	251	8	AD158059	Ad158059 Reg IV-sp	617	26	86.7	325	8	AD143963	Ad143963 Plant tra
545	26	86.7	253	3	AAQ46648	Aaq46648 Arabidops	618	26	86.7	325	8	ADI61363	Adi61363 A. thalia
546	26	86.7	253	5	ABP44996	Abp44996 Human Bly	619	26	86.7	325	8	ADO02141	Ado02141 Thalecres
547	26	86.7	253	5	ABP44992	Abp44992 Human Bly	620	26	86.7	327	3	AAV43841	Aay43841 Amino aci
548	26	86.7	253	5	ABP45515	Abp45515 Human Bly	621	26	86.7	327	3	ABBA49422	Abba49422 Listeria
549	26	86.7	253	7	ADG95823	Adg95823 Single ch	622	26	86.7	327	6	ABU32665	Abu32665 Protein e
550	26	86.7	253	7	ADG95819	Adg95819 Single ch	623	26	86.7	327	6	ADSA43619	Ads43619 Bacterial
551	26	86.7	253	7	ADG96342	Adg96342 Single ch	624	26	86.7	328	4	AAQ63570	Aaq63570 Synthetic
552	26	86.7	253	8	ADY24984	Ady24984 Plant ful	625	26	86.7	328	4	AAQ63569	Aag63569 Synthetic
553	26	86.7	254	8	ADY10383	Ady10383 Plant ful	626	26	86.7	333	5	AAM52836	Aams2836 Physcomit
554	26	86.7	254	8	ADY10544	Ady10544 Plant ful	627	26	86.7	333	6	ABJ38263	Abj38263 Apoptosis
555	26	86.7	254	8	ADY10379	Ady10379 Plant ful	628	26	86.7	340	3	AAQ55878	Aag55878 Arabidops
556	26	86.7	254	8	ADY11453	Ady11453 Plant ful	629	26	86.7	341	8	ADX93424	Adx93424 Plant ful
557	26	86.7	254	8	ADY10374	Ady10374 Plant ful	630	26	86.7	343	6	ABM68824	Abm68824 Phototrab
558	26	86.7	254	8	ADY10597	Ady10597 Plant ful	631	26	86.7	349	8	ADX93971	Adx93971 Plant ful
559	26	86.7	255	8	ADY10381	Ady10381 Plant ful	632	26	86.7	350	7	ADE08734	Ade08734 Novel pro
560	26	86.7	257	8	ADY10675	Ady10675 Plant ful	633	26	86.7	351	4	AAQ72959	Aag72959 Human olf
561	26	86.7	257	8	ADY08923	Ady08923 Plant ful	634	26	86.7	351	4	AAQ72617	Aag72617 Murine OR
562	26	86.7	258	8	ADS29521	Ads29521 Bacterial	635	26	86.7	353	4	AAQ98445	Aab98445 Human pap
563	26	86.7	258	8	ADY10348	Ady10348 Plant ful	636	26	86.7	354	5	ABG31307	Abg31307 Amino aci
564	26	86.7	258	8	ADY08800	Ady08800 Plant ful	637	26	86.7	354	8	ADN46261	Adn46261 Thermococ
565	26	86.7	260	4	ABM67201	Abm67201 Drosophi1	638	26	86.7	356	4	ABG08744	Abg08744 Novel hum
566	26	86.7	260	6	ABU52311	Abu52311 Human GPC	639	26	86.7	359	6	ABM68795	Abm68795 Phototrab
567	26	86.7	260	6	ABU52313	Abu52313 Human GPC	640	26	86.7	365	6	ADY85503	Ady85503 Catalytic
568	26	86.7	260	8	ADL23961	Adl23961 Human NOV	641	26	86.7	367	7	ABO64090	Aboc64090 Klebsiell
569	26	86.7	260	8	ADL23957	Adl23957 Human NOV	642	26	86.7	372	2	AAW04871	Aaw04871 Phosphory
570	26	86.7	264	8	ADY11817	Ady11817 Plant ful	643	26	86.7	372	2	AAW04869	Aaw04869 Cyclin-de
571	26	86.7	264	8	ADY10461	Ady10461 Plant ful	644	26	86.7	372	5	AAU75107	Aau75107 Cell cycl
572	26	86.7	264	8	ADY10797	Ady10797 Plant ful	645	26	86.7	372	6	ABU62606	Abu62606 Human p-T
573	26	86.7	267	7	ADH88388	Adh88388 Enterococ	646	26	86.7	372	7	ADFA5045	Adfa5045 Human kin
574	26	86.7	269	5	ABM78814	Abm78814 GNS1/SUR4	647	26	86.7	372	8	ADH09516	Adh09516 Human hos
575	26	86.7	270	3	AAQ54802	Aaq54802 Arabidops	648	26	86.7	372	8	ADH09519	Adh09519 Human hos
576	26	86.7	272	7	ADC79358	Adc79358 Human G p	649	26	86.7	372	8	ADH09518	Adh09518 Human hos
577	26	86.7	272	8	ADY10373	Ady10373 Plant ful	650	26	86.7	372	8	ADH09517	Adh09517 Human hos
578	26	86.7	274	8	ADY10500	Ady10500 Plant ful	651	26	86.7	372	8	ADH09521	Adh09521 Human hos
579	26	86.7	275	8	ADY08858	Ady08858 Plant ful	652	26	86.7	372	8	ADP74343	Adp74343 Human cyc
580	26	86.7	275	8	ADY25116	Ady25116 Plant ful	653	26	86.7	372	9	ADX07254	Adx07254 Cyclin-de
581	26	86.7	278	5	ABP28175	Abp28175 Streptoco	654	26	86.7	374	3	AAQ58375	Aaq58375 Lung canc
582	26	86.7	281	8	ADY11604	Ady11604 Plant ful	655	26	86.7	375	4	AAQ58375	Aaq58375 Lung canc
583	26	86.7	281	8	ADX95218	Adx95218 Plant ful	656	26	86.7	375	4	AAQ58375	Aaq58375 Lung canc
584	26	86.7	284	5	ABM50050	Abm50050 Listeria	657	26	86.7	385	5	AAO18258	Aao18258 Transport
585	26	86.7	286	6	ABU01039	Abu01039 S. pneumo	658	26	86.7	392	5	AAQ18258	Aao18258 Transport
586	26	86.7	286	6	ADK48739	Adk48739 Streptoco	659	26	86.7	393	6	ABU23256	Abu23256 Protein e
587	26	86.7	287	4	ADN06988	Adn06988 Human Bfg	660	26	86.7	394	7	ADC94140	Adc94140 E. faeciu
588	26	86.7	287	8	ADN06988	Adn06988 Human Bfg	661	26	86.7	397	2	AAW04270	Aaw04270 B. t. alka
589	26	86.7	291	8	ADP94594	Adp94594 Novel S.	662	26	86.7	398	6	ADAA3220	Ada3220 Actinocoba
590	26	86.7	291	9	AEAS58464	Aeas58464 Streptoco	663	26	86.7	404	4	ABM61292	Abm61292 Drosophi1
591	26	86.7	293	5	ABP61150	Abp61150 Human GPC	664	26	86.7	411	9	ADZ81586	Adz81586 Amino aci
592	26	86.7	296	6	ABU50507	Abu50507 Protein e	665	26	86.7	413	5	AAO15858	Aao15858 Human glu
593	26	86.7	297	4	ABG17653	Abg17653 Novel hum	666	26	86.7	415	8	ADS22070	Ads22070 Bacterial
594	26	86.7	298	4	AAQ30853	Aaq30853 Amino aci	667	26	86.7	424	4	ABM62305	Abm62305 Drosophi1
595	26	86.7	298	7	ADN03892	Adn03892 Human pro	668	26	86.7	425	8	ADK68288	Adk68288 Plant ful
596	26	86.7	302	4	AAU33999	Aau33999 Staphyloc	669	26	86.7	433	5	ABBA49901	Abba49901 Listeria
597	26	86.7	309	6	ABU26592	Abu26592 Protein e	670	26	86.7	434	8	ADY13330	Ady13330 Plant ful
598	26	86.7	309	6	ADH88714	Adh88714 Enterococ	671	26	86.7	437	6	ABU24426	Abu24426 Protein e
599	26	86.7	311	6	ABO19492	Aboc19492 Mouse GPC	672	26	86.7	438	2	AAW71488	Aaw71488 Helicobac
600	26	86.7	311	8	ABU43569	Abu43569 Protein e	673	26	86.7	445	8	ADN23434	Adn23434 Bacterial
601	26	86.7	311	8	ADQ98150	Adq98150 Mouse olf	674	26	86.7	448	8	ADN23646	Adn23646 Bacterial
602	26	86.7	312	4	AAU36839	Aau36839 Staphyloc	675	26	86.7	449	1	AAQ70317	Aaq70317 Protein N
603	26	86.7	312	6	ABU42567	Abu42567 Protein e	676	26	86.7	450	1	AAQ70317	Aaq70317 Protein N
604	26	86.7	312	6	ABU15848	Abu15848 Protein e	677	26	86.7	450	2	AAQ70317	Aaq70317 Protein N
605	26	86.7	312	6	ABM72384	Abm72384 Staphyloc	678	26	86.7	450	7	ADC37473	Adc37473 Mutant ra
606	26	86.7	314	5	ABP40560	Abp40560 Staphyloc	679	26	86.7	450	7	ADC37472	Adc37472 Mutant ra
607	26	86.7	314	5	ADSO6137	Adso6137 Staphyloc	680	26	86.7	450	7	ADC37474	Adc37474 Mutant ra
608	26	86.7	315	5	AD116516	Ad116516 Human NOV	681	26	86.7	450	7	ADC37475	Adc37475 Mutant ra

682	26	86.7	450	8	ADT89797	755	26	86.7	686	4	ABB65206	Abb65206 Drosophi1
683	26	86.7	450	8	ADT89798	756	26	86.7	689	4	AAQ91258	Aaq91258 C. glutam1
684	26	86.7	450	8	ADT89795	757	26	86.7	720	7	ADD13270	Add13270 C. glutam
685	26	86.7	450	8	ADT89800	758	26	86.7	737	5	ABP62810	Abp62810 Human pol
686	26	86.7	450	8	ADT89799	759	26	86.7	737	7	ADD14065	Add14065 Human src
687	26	86.7	450	8	ADT89796	760	26	86.7	737	7	ADDE59678	Ades59678 Human pro
688	26	86.7	450	8	ADT89801	761	26	86.7	737	7	ADDE59672	Ades59672 Human pro
689	26	86.7	458	4	ABB61099	762	26	86.7	737	7	ADDE59675	Ades59675 Human pro
690	26	86.7	462	9	ADU70079	763	26	86.7	737	7	ADDE59681	Ades59681 Human pro
691	26	86.7	467	3	AAAB49120	764	26	86.7	737	8	AD182518	Adi82518 Human mod
692	26	86.7	473	8	ADN18774	765	26	86.7	737	8	ADQ39614	Adq39614 Human myo
693	26	86.7	473	9	AEC03650	766	26	86.7	737	8	ADQ39612	Adq39612 Human myo
694	26	86.7	477	8	ADY08181	767	26	86.7	737	8	ADQ39611	Adq39611 Human myo
695	26	86.7	481	5	AAOI5026	768	26	86.7	741	4	ABG10538	Abg10538 Novel hum
696	26	86.7	487	8	ADP17500	769	26	86.7	741	4	ADCC2932	Adc2932 Human nov
697	26	86.7	488	4	ABG13825	770	26	86.7	741	9	AEB95992	Aeb95992 Human imm
698	26	86.7	488	4	ABG29639	771	26	86.7	741	9	AEB95975	Aeb95975 Human pol
699	26	86.7	491	5	ABBA48369	772	26	86.7	768	5	ABPE62811	Abpe62811 Human pol
700	26	86.7	496	9	ABM93057	773	26	86.7	768	7	ADDE15638	Adel15638 Human str
701	26	86.7	497	4	ABG26113	774	26	86.7	768	7	ADDE15637	Adel15637 Human str
702	26	86.7	498	5	ABBA49356	775	26	86.7	768	8	ABM80548	Abm80548 Tumour-as
703	26	86.7	501	7	ADM03961	776	26	86.7	768	8	ADQ39608	Adq39608 Human myo
704	26	86.7	503	7	ADD71135	777	26	86.7	768	8	ADQ39610	Adq39610 Human myo
705	26	86.7	504	8	ADJ49131	778	26	86.7	768	8	ADQ39616	Adq39616 Human myo
706	26	86.7	504	8	ADS22915	779	26	86.7	768	8	ABU35383	Abu35383 Protein e
707	26	86.7	509	5	ABP38151	780	26	86.7	789	8	ADQ31188	Ado31188 Mouse XT-
708	26	86.7	509	8	ADS07692	781	26	86.7	804	2	AAW34501	Aaw34501 Obesity x
709	26	86.7	512	8	ABBB69433	782	26	86.7	804	7	ADB12853	Adb12853 Human lep
710	26	86.7	512	5	AAEI4703	783	26	86.7	806	7	ADDE52563	Ades52563 Caerofhab
711	26	86.7	515	8	AAEI4701	784	26	86.7	809	3	ABPA1052	Abpa1052 HERV-7g e
712	26	86.7	515	8	ADS24171	785	26	86.7	815	2	AAO5701	Aao5701 Human OB
713	26	86.7	520	7	ADG73668	786	26	86.7	821	4	AAAG65911	Aag65911 Human aci
714	26	86.7	532	8	ADL05668	787	26	86.7	821	8	ADQ31184	Ado31184 Rat XT-I
715	26	86.7	537	8	ADN23981	788	26	86.7	826	8	ABO84882	AbO84882 Murine ca
716	26	86.7	538	4	ABG17323	789	26	86.7	827	9	ADZ13519	Adz13519 Murine ca
717	26	86.7	540	6	ABU20881	790	26	86.7	827	4	AAAG62909	Aag62909 Human aci
718	26	86.7	541	2	AAW98838	791	26	86.7	827	7	ADDE52564	Ades52564 Human SQV
719	26	86.7	541	4	AAU35723	792	26	86.7	827	8	ADQ31180	Ado31180 Human XT-
720	26	86.7	541	6	ABU30760	793	26	86.7	836	5	ABG91811	Abg91811 Human int
721	26	86.7	544	6	ADS23271	794	26	86.7	839	2	AAW34502	Aaw34502 Obesity x
722	26	86.7	554	9	ADM11173	795	26	86.7	861	6	ADK62984	Adk62984 Protein s
723	26	86.7	558	4	ABG06559	796	26	86.7	861	7	ADK62692	Adk62692 Disease t
724	26	86.7	560	7	ABM86595	797	26	86.7	861	8	ADN19162	Adn19162 Bacterial
725	26	86.7	567	7	ADJ68359	798	26	86.7	867	8	ADG63038	Adg63038 Human OBR
726	26	86.7	568	4	AAAG82594	799	26	86.7	868	8	ADG63030	Adg63030 Human OBR
727	26	86.7	578	5	AAAB47733	800	26	86.7	875	8	ADX95120	Adx95120 Plant ful
728	26	86.7	578	7	ADD48772	801	26	86.7	876	4	ABBB6456	Abb66456 Drosophi1
729	26	86.7	580	7	ADR73641	802	26	86.7	883	2	AAW62543	Aaw62543 Human ob-
730	26	86.7	580	8	ABM86384	803	26	86.7	887	4	ABG28071	Abg28071 Novel hum
731	26	86.7	585	4	AAE12810	804	26	86.7	887	4	ABG17316	Abg17316 Novel hum
732	26	86.7	585	5	ABE78225	805	26	86.7	892	2	AAW34260	Aaw34260 Rat ob re
733	26	86.7	611	4	AAE12809	806	26	86.7	894	2	AAW37338	Aaw37338 Ob protei
734	26	86.7	611	5	ABB78224	807	26	86.7	894	2	AAW37337	Aaw37337 Ob protei
735	26	86.7	611	7	ABR84525	808	26	86.7	895	2	AAW34258	Aaw34258 Rat ob re
736	26	86.7	618	4	ABBB63176	809	26	86.7	896	2	AAW50003	Aaw50003 Human OB-
737	26	86.7	623	8	ADX73811	810	26	86.7	896	2	AAW24052	Aaw24052 Human WSX
738	26	86.7	631	8	ABM80547	811	26	86.7	896	6	AAW14841	Aaw14841 Human hae
739	26	86.7	631	8	ADQ39606	812	26	86.7	896	6	ABU87939	Abu87939 Human WSX
740	26	86.7	631	8	ADQ39609	813	26	86.7	896	6	ABO53758	AbO53758 Human WSX
741	26	86.7	631	8	ADQ39615	814	26	86.7	896	7	ADCC08904	Adc08904 Human WSX
742	26	86.7	636	7	ADFO4273	815	26	86.7	896	7	ADDP95214	Adp95214 Human lep
743	26	86.7	640	4	ABBB62091	816	26	86.7	896	8	ADN04458	Adn04458 Antipsoi
744	26	86.7	647	6	ABU24313	817	26	86.7	896	8	ADR27661	Adr27661 Human lep
745	26	86.7	651	5	ABBB93982	818	26	86.7	896	9	ADM88112	Adm88112 Human WSX
746	26	86.7	655	4	AAAG81156	819	26	86.7	898	2	AAH88911	Aah88911 Haematopo
747	26	86.7	662	8	ADQ39613	820	26	86.7	904	2	AAW50002	Aaw50002 Human OB-
748	26	86.7	667	6	ABU00385	821	26	86.7	908	2	AAH88911	Aah88911 Haematopo
749	26	86.7	667	6	ABU18728	822	26	86.7	908	2	AAW19536	Aaw19536 Variant f
750	26	86.7	667	8	ABO84883	823	26	86.7	914	7	ADB64769	Adb64769 Human pro
751	26	86.7	667	8	ADZ13522	824	26	86.7	915	2	AAW14013	Aaw14013 Drosophi1
752	26	86.7	670	8	ADY09403	825	26	86.7	915	4	ABW70955	Abw70955 Drosophi1
753	26	86.7	681	3	AAV43772	826	26	86.7	915	4	ABB72027	Abb72027 Drosophi1
754	26	86.7	681	3	AAV54070	827	26	86.7	916	7	ADD955276	Add955276 Human lep

828	26	86.7	923	2	AAW24053	AAW24053 Human WSX	901	26	86.7	1164	3	AAW24053	AAW24053 Human WSX
829	26	86.7	923	6	ABU87940	ABU87940 Human WSX	902	26	86.7	1165	2	AAW24051	AAW24051 Human WSX
830	26	86.7	923	6	ABO53759	ABO53759 Human WSX	903	26	86.7	1165	2	AAW19116	AAW19116 Human Ob
831	26	86.7	923	7	ADC08905	ADC08905 Human WSX	904	26	86.7	1165	2	AAW13474	AAW13474 Peptide S
832	26	86.7	923	7	ADM88113	ADM88113 Human WSX	905	26	86.7	1165	4	AAE12551	AAE12551 Human Ob
833	26	86.7	925	7	ADO23831	ADO23831 Leptin re	906	26	86.7	1165	4	AAE12609	AAE12609 Human Ob
834	26	86.7	958	2	AAW38214	AAW38214 Human OB-	907	26	86.7	1165	5	AAE25455	AAE25455 Human Ob
835	26	86.7	958	2	AAW31911	AAW31911 Human OB-	908	26	86.7	1165	5	AAE25474	AAE25474 Human Ob
836	26	86.7	958	2	AAW19535	AAW19535 Human OB-	909	26	86.7	1165	5	AAE25765	AAE25765 Human Ob
837	26	86.7	958	2	AAW23773	AAW23773 Human hae	910	26	86.7	1165	5	AAE25772	AAE25772 Human Ob
838	26	86.7	960	2	AAW88910	AAW88910 Haematopo	911	26	86.7	1165	5	AAE25773	AAE25773 Human Ob
839	26	86.7	964	8	ADG63037	ADG63037 Human OBR	912	26	86.7	1165	5	AAE23859	AAE23859 Human DNA
840	26	86.7	965	8	ADG63031	ADG63031 Human OBR	913	26	86.7	1165	6	ABU87938	ABU87938 Human OB
841	26	86.7	970	2	AAW34499	AAW34499 Obesity r	914	26	86.7	1165	6	ADG62979	ADG62979 Human OBR
842	26	86.7	972	2	AAW34497	AAW34497 Obesity r	915	26	86.7	1165	6	ABO53757	ABO53757 Human ful
843	26	86.7	979	9	AEH12221	AEH12221 Streptoco	916	26	86.7	1165	7	ADC08903	ADC08903 Human WSX
844	26	86.7	985	7	ADM04189	ADM04189 Human pro	917	26	86.7	1165	7	ADG62888	ADG62888 Human Pro
845	26	86.7	999	2	AAW34498	AAW34498 Obesity r	918	26	86.7	1165	7	ADG62775	ADG62775 Human Pro
846	26	86.7	1003	6	ABP66226	ABP66226 Human nuc	919	26	86.7	1165	8	ADG63035	ADG63035 Human OBR
847	26	86.7	1015	2	AAW34259	AAW34259 Rat ob re	920	26	86.7	1165	8	ADG62979	ADG62979 Human OBR
848	26	86.7	1021	7	ADG73654	ADG73654 C. histiol	921	26	86.7	1165	8	ADG63036	ADG63036 Human OBR
849	26	86.7	1022	9	ABE55515	ABE55515 Radiochem	922	26	86.7	1165	8	ADG63034	ADG63034 Human OBR
850	26	86.7	1062	6	ADAI3347	ADAI3347 Human int	923	26	86.7	1165	9	ADM88111	ADM88111 Human WSX
851	26	86.7	1065	8	ADG63032	ADG63032 Human OBR	924	26	86.7	1165	9	AAE23210	AAE23210 Human pro
852	26	86.7	1065	8	ADQ08762	ADQ08762 Ciona int	925	26	86.7	1167	2	AAW22470	AAW22470 Streptoco
853	26	86.7	1067	8	ADG63039	ADG63039 Human OBR	926	26	86.7	1167	3	AAW22470	AAW22470 Streptoco
854	26	86.7	1071	4	AAW78903	AAW78903 Human pro	927	26	86.7	1167	3	AEH32324	AEH32324 Human pro
855	26	86.7	1075	4	AAW30852	AAW30852 Amino aci	928	26	86.7	1174	4	ABW71758	ABW71758 Drosophil
856	26	86.7	1075	8	ADP17499	ADP17499 Human nov	929	26	86.7	1181	3	AAW12266	AAW12266 SCFAL pep
857	26	86.7	1077	7	ADP31450	ADP31450 Human nov	930	26	86.7	1181	5	ABP25823	ABP25823 Streptoco
858	26	86.7	1078	9	ADZ02910	ADZ02910 Streptoco	931	26	86.7	1181	8	ADR83967	ADR83967 S. pyogen
859	26	86.7	1086	5	ABW71547	ABW71547 Drosophil	932	26	86.7	1220	2	AAW34500	AAW34500 Obesity r
860	26	86.7	1090	5	ABP28458	ABP28458 Streptoco	933	26	86.7	1221	2	AAW62544	AAW62544 Human ob-
861	26	86.7	1094	4	AAW79887	AAW79887 Human pro	934	26	86.7	1234	2	ADG95278	ADG95278 Human lep
862	26	86.7	1095	4	ABG05128	ABG05128 Novel hum	935	26	86.7	1234	8	ADR27663	ADR27663 OB-R LUC
863	26	86.7	1095	6	ABJ38262	ABJ38262 Apoptosis	936	26	86.7	1277	5	AAU93150	AAU93150 Arabidops
864	26	86.7	1095	6	ABJ38262	ABJ38262 Apoptosis	937	26	86.7	1283	8	ADP74638	ADP74638 Amino aci
865	26	86.7	1095	7	ADB85259	ADB85259 Human KIA	938	26	86.7	1358	5	ABW80603	ABW80603 Human sbg
866	26	86.7	1095	8	ADN04613	ADN04613 Antipiori	939	26	86.7	1416	2	AAE67358	AAE67358 Human ast
867	26	86.7	1095	8	ADRI4045	ADRI4045 Human NF-	940	26	86.7	1471	4	ABW58739	ABW58739 Drosophil
868	26	86.7	1095	9	ADX06623	ADX06623 Cyclin-de	941	26	86.7	1663	8	AD182104	AD182104 Complemen
869	26	86.7	1099	9	ADP17498	ADP17498 Human MEG	942	26	86.7	1663	9	ADX26439	ADX26439 Novel cel
870	26	86.7	1103	9	ADZ02909	ADZ02909 Streptoco	943	26	86.7	1802	3	AAW18217	AAW18217 Plasmodu
871	26	86.7	1109	9	ADZ02908	ADZ02908 Streptoco	944	26	86.7	2222	6	AAW70220	AAW70220 Photorhab
872	26	86.7	1115	5	AAE23383	AAE23383 Human int	945	26	86.7	2225	4	ABW71877	ABW71877 Drosophil
873	26	86.7	1115	5	ADG63033	ADG63033 Human OBR	946	26	86.7	2400	6	ABW70712	ABW70712 Photorhab
874	26	86.7	1120	8	ADX95092	ADX95092 Plant ful	947	26	86.7	2424	4	ABW68256	ABW68256 Drosophil
875	26	86.7	1127	4	ABG07720	ABG07720 Novel hum	948	26	86.7	3105	5	ABW80604	ABW80604 Human sbg
876	26	86.7	1130	8	ADN46433	ADN46433 Thermococ	949	26	86.7	4572	8	ADN17335	ADN17335 O. sativa
877	26	86.7	1134	8	ABP29883	ABP29883 Streptoco	950	26	86.7	4572	5	AAW70923	AAW70923 CDRI of t
878	26	86.7	1134	8	ADOL0473	ADOL0473 Group B S	951	26	86.7	4572	5	ADU38844	ADU38844 Mouse ant
879	26	86.7	1134	3	ADZ02907	ADZ02907 Streptoco	952	26	86.7	4572	5	ADU38844	ADU38844 Human IL-
880	26	86.7	1138	3	AAW18229	AAW18229 Plasmodu	953	26	86.7	4572	10	AAW87018	AAW87018 HPV type
881	26	86.7	1141	4	ABG20072	ABG20072 Novel hum	954	26	86.7	4572	10	ADK08397	ADK08397 Human pap
882	26	86.7	1141	5	ABP66341	ABP66341 Bifidobac	955	26	86.7	4572	10	ADK08041	ADK08041 Human pap
883	26	86.7	1145	4	AAW82169	AAW82169 S. epider	956	26	86.7	4572	14	ADX17325	ADX17325 Human sex
884	26	86.7	1146	6	ABW72999	ABW72999 Streptoco	957	26	86.7	4572	20	AAW15555	AAW15555 Immunop
885	26	86.7	1150	2	AAW22471	AAW22471 Streptoco	958	26	86.7	4572	20	AAW7019	AAW7019 pex12mer/
886	26	86.7	1150	2	AAW22471	AAW22471 Streptoco	959	26	86.7	4572	20	AAW7019	AAW7019 pex12mer/
887	26	86.7	1150	8	ADU69611	ADU69611 S agalact	960	26	86.7	4572	20	AAW7019	AAW7019 pex12mer/
888	26	86.7	1150	8	ADV88737	ADV88737 Streptoco	961	26	86.7	4572	20	AAW7019	AAW7019 pex12mer/
889	26	86.7	1150	8	ADV79990	ADV79990 Streptoco	962	26	86.7	4572	20	AAW7019	AAW7019 pex12mer/
890	26	86.7	1150	8	ADV82129	ADV82129 Streptoco	963	26	86.7	4572	20	AAW7019	AAW7019 pex12mer/
891	26	86.7	1151	5	ABP38397	ABP38397 Staphyloc	964	26	86.7	4572	20	AAW7019	AAW7019 pex12mer/
892	26	86.7	1151	5	ABP38397	ABP38397 Staphyloc	965	26	86.7	4572	20	AAW7019	AAW7019 pex12mer/
893	26	86.7	1155	7	ADG39174	ADG39174 Novel hum	966	26	86.7	4572	20	AAW7019	AAW7019 pex12mer/
894	26	86.7	1155	7	ADG63040	ADG63040 Human OBR	967	26	86.7	4572	20	AAW7019	AAW7019 pex12mer/
895	26	86.7	1161	7	ADG95280	ADG95280 Human lep	968	26	86.7	4572	20	AAW7019	AAW7019 pex12mer/
896	26	86.7	1161	8	ADG63041	ADG63041 Human OBR	969	26	86.7	4572	20	AAW7019	AAW7019 pex12mer/
897	26	86.7	1162	8	ADR27665	ADR27665 OB-R YFP	970	26	86.7	4572	20	AAW7019	AAW7019 pex12mer/
898	26	86.7	1162	8	AAW23399	AAW23399 Rat ob re	971	26	86.7	4572	20	AAW7019	AAW7019 pex12mer/
899	26	86.7	1162	8	AAW23398	AAW23398 Rat ob re	972	26	86.7	4572	20	AAW7019	AAW7019 pex12mer/
900	26	86.7	1164	2	AAW34257	AAW34257 Rat wild-	973	26	86.7	4572	20	AAW7019	AAW7019 pex12mer/
					AAW22469	Streptoco							

974	25	83.3	38	4	AAU22778	AAU22778 Human pro
975	25	83.3	38	7	ADH59005	ADH59005 Human pro
976	25	83.3	38	7	ADJ09351	ADJ09351 Human pro
977	25	83.3	44	4	AAU86482	AAU86482 Novel hum
978	25	83.3	44	7	ADB59816	ADB59816 Connectiv
979	25	83.3	45	4	ABB67634	ABB67634 Drosophi1
980	25	83.3	46	4	AAU86830	AAU86830 Novel hum
981	25	83.3	46	7	ADB60164	ADB60164 Connectiv
982	25	83.3	47	8	ADS05205	ADS05205 Staphy1oc
983	25	83.3	48	8	ADS06696	ADS06696 Staphy1oc
984	25	83.3	50	4	AAU81922	AAU81922 Human hae
985	25	83.3	54	2	AAW77719	AAW77719 Staphy1oc
986	25	83.3	55	9	AEI12002	AEI12002 HPV16 E2
987	25	83.3	55	9	AEI12009	AEI12009 HPV16 E2
988	25	83.3	58	5	ABP04456	ABP04456 Human ORF
989	25	83.3	60	6	ABP97609	ABP97609 Amino ac1
990	25	83.3	61	4	AAU63721	AAU63721 Propionib
991	25	83.3	61	5	ABB72315	ABB72315 Rat prote
992	25	83.3	61	6	ABM60240	ABM60240 Propionib
993	25	83.3	62	8	ADX73255	ADX73255 Plant ful
994	25	83.3	64	4	AAU81483	AAU81483 Human hae
995	25	83.3	70	4	AAU21996	AAU21996 Human car
996	25	83.3	70	7	ADE45964	ADE45964 Human car
997	25	83.3	70	8	ADJ07382	ADJ07382 Human car
998	25	83.3	75	2	AAU27864	AAU27864 Human sec
999	25	83.3	75	6	ABO14361	ABO14361 Novel hum
1000	25	83.3	75	8	ADG78770	ADG78770 Human sec

ALIGNMENTS

RESULT 1

AAW27347 standard; peptide; 5 AA.

AAW27347;

27-AUG-2003 (revised)
12-DEC-1997 (first entry)

CDR1 from murine anti-human IGE receptor antibody light chain.

Complementarity determining region; CDR1; murine; mouse; human;
high affinity; immunoglobulin E; receptor; monoclonal antibody; IGE; Mab;
light chain; variable region; humanised; semi-chimeric; chimeric;
treatment; prevention; disease; allergy.

Mus sp.

JP09191886-A;

29-JUL-1997.

19-JAN-1996; 96JP-00024816.

19-JAN-1996; 96JP-00024816.

(ASAHI BREWERIES LTD.

(TORI) TORII YAKUHI KK.

(NIKK-) NIKKA WHISKY KK.

(TSUR/) TSURA T.

WPI; 1997-429186/40.

Humanised, semi-chimeric and chimeric antibodies against human high-

affinity IGE receptor - useful medicinally and have low antigenicity in

humans.
Claim 1; Page 13; 26pp; Japanese.
The present complementarity determining region 1 (CDR1), which is from a
murine, anti-human high affinity immunoglobulin E (IGE) receptor,

monoclonal antibody (Mab) light chain variable region, can be used in the
preparation of humanised or semi-chimeric anti-human high affinity IGE
receptor Mab. The Mab can be used to treat or prevent diseases,
specifically allergies, associated with the receptor. The humanised, semi-
chimeric or chimeric Mab have very low antigenicity in humans. (Updated
on 27-AUG-2003 to correct OS field.)

Sequence 5 AA;
Query Match 100.0%; Score 30; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 5; Conservative 0; Mismatches 0; Gaps 0;

1 SYVIH 5
1 SYVIH 5

RESULT 2

ADO32085 standard; peptide; 5 AA.

ADO32085;

12-AUG-2004 (first entry)

Mouse anti-CD3 antibody My9-6 heavy chain CDR1 SEQ ID NO:1.

anti-CD3 antibody; epitope-binding fragment;
complementarity-determining region; CDR; immunoglobulin; cytostatic;
antibody; myelodysplastic syndrome; acute myeloid leukaemia;
chronic myeloid leukaemia; pro-myelocytic leukaemia; mouse; My9-6;
heavy chain.

Mus musculus.

WO2004043344-A2.

27-MAY-2004.

05-NOV-2003; 2003MO-US032737.

07-NOV-2002; 2002US-0424332P.

(IMMU-) IMMUNOGEN INC.

Hofee MG, Tavares D, Lutz RJ;

WPI; 2004-411619/38.

New antibodies that bind to CD3, useful for treating a disease
associated with CD3 expression, such as myelodysplastic syndrome, acute
or chronic myeloid leukemia.
Claim 1; SEQ ID NO 1; 124pp; English.

The present invention describes an isolated anti-CD3 antibody or its
epitope-binding fragment comprising: (a) at least one complementarity-
determining region (CDR); or (b) at least heavy chain variable region
comprising 3 CDRs, and at least one light chain variable region, where
the CDR has the ability to bind CD3. Also described: (1) an
immunoglobulin comprising the antibody or its epitope-binding fragment
linked to a drug or prodrug; (2) a composition comprising the antibody or
epitope-binding fragment and a drug or prodrug; (3) a pharmaceutical
composition comprising the immunoglobulin, composition or the antibody
defined above, or its epitope-binding fragment, and a pharmaceutical
agent; (4) a diagnostic reagent comprising the antibody defined above,
where the antibody or antibody fragment is labelled; (5) inhibiting the
growth of a cell expressing CD3 by contacting the cell with the above
defined antibody or its epitope-binding fragment, immunoglobulin, or
(pharmaceutical) composition; (6) determining whether a biological sample
contains a myelogenous cancer cell; (7) an improved antibody or its
epitope-binding fragment that specifically binds to CD3; (8) an isolated

CC (pharmaceutical) composition; (6) determining whether a biological sample
CC contains a myelogenous cancer cell; (7) an improved antibody or its epitope
CC epitope-binding fragment that specifically binds to CD33; (8) an isolated
CC polynucleotide encoding the antibody or its epitope-binding fragment
CC defined above; (9) an isolated polynucleotide encoding a light or heavy
CC chain of the antibody defined above or its epitope-binding fragment; (10)
CC a recombinant vector comprising the polynucleotide; (11) a host cell
CC transformed with the recombinant vector; (12) producing an antibody or
CC its epitope-binding fragment having the ability to bind CD33; and (13)
CC obtaining CD33 from a biological material. The anti-CD33 antibody has
CC cytostatic activity. The antibody or its epitope-binding fragment,
CC immunocjugate, composition can be used for treating a subject having a
CC disease where CD33 is expressed, such as myelodysplastic syndrome, acute
CC myeloid leukemia, chronic myeloid leukemia or pro-myelocytic leukaemia.
CC It can also be used for inhibiting the growth of cells expressing CD33,
CC and for in vivo imaging or as affinity purification agents. The present
CC sequence represents the mouse anti-CD33 antibody My9-6 AbMheavy chain
CC CD31, which is used in an example from the present invention.
XX
SQ Sequence 10 AA:
Query Match 100.0%; Score 30; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 SYTH 5
Db 6 SYTH 10
RESULT 5
AAG36825
ID AAG36825 standard; protein, 47 AA.
XX
AC AAG36825;
DT 18-OCT-2000 (first entry)
XX
XX Arabidopsis thaliana protein fragment SEQ ID NO: 45183.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 45183.
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
XX 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
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PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
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PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
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PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
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PR 07-JUN-1999; 99US-0137724P.
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PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
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PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
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PR 22-JUL-1999; 99US-0145192P.

PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
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PR 28-JUL-1999; 99US-0145951P.
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PR 30-AUG-1999; 99US-0151080P.
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PR 26-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
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PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158359P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
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PR 21-OCT-1999; 99US-0160815P.

PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
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PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 100.0%; Score 30; DB 3; Length 47;
Best Local Similarity 100.0%; Pred. No. 1.1e+02; Mismatches 0; Gaps 0;
Matches 5; Conservative 0; Indels 0;

QY 1 SYIYH 5
Db 8 SYIYH 12

RESULT 6
AAM85069
ID AAM85069 standard; protein; 50 AA.
XX
AC AAM85069;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen SEQ ID NO:12662.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytosolic; gene therapy; vaccine; metastasis.
XX
OS Homo sapiens.
XX
PN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001354.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
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PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
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PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
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PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.

Db 23 SYTH 27

RESULT 7
AAG36823
ID AAG36823 standard; protein, 53 AA.
XX
AC AAG36823;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 45181.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PE 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128271P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 28-APR-1999; 99US-0130891P.
PR 30-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
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PR 05-MAY-1999; 99US-0132485P.
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PR 27-MAY-1999; 99US-0136382P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139482P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.

PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139753P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142380P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144335P.
PR 19-JUL-1999; 99US-0144335P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144684P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145919P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148319P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.

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PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161929P.
PR 28-OCT-1999; 99US-0161935P.
PR 29-OCT-1999; 99US-0162142P.

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Query Match 100.0%; Score 30; DB 3; Length 53;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 SYTH 5
   |||||
Db 14 SYTH 18

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```

RESULT 8
ADW97154
ID ADW97154 standard; protein; 93 AA.
XX

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AC ADW97154;
XX 21-APR-2005 (first entry)
DT Human IL-17A/F Fab heavy chain variable region FR and CDR from clone #9.
XX Interleukin-17; cytokine; lymphokine; immune modulation;
DE animal disease model; immunotherapy; pharmaceutical; diagnosis;
XX prognosis; drug screening; systemic lupus erythematosus;
KM antiinflammatory; dermatological; immunosuppressive;
KM rheumatoid arthritis; antirheumatic; antirheumatic; osteoarthritis;
KM osteoarthritis; arthritis; inflammation; arthropathy; scleroderma;
KM myopathy; Sjogrens syndrome; vasculitis; sarcoidosis;
KM autoimmune hemolytic anemia; anemic; thrombocytopenia; hemostatic;
KM thyroiditis; antithyroid; diabetes mellitus; renal disease; nephrotropic;
KM demyelinating disease; neuroprotective; neuropathy;
KM guillain barre syndrome; cns-gen.; hepatobiliary disease; hepatitis;
KM primary biliary cirrhosis; hepatotropic; primary sclerosing cholangitis;
KM inflammatory bowel disease; gastrointestinal-gen.; enteropathy;
KM lipodystrophy; antilipemic; inflammatory skin disease;
KM bullous skin disease; erythema; contact dermatitis; psoriasis; allergy;
KM antiallergic; asthma; antiasthmatic; allergic rhinitis;
KM atopic dermatitis; food hypersensitivity; urticaria; pulmonary disease;
KM pneumonia; infection; pulmonary fibrosis; respiratory-gen.;
KM transplantation associated disease; graft rejection;
KM graft versus host disease; chimeric antibody; fab;
XX heavy chain variable region.
XX Homo sapiens.
OS Chimeric.
OS Undifferentiated.
XX
FH Key Location/Qualifiers
FT Region 7..16 /note="Complementarity determining region (CDR)-H1"
FT Region 30..46 /note="Complementarity determining region (CDR)-H2"
FT Region 78..87 /note="Complementarity determining region (CDR)-H3"
XX
XX W0205010044-A2.
XX
XX 03-FEB-2005.
XX
XX 02-JUN-2004; 2004WO-US017581.
XX
XX 08-JUL-2003; 2003US-0485559P.
XX 11-JUL-2003; 2003US-0486457P.
XX
XX (GENTECH) GENENTECH INC.
XX
XX Arnoct D, Gurney A, Hase P, Lee J, Wu Y;
XX WPI; 2005-123127/13.
XX
XX N-PSDB; ADW97188.
XX
XX New isolated nucleic acid molecules and encoded IL-17 A/F polypeptides
XX useful for diagnosing or treating degenerative cartilaginous disorders
XX and other immune diseases (e.g. inflammation, rheumatoid arthritis or
XX diabetes).
XX
XX Claim 40; SEQ ID NO 17; 154pp; English.
XX
XX The present invention is related to novel human cytokine that is
XX comprised of a heterodimer of interleukin-17 and interleukin-17F
XX designated as interleukin-17A/F (IL-17A/F). The invention is useful for
XX diagnosing and treating degenerative cartilaginous disorders and other
XX immune related disorders such as systemic lupus erythematosus, rheumatoid
XX arthritis, osteoarthritis, juvenile chronic arthritis, a
XX spondyloarthropathy, systemic sclerosis, an idiopathic inflammatory
XX myopathy, Sjogren's syndrome, systemic vasculitis, sarcoidosis,
XX autoimmune hemolytic anemia, autoimmune chromocytopenia, thyroiditis,
XX diabetes mellitus, immune-mediated renal disease, a demyelinating disease

```

CC of the central or peripheral nervous system, idiopathic demyelinating
 CC polyneuropathy, Guillain-Barre syndrome, a chronic inflammatory
 CC demyelinating polyneuropathy, hepatobiliary disease, infectious or
 CC autoimmune chronic active hepatitis, primary biliary cirrhosis
 CC granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel
 CC disease, gluten-sensitive enteropathy, Whipple's disease, an autoimmune
 CC or immune-mediated skin disease, a bullous skin disease, erythema
 CC multiforme, contact dermatitis, psoriasis, an allergic disease, asthma,
 CC allergic rhinitis, atopic dermatitis, food hypersensitivity, urticaria,
 CC an immunologic disease of the lung, eosinophilic pneumonia, idiopathic
 CC pulmonary fibrosis, hypersensitivity pneumonitis, a transplantation
 CC associated disease, graft rejection and graft-versus-host-disease. The
 CC invention is also used in drug screening purposes. The present sequence
 CC is human interleukin-17A/F (IL-17A/F) Fab heavy chain variable region FR
 CC and CDR protein. The Fab heavy chain variable contains human frame work
 CC (FR) region residues and nonhuman complementarity determining regions
 CC (CDR) residues. This sequence is used in the phage library screening for
 CC antibodies that bind to interleukin-17A/F.

XX Sequence 93 AA;

Query Match 100.0%; Score 30; DB 9; Length 93;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02; Mismatches 0; Gaps 0;
 Matches 5; Conservative 0; Indels 0;

OY 1 SYTH 5
 |||||
 Db 12 SYTH 16

RESULT 9
 AAM22418
 ID AAM22418 standard; protein; 116 AA.

AC AAM22418;

DT 08-DEC-1997 (first entry)

DE Reshaped human AUK12-20 VH.

XX Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6; asthma;
 KW atherosclerosis; AIDS; dementia; diabetes; tumour; metastasis;
 KW inflammatory bowel disease; rheumatoid arthritis; transplant rejection;
 KW graft versus host disease; nephritis; atopic dermatitis; psoriasis;
 KW myocardial ischaemia; acute leukocyte mediated lung injury; therapy;
 KW AUK12-20.

XX Homo; sapiens.
 OS Synthetic.
 OS Chimeric.

PH Key Location/Qualifiers

FT Region 1..30 /label= FR1
 FT Region 31..35 /label= CDRI
 FT Region 36..49 /label= FR2
 FT Region 50..66 /label= CDR2
 FT Region 67..98 /label= FR3
 FT Region 99..105 /label= CDR3
 FT Region 106..116 /label= FR4

XX WO9718838-A1.

PD 29-MAY-1997.

PF 21-NOV-1996; 96WO-US018807.

XX

PR 21-NOV-1995; 95US-00561521.

XX (ATHE-) ATHENA NEUROSCIENCES INC.

PI Bendig MM, Leger OJ, Saldanha J, Jones ST, Vednock TA;

DR WPI; 1997-297879/27.

XX Uses of humanised alpha-4 integrin antibody - for treatment of asthma,
 PT atherosclerosis, AIDS, dementia, etc.

XX Example 6, Page 44; 107pp; English.

PS This polypeptide comprises version 'b', of a reshaped human antibody
 CC AUK12-20 VH region. A DNA fragment encoding the polypeptide was subcloned
 CC into vector pUC19 for use as a template for PCR amplification and
 CC production of version 'a' of a reshaped human 21.6 VH region (see
 CC AAM22413) that can be used in the construction of novel humanised anti-
 CC alpha-4 integrin antibodies. Claimed humanised antibodies are useful in
 CC the treatment of asthma, atherosclerosis, AIDS, dementia, diabetes,
 CC inflammatory bowel disease, rheumatoid arthritis, transplant rejection,
 CC graft versus host disease, tumour metastasis, nephritis, atopic
 CC dermatitis, psoriasis, myocardial ischaemia, and acute leukocyte mediated
 CC lung injury

XX Sequence 116 AA;

Query Match 100.0%; Score 30; DB 2; Length 116;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02; Mismatches 0; Gaps 0;
 Matches 5; Conservative 0; Indels 0;

OY 1 SYTH 5
 |||||
 Db 31 SYTH 35

RESULT 10
 ADR40409
 ID ADR40409 standard; protein; 116 AA.

AC ADR40409;

DT 04-NOV-2004 (first entry)

DE Amino acid fragment of Vh a425.

XX Sulphonylamine; remyelination; demyelinating disease;
 KW lymphocyte infiltration; paralysis; neuroprotective; muscular;
 KW cytoskeletal; antiinflammatory; vulnery;
 KW selective adhesion molecule inhibitor; SAM1; antibody; 21.6.

XX Synthetic.

XX WO2004066931-A2.

PD 12-AUG-2004.

PF 26-JAN-2004; 2004WO-US002028.

PR 24-JAN-2003; 2003US-0442171P.

PR 05-SEP-2003; 2003US-0500316P.

XX (ELAN-) ELAN PHARM INC.

PI Karlik SJ, Pleiss MA, Konradi AW, Grant FS, Semko CM, Dressen D;

PI Messersmith E, Freedman S, Vednock T;

DR WPI; 2004-593990/57.

PT Use of sulfonylamine compounds as selective adhesion molecule inhibitors
 PT to treat demyelinating disease e.g. multiple sclerosis, by inhibiting
 PT lymphocyte infiltration and promoting remyelination to treat paralysis.

XX

PS Example 3; Page 445; 573pp; English.

XX The invention relates to sulphonylamine compounds (A) of specified
CC formulae. The compounds are used to prepare a medicament to promote
CC remyelination of nerve cells in a mammal for treatment of a demyelinating
CC disease and to inhibit lymphocyte infiltration of immune cells in the
CC spinal cord to promote remyelination of nerve cells in the spinal cord,
CC thus treating paralysis. The method of inhibiting lymphocyte infiltration
CC of immune cells in the spinal cord to promote remyelination of nerve
CC cells in the spinal cord and thus treating paralysis further comprises co
CC -administering an immunosuppressant such as adrenocorticotrophic hormone,
CC a corticosteroid (e.g. prednisone, methylprednisolone, dexamethasone
CC cortisone, cortisone, fludrocortisone, prednisolone, alpha-
CC methylprednisolone, triamcinolone or betamethasone) or an interferon
CC (e.g. interferon beta-1b or interferon beta-1a). (A) is used to prepare a
CC medicament for treating paralysis, a congenital metabolic disorder, a
CC neuropathy with abnormal myelination, drug induced demyelination,
CC radiation induced demyelination, hereditary demyelinating condition,
CC prion induced demyelinating condition, encephalitis induced demyelination
CC or spinal cord injury. The present sequence [represents a Vh 4425 fragment
CC used in the construction of reshaped human 21.6 antibody.

XX

SQ Sequence 116 AA;

QY Query Match 100.0%; Score 30; DB 8; Length 116;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 SYTYH 5
|||||
31 SYTYH 35

Db

RESULT 11
ADR40327 standard; protein; 116 AA.

XX

AC ADR40327;

XX

DT 04-NOV-2004 (first entry)

XX

DE Amino acid fragment of Vh 4425.

XX

KW Remyelination; demyelinating disease; lymphocyte infiltration; paralysis;
KW neuroprotective; muscular; cytosratic; antiinflammatory; vulnetary;
KW selective adhesion molecule inhibitor; SAM; antibody; 21.6.

XX

OS Synthetic.

XX

PN WO2004066932-A2.

XX

PD 12-AUG-2004.

XX

PF 26-JAN-2004; 2004WO-US002039.

XX

PR 24-JAN-2003; 2003US-044217P.
PR 05-SEP-2003; 2003US-0500316P.

XX

PA (ELAN-) ELAN PHARM INC.

XX

PI Karlik SJ, Pleiss MA, Konradi AW, Grant FS, Semko CM, Dreesen D;
PI Messersmith E, Freedman S, Yednock T;

XX

DR WPI; 2004-593991/57.

XX

PT Use of remyelinating agent such as natalizumab for preparation of
PT medicament for treating demyelinating diseases and paralysis by promoting
PT remyelination of nerve cells in mammal.

XX

PS Example 3; Page 445; 495pp; English.

XX

CC The invention relates to remyelinating agents (A) that are used to
CC prepare a medicament to promote remyelination of nerve cells in a mammal

CC for treatment of a demyelinating disease and to inhibit lymphocyte
CC infiltration of immune cells in the spinal cord to promote remyelination
CC of nerve cells in the spinal cord, thus treating paralysis. The method of
CC inhibiting lymphocyte infiltration of immune cells in the spinal cord to
CC promote remyelination of nerve cells in the spinal cord and thus treating
CC paralysis further comprises co-administering an immunosuppressant such as
CC adrenocorticotrophic hormone, a corticosteroid (e.g. prednisone,
CC methylprednisolone, dexamethasone cortisone, cortisone, fludrocortisone,
CC prednisolone, alpha-methylprednisolone, triamcinolone or betamethasone)
CC or an interferon (e.g. interferon beta-1b or interferon beta-1a). (A) is
CC used to prepare a medicament for treating paralysis, a congenital
CC metabolic disorder, a neuropathy with abnormal myelination, drug induced
CC demyelination, radiation induced demyelination, hereditary demyelinating
CC condition, prion induced demyelinating condition, encephalitis induced
CC demyelination or spinal cord injury. The present sequence [represents a Vh
CC 4425 fragment used in the construction of reshaped human 21.6 antibody.

XX

SQ Sequence 116 AA;

QY Query Match 100.0%; Score 30; DB 8; Length 116;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 SYTYH 5
|||||
31 SYTYH 35

Db

RESULT 12
AEB21875 standard; protein; 116 AA.

XX

ID AEB21875

XX

AC AEB21875;

XX

DT 08-SEP-2005 (first entry)

XX

DE Human DC-SIGN antibody, heavy chain, SEQ ID NO:31.

XX

KW antibody; DC-SIGN; dendritic cell-specific ICAM-3 grabbing non-integrin;
KW cancer; neoplasm; cytostatic; inflammation; antiinflammatory;
KW ectoparasite infection; antiparasitic; infection; viral infection;
KW bacterial infection; antibacterial; virucide; autoimmune disease;
KW immunosuppressive; immune disorder; allergy; antiallergic; immunotherapy;
KW transplant rejection; humanized antibody; single chain antibody;
KW heavy chain.

XX

OS Homo sapiens.

XX

PN WO2005058244-A2.

XX

PD 30-JUN-2005.

XX

PF 15-DEC-2004; 2004WO-US041788.

XX

PR 15-DEC-2003; 2003US-0529517P.

XX

PA (ALEX-) ALEXION PHARM INC.

XX

PI Bowdish KS, Kretz-Rommel A;

XX

DR WPI; 2005-506067/51.

XX

PT Novel antibody capable of binding or recognizing human dendritic cell-
PT specific intercellular adhesion molecule-3 grabbing non-integrin receptor
PT on cell, useful for treating cancer, and viral and bacterial infections.

XX

PS Example 5; SEQ ID NO 31; 44pp; English.

XX

CC The invention relates to an antibody (I) capable of binding human
CC Dendritic cell-specific intercellular adhesion molecule (ICAM)-3 grabbing
CC non-integrin (DC-SIGN) or recognizing a DC-SIGN receptor on a cell,
CC comprising an amino acid sequence having at least 80% homology to any one
CC of 18 fully defined 4-10 amino acid sequences (AEB21889 to AEB21906). An

CC antibody (I) capable of binding human DC-SIGN or recognizing a DC-SIGN
 CC receptor on a cell, is chosen from: an antibody (A1) capable of binding
 CC human DC-SIGN or recognizing a DC-SIGN receptor on a cell; and an
 CC antibody (A4) capable of recognizing a DC-SIGN receptor on a cell. A4
 CC effectively blocks binding of a virus to the cell, blocks infection of
 CC the cell by a virus, and/or blocks transmission of a virus from the cell
 CC to another cell, where the virus is chosen from HIV, hepatitis C virus
 CC (HCV), Ebola, severe acute respiratory syndrome (SARS), cytomegalovirus
 CC (CMV), Sindbis and Dengue; or effectively blocks binding of a bacteria or
 CC parasite to the cell, blocks infection of the cell by a bacteria or
 CC parasite, and/or blocks transmission of a bacteria or parasite from the
 CC cell to another cell, where the bacteria is chosen from *Helicobacter*
 CC *pylori*, *Klebsiella pneumoniae*, *Mycobacterium tuberculosis* and *M. bovis*,
 CC and the parasite is chosen from *Leishmania pifanoi* and *Schistosoma*
 CC *mansonii*. Also described are: a vaccine comprising A1; a composition
 CC comprising A1 and a carrier; a diagnostic agent (II) for a tumor
 CC characterized by increased DC-SIGN expression, comprising (I); a
 CC diagnostic kit comprising (II); a therapeutic agent for treating a cancer
 CC characterized by increased DC-SIGN expression, comprising A1; treating
 CC (M1) a cancer, involves administering to a subject, a cancer cell killing
 CC amount of a composition comprising A1; and treating (M2) an inflammatory
 CC disease, which involves administering to a subject, a dendritic cell
 CC killing amount of a composition comprising A1. A1 further comprises a
 CC peptide attached to it. The peptide comprises an antigen, where the
 CC antigen comprises a cancer antigen. A1 is humanized antibody or an scFv.
 CC The amino acid sequence appears in the heavy chain CDR3 of the antibody
 CC or the light chain CDR3 of the antibody. A4 capable of blocking and
 CC transmitting virus, also binds to L-SIGN. (I) is useful in interfering
 CC with the interaction of DC-SIGN expressing cells and ICAM-expressing
 CC cells, which involves administering immune-modulating amount of (I), to a
 CC subject. (I) is useful for generating an immune response, which involves
 CC administering immune-modulating amount of (I), to a subject. It is useful
 CC for delivering an antigen to DC-SIGN expressing cells, which involves
 CC attaching the antigen to (I). (I) is useful for diagnosing cancer, which
 CC involves obtaining a tissue sample from a subject suspected of having
 CC cancer, and determining the degree to which the tissue sample binds with
 CC (I), where an increase in the degree of binding compared to corresponding
 CC normal tissue indicates the presence of cancer. The determining step
 CC involves staining for the presence of DC-SIGN. (I) is useful for treating
 CC cancer or inflammatory diseases. (I) is useful for blocking binding of a
 CC virus, bacteria or parasite to the cell, blocking transmission of a
 CC by a virus, bacteria or parasite, and/or blocking transmission of a
 CC virus, bacteria or parasite from the cell to another cell, where the
 CC virus is chosen from HIV, HCV, Ebola, SARS, CMV, Sindbis and Dengue, the
 CC bacteria is chosen from *H. pylori*, *K. pneumoniae*, *M. tuberculosis* and
 CC *M. bovis*, and the parasite is chosen from *L. pifanoi* and *S. mansoni*. (I) is
 CC useful in treating autoimmune diseases (e.g., Rheumatoid arthritis,
 CC systemic lupus erythematosus, multiple sclerosis), preventing transplant
 CC rejection, preventing and treating allergies, and to prevent, inhibit or
 CC at least delay T cell activation for slowing the onset and/or the
 CC progress of a viral disease such as HIV. (I) is useful in inducing
 CC tolerance, immunotherapy, and in diagnostic and research for studying
 CC dendritic cells and/or their function and interaction, studying immune
 CC system and for detecting dendritic cells and/or C-type lectins in
 CC biological samples. The present sequence represents a human DC-SIGN
 CC antibody, heavy chain, SEQ ID NO.31.

XX
 SQ Sequence 116 AA;

Query Match 100.0%; Score 30; DB 9; Length 116;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTYH 5
 |||||
 Db 31 SYTYH 35

RESULT 13
 ADO32157
 ID ADO32157 standard; procein; 117 AA.
 XX
 AC ADO32157;

XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Mouse anti-CD3 antibody heavy chain homologous protein SEQ ID NO:73.
 XX
 KW anti-CD3 antibody; epitope-binding fragment;
 XX complementarity-determining region; CDR; immunoglobulin; cytostatic;
 KW antibody; myelodysplastic syndrome; acute myeloid leukaemia;
 KW chronic myeloid leukaemia; pro-myelocytic leukaemia; mouse; heavy chain.
 XX
 OS Mus musculus.
 XX
 PN W02004043344-A2.
 XX
 PD 27-MAY-2004.
 XX
 PF 05-NOV-2003; 2003MO-US032737.
 XX
 PR 07-NOV-2002; 2002US-0424332P.
 XX
 PA (IMMU-) IMMUNOGEN INC.
 XX
 PI Hoffee MG, Tavares D, Lutz RJ;
 XX
 DR WPI; 2004-411619/38.
 XX
 PT New antibodies that bind to CD33, useful for treating a disease
 PT associated with CD33 expression, such as myelodysplastic syndrome, acute
 PT or chronic myeloid leukemia.
 XX
 PS Example 3; SEQ ID NO 73; 124bp; English.

XX
 CC The present invention describes an isolated anti-CD33 antibody or its
 CC epitope-binding fragment comprising: (a) at least one complementarity-
 CC determining region (CDR); or (b) at least heavy chain variable region
 CC comprising 3 CDRs, and at least one light chain variable region, where
 CC the CDR has the ability to bind CD33. Also described: (1) an
 CC immunoglobulin comprising the antibody or its epitope-binding fragment
 CC linked to a drug or prodrug; (2) a composition comprising the antibody or
 CC epitope-binding fragment and a drug or prodrug; (3) a pharmaceutical
 CC composition comprising the immunoglobulin, composition or the antibody
 CC defined above, or its epitope-binding fragment, and a pharmaceutical
 CC agent; (4) a diagnostic reagent comprising the antibody defined above,
 CC where the antibody or antibody fragment is labelled; (5) inhibiting the
 CC growth of a cell expressing CD33 by contacting the cell with the above
 CC defined antibody or its epitope-binding fragment, immunoglobulin, or
 CC (pharmaceutical) composition; (6) determining whether a biological sample
 CC contains a myelogenous cancer cell; (7) an improved antibody or its
 CC epitope-binding fragment that specifically binds to CD33; (8) an isolated
 CC polynucleotide encoding the antibody or its epitope-binding fragment
 CC defined above; (9) an isolated polynucleotide encoding a light or heavy
 CC chain of the antibody defined above or its epitope-binding fragment; (10)
 CC a recombinant vector comprising the polynucleotide; (11) a host cell
 CC transformed with the recombinant vector; (12) producing an antibody or
 CC its epitope-binding fragment having the ability to bind CD33; and (13)
 CC obtaining CD33 from a biological material. The anti-CD33 antibody has
 CC cytostatic activity. The antibody or its epitope-binding fragment,
 CC immunoglobulin, composition can be used for treating a subject having a
 CC disease where CD33 is expressed, such as myelodysplastic syndrome, acute
 CC myeloid leukaemia, chronic myeloid leukaemia or pro-myelocytic leukaemia.
 CC It can also be used for inhibiting the growth of cells expressing CD33,
 CC and for in vivo imaging or as affinity purification agents. The present
 CC sequence represents a mouse anti-CD33 antibody heavy chain homologous
 CC amino acid sequence, which is used in an example from the present
 CC invention.

XX
 SQ Sequence 117 AA;

Query Match 100.0%; Score 30; DB 8; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTYH 5

```

Db          31 SYTH 35
|||||
RESULT 14
AAR79159 standard; peptide; 118 AA.
XX
AC AAR79159;
XX
DT 25-MAR-2003 (revised)
DT 04-MAR-1996 (first entry)
XX
DE Human Ige receptor-binding antibody-related peptide heavy chain.
XX
KW Immunoglobulin E; antibody; receptor; monoclonal; detection;
KW complementarity determining region.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Region 31..35
FT /label= CDR1H
FT /note= "all CDR regions are claimed"
FT Region 50..66
FT /label= CDR2H
FT /note= "all CDR regions are claimed"
FT Region 99..107
FT /label= CDR3H
FT /note= "all CDR regions are claimed"
XX
PN JF07165799-A.
XX
PD 27-JUN-1995.
XX
PF 22-OCT-1993; 93JP-00264792.
XX
PR 22-OCT-1993; 93JP-00264792.
XX
PA (TSUR/) TSURA T.
PA (ASAK ) ASAH1 BREWERIES LTD.
PA (TORI ) TORII YAKUHIN KK.
PA (NIKK-) NIKKA WHISKEY KK.
XX
DR WPI: 1995-261292/34.
DR N-PSDB; AAQ96286.
XX
PT Novel monoclonal antibody against human high-affinity Ige receptor - and
PT DNA fragment encoding the Mab, for the specific identification of human
PT Fc-epsilon RI.
XX
PS Claim 7; Page 15; 20pp; Japanese.
XX
CC Polypeptides which specifically recognise human Ige receptor (Fc- epsilon
CC -RI) have been isolated and sequenced. The new peptides are related to a
CC monoclonal antibody against Fc-epsilon-RI and are either heavy or light
CC chain molecules. The heavy chain molecules have the general formula R1-
CC CDR1H-FR2-CDR2H-FR3-CDR3H-FR4 (corresp. to AAR79153, AAR79155, AAR79157,
CC AAR79159 and AAR79161) and are encoded by AAQ96280, AAQ96282, AAQ96284,
CC AAQ96286 and AAQ96288. FR1 is a polypeptide having 29-36 amino acids
CC (aa), FR2 is a 10-16 aa polypeptide, FR3 is a 33-35 aa polypeptide and FR4
CC is a 12-14 aa polypeptide. Similarly the light chains have the general
CC formula FR5-CDR1L-FR6-CDR2L-FR7- CDR3L-FR8, (corresp. to AAR79154,
CC AAR79156, AAR79158, AAR79160 and AAR79162) and are encoded by AAQ96281,
CC AAQ96283, AAQ96285, AAQ96287 and AAQ96289. FR5 is a 23-28 aa polypeptide,
CC FR6 is a 14-16 aa polypeptide, FR7 is a 30-34 aa polypeptide and FR8 is a
CC 9-11 aa polypeptide. All the peptides are derived from mouse hybridoma
CC cells and are useful in the detection of the human Fc-epsilon-RI or for
CC the elucidation of an antigen recognising region of a monoclonal antibody
CC against human Fc-epsilon-RI. (Updated on 25-MAR-2003 to correct PA
CC field.)
XX
SQ Sequence 118 AA;

```

```

Query Match 100.0%; Score 30; DB 2; Length 118;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
   |||||
Db 31 SYTH 35

RESULT 15
AAW27356 standard; protein; 118 AA.
XX
AC AAW27356;
XX
DT 16-DEC-1997 (first entry)
XX
DE Heavy chain variable region of human CRA4 antibody.
XX
KW Complementarity determining region; CDR; murine; mouse; human;
KW high affinity; immunoglobulin E; receptor; monoclonal antibody; Ige; Mab;
KW heavy chain; variable region; humanised; semi-chimeric; chimeric;
KW treatment; prevention; disease; allergy; CRA4.
XX
OS Homo sapiens.
XX
PN JF09191886-A.
XX
PD 29-JUL-1997.
XX
PF 19-JAN-1996; 96JP-00024816.
XX
PR 19-JAN-1996; 96JP-00024816.
XX
PA (ASAK ) ASAH1 BREWERIES LTD.
PA (TORI ) TORII YAKUHIN KK.
PA (NIKK-) NIKKA WHISKEY KK.
PA (TSUR/) TSURA T.
XX
DR WPI: 1997-429186/40.
DR N-PSDB; AAT90027.
XX
PT Humanised, semichimeric and chimeric antibodies against human high-
PT affinity Ige receptor - useful medicinally and have low antigenicity in
PT humans.
XX
PS Disclosure; Fig 2; 26pp; Japanese.
XX
CC The CDNA encoding the present sequence, the heavy chain variable region
CC of the human antibody (Ab) CRA4, was used in the preparation of a
CC humanised or semi-chimeric monoclonal Ab (MAB), comprising
CC complementarity determining regions (CDR) from a murine, anti-human high
CC affinity immunoglobulin E (Ige) receptor, Mab. The humanised, semi-
CC chimeric or chimeric Mab can be used to treat or prevent diseases,
CC specifically allergic, associated with the receptor, and has very low
CC antigenicity in humans
XX
SQ Sequence 118 AA;

Query Match 100.0%; Score 30; DB 2; Length 118;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
   |||||
Db 31 SYTH 35

RESULT 16
AAW27528 standard; protein; 118 AA.
XX

```


AC AAW27528;
 XX 16-DEC-1997 (first entry)
 DT
 XX Heavy chain variable region of human CRA4 antibody.
 DE
 XX Complementarity determining region; CDR; murine; mouse; human;
 KW high affinity; immunoglobulin E; receptor; monoclonal antibody; IgE; Mab;
 KM heavy chain; variable region; humanised; semi-chimeric; chimeric;
 KW treatment; prevention; disease; allergy; CRA4.
 XX
 OS Homo sapiens.
 OS JP09191886-A.
 PN
 XX 29-JUL-1997.
 PD
 XX 19-JAN-1996; 96JP-00024816.
 PF
 XX 19-JAN-1996; 96JP-00024816.
 PR
 XX 19-JAN-1996; 96JP-00024816.
 PS
 XX (ASAK) ASAH BWERIES LTD.
 PA (TORI) TORII YAKUHIN KK.
 PA (NIKK-) NIKKA WHISKEY KK.
 PA (TSUR/) TSURA T.
 XX
 DR WPI; 1997-429186/40.
 XX
 PT Humanised, semichimeric and chimeric antibodies against human high-
 PT affinity IGE receptor - useful medicinally and have low antigenicity in
 PT humans.
 PS
 XX Claim 2; Page 14; 26pp; Japanese.
 CC
 XX The present sequence, the heavy chain variable region of the human
 CC antibody (Ab) CRA4, was used in the preparation of a humanised or semi-
 CC chimeric monoclonal Ab (Mab), comprising complementarity determining
 CC regions (CDR) from a murine, anti-human high affinity immunoglobulin E
 CC (IGE) receptor, Mab. The humanised, semi-chimeric or chimeric Mab can be
 CC used to treat or prevent diseases, specifically allergies, associated
 CC with the receptor, and has very low antigenicity in humans
 CC
 SQ Sequence 118 AA;
 QY
 DB 1 SYTYH 5
 31 SYTYH 35
 Query Match 100.0%; Score 30; DB 2; Length 118;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0;
 RESULT 17
 AAW27359
 ID AAW27359 standard; protein; 118 AA.
 XX
 AC AAW27359;
 XX
 DT 16-DEC-1997 (first entry)
 DE
 XX Heavy chain variable region of chimeric human CRA4 antibody.
 DE
 XX Complementarity determining region; CDR; murine; mouse; human;
 KW high affinity; immunoglobulin E; receptor; monoclonal antibody; IgE; Mab;
 KM heavy chain; variable region; humanised; semi-chimeric; chimeric;
 KW treatment; prevention; disease; allergy; CRA4.
 XX
 OS Homo sapiens.
 OS Mus; spp.
 OS Synthetic.
 OS Chimeric.
 XX

PN JP09191886-A.
 XX
 PD 29-JUL-1997.
 XX
 XX 19-JAN-1996; 96JP-00024816.
 PF
 XX 19-JAN-1996; 96JP-00024816.
 PR
 XX 19-JAN-1996; 96JP-00024816.
 PS
 XX (ASAK) ASAH BWERIES LTD.
 PA (TORI) TORII YAKUHIN KK.
 PA (NIKK-) NIKKA WHISKEY KK.
 PA (TSUR/) TSURA T.
 XX
 DR WPI; 1997-429186/40.
 XX
 PT Humanised, semichimeric and chimeric antibodies against human high-
 PT affinity IGE receptor - useful medicinally and have low antigenicity in
 PT humans.
 PS
 XX Claim 8; Page 16; 26pp; Japanese.
 CC
 XX The present sequence, the heavy chain variable region of a chimeric human
 CC CRA4 antibody (Ab), comprises complementarity determining regions (CDR)
 CC from a murine, anti-human high affinity immunoglobulin E (IGE) receptor,
 CC monoclonal Ab (Mab). The humanised chimeric Mab can be used to treat or
 CC prevent diseases, specifically allergies, associated with the receptor,
 CC and has very low antigenicity in humans
 CC
 SQ Sequence 118 AA;
 QY
 DB 1 SYTYH 5
 31 SYTYH 35
 Query Match 100.0%; Score 30; DB 2; Length 118;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0;
 RESULT 18
 ADE25828
 ID ADE25828 standard; protein; 118 AA.
 XX
 AC ADE25828;
 XX
 DT 26-FEB-2004 (first entry)
 DE
 XX Anti-alpha-v-beta-6 monoclonal Ab heavy chain variable domain SEQ:35.
 DE
 XX monoclonal antibody; alpha-v-beta-6; latency associated peptide; LAP;
 KW cytostratic; dermatological; vulnery; hepatocytic; immunosuppressive;
 KW vaccine; fibrosis; scleroderma; scarring; liver fibrosis;
 KW kidney fibrosis; lung fibrosis; psoriasis; cancer; Alport's syndrome.
 XX
 OS Synthetic.
 OS
 PN WO2003100033-A2.
 XX
 PD 04-DEC-2003.
 DE
 XX 13-MAR-2003; 2003WO-US008048.
 PF
 XX 13-MAR-2002; 2002US-0364991P.
 PR
 XX 13-NOV-2002; 2002US-0426286P.
 PA (BIOU) BIOGEN INC.
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Violette SM, Weinreb PH, Simon KJ, Sheppard D, Leone DR;
 DR WPI; 2004-035139/03.
 XX
 PT New monoclonal antibody that specifically binds to alpha-v-beta-6, and

PT inhibits the binding of alpha v beta 6 to latency associated peptide
PT (LAP), useful for treating fibrosis, psoriasis, cancer, or Alport's
XX syndrome.
PS Claim 18; SEQ ID NO 35; 83pp; English.
XX
CC The present invention describes a monoclonal antibody (1) that
CC specifically binds to alpha-v-beta-6, and inhibits the binding of alpha-v-
CC beta-6 to latency associated peptide (LAP) with an IC50 value lower than
CC that of 10D5. Also described: (1) an anti-alpha-v-beta-6 antibody
CC comprising heavy chain complementarily determining regions (CDR) 1, 2,
CC and 3, or a heavy and light chain variable domain sequence; (2) a
CC monoclonal antibody that specifically binds to alpha-v-beta-6 but does
CC not inhibit binding of alpha-v-beta-6 to LAP; (3) a composition for
CC preventing or treating a disease mediated by alpha-v-beta-6 in a mammal
CC comprising the antibody and a carrier; (4) a method for treating a
CC subject having or at risk of having a disease mediated by alpha-v-beta-6
CC by administering to the subject the composition described above, and so
CC alleviating or postponing the onset of the disease; (5) a method of
CC detecting alpha-v-beta-6 in a tissue sample by contacting the tissue
CC sample with the antibody; and (6) a cell hybridoma 6.1A8, 6.3G9, 6.8G6,
CC 6.2B1, 7.1G10, 7.7G5, or 7.1Cr, which respectively comprises American
CC Type Culture Collection (ATCC) Accession number PTA-3647, PTA-3649, PTA-
CC 3645, PTA-3646, PTA-3898, PTA-3899, or PTA-3900. (1) has cytosratic,
CC dermatological, vulnery, hepatotropic and immunosuppressive activities,
CC and can be used in vaccines. The antibodies, compositions and methods of
CC the present invention can be used for preventing or treating a disease
CC mediated by alpha-v-beta-6, e.g. fibrosis such as scleroderma, scarring,
CC liver fibrosis, kidney fibrosis or lung fibrosis; psoriasis; cancer,
CC preferably epithelial cancer, oral, skin, cervical, pharyngeal,
CC laryngeal, oesophageal, lung, breast, kidney or colorectal cancer; or
CC Alport's syndrome. The present sequence is used in the exemplification of
CC the present invention.
XX
SQ Sequence 118 AA;
XX
Query Match 100.0%; Score 30; DB 8; Length 118;
Best Local Similarity 100.0%; Pred. No. 2,7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 SYTYH 5
|||
|||
Db 31 SYTYH 35
XX
RESULT 19
ADE25829 100.0%; Score 30; DB 8; Length 118;
ID ADE25829 standard; protein; 118 AA.
XX
AC ADE25829;
XX
DT 26-FEB-2004 (first entry)
XX
XX Anti-alpha-v-beta-6 monoclonal Ab heavy chain variable domain SEQ.36.
XX
XX monoclonal antibody; alpha-v-beta-6; latency associated peptide; LAP;
KW cytosratic; dermatological; vulnery; hepatotropic; immunosuppressive;
KW vaccine; fibrosis; scleroderma; scarring; liver fibrosis;
KW kidney fibrosis; lung fibrosis; psoriasis; cancer; Alport's syndrome.
XX
OS Synthetic.
XX
PN WO0003100033-A2.
XX
PD 04-DEC-2003.
XX
PF 13-MAR-2003; 2003WO-US008048.
XX
PR 13-MAR-2002; 2002US-0364991P.
XX
PR 13-NOV-2002; 2002US-0426286P.
XX
PA (BIOJ) BIOGEN INC.
PA (REGC) UNIV CALIFORNIA.

XX
PI Violette SM, Weinreb PH, Simon KU, Shepard D, Leone DB;
XX WPI; 2004-035139/03.
XX
DR
XX
XX New monoclonal antibody that specifically binds to alpha-v-beta-6, and
PT inhibits the binding of alpha v beta 6 to latency associated peptide
PT (LAP), useful for treating fibrosis, psoriasis, cancer, or Alport's
PT syndrome.
XX
PS Claim 18; SEQ ID NO 36; 83pp; English.
XX
XX The present invention describes a monoclonal antibody (1) that
CC specifically binds to alpha-v-beta-6, and inhibits the binding of alpha-v-
CC beta-6 to latency associated peptide (LAP) with an IC50 value lower than
CC that of 10D5. Also described: (1) an anti-alpha-v-beta-6 antibody
CC comprising heavy chain complementarily determining regions (CDR) 1, 2,
CC and 3, or a heavy and light chain variable domain sequence; (2) a
CC monoclonal antibody that specifically binds to alpha-v-beta-6 but does
CC not inhibit binding of alpha-v-beta-6 to LAP; (3) a composition for
CC preventing or treating a disease mediated by alpha-v-beta-6 in a mammal
CC comprising the antibody and a carrier; (4) a method for treating a
CC subject having or at risk of having a disease mediated by alpha-v-beta-6
CC by administering to the subject the composition described above, and so
CC alleviating or postponing the onset of the disease; (5) a method of
CC detecting alpha-v-beta-6 in a tissue sample by contacting the tissue
CC sample with the antibody; and (6) a cell hybridoma 6.1A8, 6.3G9, 6.8G6,
CC 6.2B1, 7.1G10, 7.7G5, or 7.1Cr, which respectively comprises American
CC Type Culture Collection (ATCC) Accession number PTA-3647, PTA-3649, PTA-
CC 3645, PTA-3646, PTA-3898, PTA-3899, or PTA-3900. (1) has cytosratic,
CC dermatological, vulnery, hepatotropic and immunosuppressive activities,
CC and can be used in vaccines. The antibodies, compositions and methods of
CC the present invention can be used for preventing or treating a disease
CC mediated by alpha-v-beta-6, e.g. fibrosis such as scleroderma, scarring,
CC liver fibrosis, kidney fibrosis or lung fibrosis; psoriasis; cancer,
CC preferably epithelial cancer, oral, skin, cervical, pharyngeal,
CC laryngeal, oesophageal, lung, breast, kidney or colorectal cancer; or
CC Alport's syndrome. The present sequence is used in the exemplification of
CC the present invention.
XX
SQ Sequence 118 AA;
XX
Query Match 100.0%; Score 30; DB 8; Length 118;
Best Local Similarity 100.0%; Pred. No. 2,7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 SYTYH 5
|||
|||
Db 31 SYTYH 35
XX
RESULT 20
ADE25823 100.0%; Score 30; DB 8; Length 118;
ID ADE25823 standard; protein; 118 AA.
XX
AC ADE25823;
XX
DT 26-FEB-2004 (first entry)
XX
XX Anti-alpha-v-beta-6 monoclonal Ab heavy chain variable domain SEQ.30.
XX
XX monoclonal antibody; alpha-v-beta-6; latency associated peptide; LAP;
KW cytosratic; dermatological; vulnery; hepatotropic; immunosuppressive;
KW vaccine; fibrosis; scleroderma; scarring; liver fibrosis;
KW kidney fibrosis; lung fibrosis; psoriasis; cancer; Alport's syndrome.
XX
OS Synthetic.
XX
PN WO0003100033-A2.
XX
PD 04-DEC-2003.
XX
PF 13-MAR-2003; 2003WO-US008048.
XX

```

XX 13-MAR-2002; 2002US-0364991P.
PR 13-NOV-2002; 2002US-0426286P.
XX
XX (BIOJ ) BIOGEN INC.
PA (REGC ) UNIV CALIFORNIA.
XX
XX Violette SM, Weinreb PH, Simon KJ, Sheppard D, Leone DR;
XX WPI: 2004-035139/03.
XX
XX New monoclonal antibody that specifically binds to alpha-v-beta-6, and
PT inhibits the binding of alpha v beta 6 to latency associated peptide
PT (LAP), useful for treating fibrosis, psoriasis, cancer, or Alport's
PT syndrome.
XX
XX Claim 18; SEQ ID NO 30; 83pp; English.
XX
XX The present invention describes a monoclonal antibody (1) that
CC specifically binds to alpha-v-beta-6, and inhibits the binding of alpha-v-
CC beta-6 to latency associated peptide (LAP) with an IC50 value lower than
CC that of 10D5. Also described: (1) an anti-alpha-v-beta-6 antibody
CC comprising heavy chain complementarily determining regions (CDR) 1, 2,
CC and 3, or a heavy and light chain variable domain sequence; (2) a
CC monoclonal antibody that specifically binds to alpha-v-beta-6 but does
CC not inhibit binding of alpha-v-beta-6 to LAP; (3) a composition for
CC preventing or treating a disease mediated by alpha-v-beta-6 in a mammal
CC comprising the antibody and a carrier; (4) a method for treating a
CC subject having or at risk of having a disease mediated by alpha-v-beta-6
CC by administering to the subject the composition described above, and so
CC alleviating or postponing the onset of the disease; (5) a method of
CC detecting alpha-v-beta-6 in a tissue sample by contacting the tissue
CC sample with the antibody; and (6) a cell hybridoma 6.1A8, 6.3G9, 6.8G6,
CC 6.2B1, 7.1G10, 7.7G5, or 7.1Cr, which respectively comprises American
CC Type Culture Collection (ATCC) Accession number PTA-3647, PTA-3649, PTA-
CC 3645, PTA-3646, PTA-3898, PTA-3899, or PTA-3900. (1) has cytosstatic,
CC dermatological, vulnery, hepatotropic and immunosuppressive activities,
CC and can be used in vaccines. The antibodies, compositions and methods of
CC the present invention can be used for preventing or treating a disease
CC mediated by alpha-v-beta-6, e.g. fibrosis such as scleroderma, scarring,
CC liver fibrosis, kidney fibrosis or lung fibrosis; psoriasis; cancer,
CC preferably epithelial cancer, oral, skin, cervical, pharyngeal,
CC laryngeal, esophageal, lung, breast, kidney or colorectal cancer; or
CC Alport's syndrome. The present sequence is used in the exemplification of
CC the present invention.
XX
XX Sequence 118 AA;
SQ
Query Match 100.0%; Score 30; DB 8; Length 118;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SYTYH 5
Db 31 SYTYH 35
|||||
RESULT 21
ADE25824
ID ADE25824 standard; protein; 118 AA.
XX
AC ADE25824;
XX
XX 26-FEB-2004 (first entry)
XX
XX Anti-alpha-v-beta-6 monoclonal Ab heavy chain variable domain SEQ.31.
XX
XX monoclonal antibody; alpha-v-beta-6; latency associated peptide; LAP;
XX cytosstatic; dermatological; vulnary; hepatotropic; immunosuppressive;
XX vaccine; fibrosis; scleroderma; scarring; liver fibrosis;
XX kidney fibrosis; lung fibrosis; psoriasis; cancer; Alport's syndrome.
XX
XX Synthetic.
OS

```

```

XX WO2003100033-A2.
XX
XX 04-DEC-2003.
XX
XX 13-MAR-2003; 2003WO-US008048.
XX
XX 13-MAR-2002; 2002US-0364991P.
PR 13-NOV-2002; 2002US-0426286P.
XX
XX (BIOJ ) BIOGEN INC.
PA (REGC ) UNIV CALIFORNIA.
XX
XX Violette SM, Weinreb PH, Simon KJ, Sheppard D, Leone DR;
XX WPI: 2004-035139/03.
XX
XX New monoclonal antibody that specifically binds to alpha-v-beta-6, and
PT inhibits the binding of alpha v beta 6 to latency associated peptide
PT (LAP), useful for treating fibrosis, psoriasis, cancer, or Alport's
PT syndrome.
XX
XX Claim 18; SEQ ID NO 31; 83pp; English.
XX
XX The present invention describes a monoclonal antibody (1) that
CC specifically binds to alpha-v-beta-6, and inhibits the binding of alpha-v-
CC beta-6 to latency associated peptide (LAP) with an IC50 value lower than
CC that of 10D5. Also described: (1) an anti-alpha-v-beta-6 antibody
CC comprising heavy chain complementarily determining regions (CDR) 1, 2,
CC and 3, or a heavy and light chain variable domain sequence; (2) a
CC monoclonal antibody that specifically binds to alpha-v-beta-6 but does
CC not inhibit binding of alpha-v-beta-6 to LAP; (3) a composition for
CC preventing or treating a disease mediated by alpha-v-beta-6 in a mammal
CC comprising the antibody and a carrier; (4) a method for treating a
CC subject having or at risk of having a disease mediated by alpha-v-beta-6
CC by administering to the subject the composition described above, and so
CC alleviating or postponing the onset of the disease; (5) a method of
CC detecting alpha-v-beta-6 in a tissue sample by contacting the tissue
CC sample with the antibody; and (6) a cell hybridoma 6.1A8, 6.3G9, 6.8G6,
CC 6.2B1, 7.1G10, 7.7G5, or 7.1Cr, which respectively comprises American
CC Type Culture Collection (ATCC) Accession number PTA-3647, PTA-3649, PTA-
CC 3645, PTA-3646, PTA-3898, PTA-3899, or PTA-3900. (1) has cytosstatic,
CC dermatological, vulnery, hepatotropic and immunosuppressive activities,
CC and can be used in vaccines. The antibodies, compositions and methods of
CC the present invention can be used for preventing or treating a disease
CC mediated by alpha-v-beta-6, e.g. fibrosis such as scleroderma, scarring,
CC liver fibrosis, kidney fibrosis or lung fibrosis; psoriasis; cancer,
CC preferably epithelial cancer, oral, skin, cervical, pharyngeal,
CC laryngeal, esophageal, lung, breast, kidney or colorectal cancer; or
CC Alport's syndrome. The present sequence is used in the exemplification of
CC the present invention.
XX
XX Sequence 118 AA;
SQ
Query Match 100.0%; Score 30; DB 8; Length 118;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SYTYH 5
Db 31 SYTYH 35
|||||
RESULT 22
ADE25827
ID ADE25827 standard; protein; 118 AA.
XX
AC ADE25827;
XX
XX 26-FEB-2004 (first entry)
XX
XX Anti-alpha-v-beta-6 monoclonal Ab heavy chain variable domain SEQ.34.
XX

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KM monoclonal antibody; alpha-v-beta-6; latency associated peptide; LAP;
 KM cyclostatic; dermatological; vulnary; hepatocytic; immunosuppressive;
 KM vaccine; fibrosis; scleroderma; scarring; liver fibrosis;
 KM kidney fibrosis; lung fibrosis; psoriasis; cancer; Alport's syndrome.
 OS Synthetic.
 XX W02003100033-A2.
 XX
 XX
 PD 04-DEC-2003.
 XX
 PF 13-MAR-2003; 2003WO-US008048.
 XX
 PR 13-MAR-2002; 2002US-0354991P.
 PR 13-NOV-2002; 2002US-0426286P.
 XX
 PA (BIOJ) BIOGEN INC.
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Violette SM, Weinreb PH, Simon KJ, Sheppard D, Leone DR;
 XX
 DR WPI; 2004-035139/03.
 XX
 PT New monoclonal antibody that specifically binds to alpha-v-beta-6, and
 PT inhibits the binding of alpha v beta 6 to latency associated peptide
 PT (LAP), useful for treating fibrosis, psoriasis, cancer, or Alport's
 PT syndrome.
 PS
 PS Claim 18; SEQ ID NO 34; 83pp; English.
 XX
 CC The present invention describes a monoclonal antibody (1) that
 CC specifically binds to alpha-v-beta-6, and inhibits the binding of alpha-v-
 CC beta-6 to latency associated peptide (LAP) with an IC50 value lower than
 CC that of 10D5. Also described: (1) an anti-alpha-v-beta-6 antibody
 CC comprising heavy chain complementarily determining regions (CDR) 1, 2,
 CC and 3, or a heavy and light chain variable domain sequence; (2) a
 CC monoclonal antibody that specifically binds to alpha-v-beta-6 but does
 CC not inhibit binding of alpha-v-beta-6 to LAP; (3) a composition for
 CC preventing or treating a disease mediated by alpha-v-beta-6 in a mammal
 CC comprising the antibody and a carrier; (4) a method for treating a
 CC subject having or at risk of having a disease mediated by alpha-v-beta-6
 CC by administering to the subject the composition described above, and so
 CC alleviating or postponing the onset of the disease; (5) a method of
 CC detecting alpha-v-beta-6 in a tissue sample by contacting the tissue
 CC sample with the antibody; and (6) a cell hybridoma 6.1A8, 6.3G9, 6.8G6,
 CC 6.2B1, 7.1G10, 7.7G5, or 7.1C7, which respectively comprises American
 CC Type Culture Collection (ATCC) Accession number PTA-3647, PTA-3649, PTA-
 CC 3645, PTA-3646, PTA-3898, PTA-3899, or PTA-3900. (1) has cyclostatic,
 CC dermatological, vulnary, hepatocytic and immunosuppressive activities,
 CC and can be used in vaccines. The antibodies, compositions and methods of
 CC the present invention can be used for preventing or treating a disease
 CC mediated by alpha-v-beta-6, e.g. fibrosis such as scleroderma, scarring,
 CC liver fibrosis, kidney fibrosis or lung fibrosis; psoriasis; cancer,
 CC preferably epithelial cancer, oral, skin, cervical, pharyngeal,
 CC laryngeal, oesophageal, lung, breast, kidney or colorectal cancer; or
 CC Alport's syndrome. The present sequence is used in the exemplification of
 CC the present invention.
 CC
 XX
 SQ Sequence 118 AA;
 Query Match 100.0%; Score 30; DB 8; Length 118;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 SYTH 5
 |||||
 Db 31 SYTH 35
 RESULT 23
 ADO32091
 ID ADO32091 standard; protein; 118 AA.
 XX

AC ADO32091;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Mouse anti-CD33 antibody My9-6 heavy chain variable region SEQ ID NO:7.
 XX
 KM anti-CD33 antibody; epitope-binding fragment;
 KM complementarity-determining region; CDR; immunocjugate; cyclostatic;
 KM antibody; myelodysplastic syndrome; acute myeloid leukaemia;
 KM chronic myeloid leukaemia; pro-myelocytic leukaemia; mouse; My9-6;
 KM heavy chain.
 XX
 OS Mus musculus.
 XX
 PN W02004043344-A2.
 XX
 PD 27-MAY-2004.
 XX
 PF 05-NOV-2003; 2003WO-US032737.
 XX
 PR 07-NOV-2002; 2002US-0424332P.
 XX
 PA (IMMU-) IMMUNOGEN INC.
 PA
 PI Hoffee MG, Tavares D, Lutz RJ;
 XX
 DR WPI; 2004-411619/38.
 DR N-PSDB; ADO32140.
 XX
 PT New antibodies that bind to CD33, useful for treating a disease
 PT associated with CD33 expression, such as myelodysplastic syndrome, acute
 PT or chronic myeloid leukemia.
 PS
 PS Claim 5; SEQ ID NO 7; 124pp; English.
 XX
 CC The present invention describes an isolated anti-CD33 antibody or its
 CC epitope-binding fragment comprising: (a) at least one complementarity-
 CC determining region (CDR); or (b) at least heavy chain variable region
 CC comprising 3 CDRs, and at least one light chain variable region, where
 CC the CDR has the ability to bind CD33. Also described: (1) an
 CC immunocjugate comprising the antibody or its epitope-binding fragment
 CC linked to a drug or prodrug; (2) a composition comprising the antibody or
 CC epitope-binding fragment and a drug or prodrug; (3) a pharmaceutical
 CC composition comprising the immunocjugate, composition or the antibody
 CC defined above, or its epitope-binding fragment, and a pharmaceutical
 CC agent; (4) a diagnostic reagent comprising the antibody defined above,
 CC where the antibody or antibody fragment is labelled; (5) inhibiting the
 CC growth of a cell expressing CD33 by contacting the cell with the above
 CC defined antibody or its epitope-binding fragment, immunocjugate, or
 CC (pharmaceutical) composition; (6) determining whether a biological sample
 CC contains a myelogenous cancer cell; (7) an improved antibody or its
 CC epitope-binding fragment that specifically binds to CD33; (8) an isolated
 CC polynucleotide encoding the antibody or its epitope-binding fragment
 CC defined above; (9) an isolated polynucleotide encoding a light or heavy
 CC chain of the antibody defined above or its epitope-binding fragment; (10)
 CC a recombinant vector comprising the polynucleotide; (11) a host cell
 CC transformed with the recombinant vector; (12) producing an antibody or
 CC its epitope-binding fragment having the ability to bind CD33; and (13)
 CC obtaining CD33 from a biological material. The anti-CD33 antibody has
 CC cyclostatic activity. The antibody or its epitope-binding fragment,
 CC immunocjugate, composition can be used for treating a subject having a
 CC disease where CD33 is expressed, such as myelodysplastic syndrome, acute
 CC myeloid leukaemia, chronic myeloid leukaemia or pro-myelocytic leukaemia.
 CC It can also be used for inhibiting the growth of cells expressing CD33,
 CC and for in vivo imaging or as affinity purification agents. The present
 CC sequence represents the mouse anti-CD33 antibody My9-6 heavy chain
 CC variable region, which is used in an example from the present invention.
 XX
 SQ Sequence 118 AA;
 Query Match 100.0%; Score 30; DB 8; Length 118;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX

OY 1 SYTH 5
|||
31 SYTH 35

RESULT 24

AD032093 standard; protein; 118 AA.

AC AD032093;

DT 12-AUG-2004 (first entry)

DE Humanised mouse anti-CD33 antibody My9-6 heavy chain SEQ ID NO:9.

XX anti-CD33 antibody; epitope-binding fragment;
XX complementarily-determining region; CDR; immunoglobulin; cytosolic;
XX antibody; myelodysplastic syndrome; acute myeloid leukaemia;
XX chronic myeloid leukaemia; pro-myelocytic leukaemia; mouse; humanised;
XX My9-6; heavy chain.

OS Mus musculus.
OS Homo sapiens.
OS Synthetic.

PN WO2004043344-A2.

PD 27-MAY-2004.

XX 05-NOV-2003; 2003WO-US032737.

XX 07-NOV-2002; 2002US-0424332P.

XX (IMMU-) IMMUNOGEN INC.

PI Hoffee MG, Tavares D, Lutz RJ;

XX WPI; 2004-411619/38.

PT New antibodies that bind to CD33, useful for treating a disease
PT associated with CD33 expression, such as myelodysplastic syndrome, acute
PT or chronic myeloid leukemia.

XX Claim 11; SEQ ID NO 9; 124pp; English.

XX The present invention describes an isolated anti-CD33 antibody or its
XX epitope-binding fragment comprising: (a) at least one complementarily-
XX determining region (CDR); or (b) at least one heavy chain variable region
XX comprising 3 CDRs, and at least one light chain variable region, where
XX the CDR has the ability to bind CD33. Also described: (1) an
XX immunoglobulin comprising the antibody or its epitope-binding fragment
XX linked to a drug or prodrug; (2) a composition comprising the antibody or
XX epitope-binding fragment and a drug or prodrug; (3) a pharmaceutical
XX composition comprising the immunoglobulin, composition or the antibody
XX defined above, or its epitope-binding fragment, and a pharmaceutical
XX agent; (4) a diagnostic reagent comprising the antibody defined above,
XX where the antibody or antibody fragment is labelled; (5) inhibiting the
XX growth of a cell expressing CD33 by contacting the cell with the above
XX defined antibody or its epitope-binding fragment, immunoglobulin, or
XX (pharmaceutical) composition; (6) determining whether a biological sample
XX contains a myelogenous cancer cell; (7) an improved antibody or its
XX epitope-binding fragment that specifically binds to CD33; (8) an isolated
XX polynucleotide encoding the antibody or its epitope-binding fragment
XX defined above; (9) an isolated polynucleotide encoding a light or heavy
XX chain of the antibody defined above or its epitope-binding fragment; (10)
XX a recombinant vector comprising the polynucleotide; (11) a host cell
XX transformed with the recombinant vector; (12) producing an antibody or
XX its epitope-binding fragment having the ability to bind CD33; and (13)
XX obtaining CD33 from a biological material. The anti-CD33 antibody has
XX cytostatic activity. The antibody or its epitope-binding fragment,
XX immunoglobulin, composition can be used for treating a subject having a
XX disease where CD33 is expressed, such as myelodysplastic syndrome, acute

CC myeloid leukaemia, chronic myeloid leukaemia or pro-myelocytic leukaemia.
CC It can also be used for inhibiting the growth of cells expressing CD33,
CC and for in vivo imaging or as affinity purification agents. The present
CC sequence represents a humanised mouse anti-CD33 antibody My9-6 heavy
CC chain variable region, which is used in an example from the present
CC invention.

XX Sequence 118 AA;

Query Match 100.0%; Score 30; DB 8; Length 118;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYTH 5
|||
31 SYTH 35

RESULT 25

ADU77882 standard; protein; 118 AA.

AC ADU77882;

DT 10-FEB-2005 (first entry)

DE Humanized mouse H chain protein - SEQ ID 19.

XX antibody production; H chain; humanized protein.

OS Mus sp.
OS Synthetic.

PN JP2004331569-A.

PD 25-NOV-2004.

XX 07-MAY-2003; 2003JP-00129554.

XX 07-MAY-2003; 2003JP-00129554.

XX (SERE-) SERESUTTA REKISHIKO SCI KK.

PI WPI; 2004-826797/82.

PT Apparatus for producing antibody, has unit for acquiring information of
PT complementarily determining and framework region of antibody, division
PT unit, search unit, mutation unit, activity determination unit, and
PT mutation determination unit.

XX Disclosure; SEQ ID NO 19; 77pp; Japanese.

XX The invention comprises an apparatus for producing an antibody. The
XX apparatus contains: an acquisition unit for acquiring information for an
XX antibody - information of complementarily determining and/or framework
XX region; a division unit; a unit for determining corresponding and similar
XX information of a predetermined antibody fragment; a unit for mutating
XX antibody fragment; a unit for determining active maintenance factor of
XX the antibody; and a unit for determining mutated antibody. The apparatus
XX of the invention is useful for producing an antibody. The present amino
XX acid sequence represents a humanized mouse H chain protein.

XX Sequence 118 AA;

Query Match 100.0%; Score 30; DB 8; Length 118;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYTH 5
|||
31 SYTH 35

RESULT 26
ADU77875
ID ADU77875 standard; protein; 118 AA.
AC ADU77875;
XX
DT 10-FEB-2005 (first entry)
XX
DE Humanized mouse H chain protein - SEQ ID 12.
XX
KM antibody production; H chain; humanized protein.
XX
OS Mus sp.
XX Synthetic.
PN JP2004331569-A.
XX
PD 25-NOV-2004.
XX
PF 07-MAY-2003; 2003JP-00129554.
XX
PR 07-MAY-2003; 2003JP-00129554.
XX
PA (SERE-) SERESUTA REKISHIKO SCI KK.
XX
DR WPI; 2004-826797/82.
XX
PT Apparatus for producing antibody, has unit for acquiring information of
PT complementary determining and framework region of antibody, division
PT unit, search unit, mutation unit, activity determination unit, and
PT mutation determination unit.
XX
PS Disclosure; SEQ ID NO 12; 77pp; Japanese.
XX
CC The invention comprises an apparatus for producing an antibody. The
CC apparatus contains: an acquisition unit for acquiring information for an
CC antibody - information of complementarity determining and/or framework
CC region; a division unit; a unit for determining corresponding and similar
CC information of a predetermined antibody fragment; a unit for mutating
CC antibody fragment; and a unit for determining active maintenance factor of
CC the antibody; and a unit for determining mutated antibody. The apparatus
CC of the invention is useful for producing an antibody. The present amino
CC acid sequence represents a humanized mouse H chain protein.
XX
SQ Sequence 118 AA;
XX
Query Match 100.0%; Score 30; DB 8; Length 118;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 SYTYH 5
|||
31 SYTYH 35
DB
RESULT 27
ADU77879
ID ADU77879 standard; protein; 118 AA.
AC ADU77879;
XX
DT 10-FEB-2005 (first entry)
XX
DE Humanized mouse H chain protein - SEQ ID 16.
XX
KM antibody production; H chain; humanized protein.
XX
OS Mus sp.
XX Synthetic.
PN JP2004331569-A.
XX
PD 25-NOV-2004.
XX

XX
PF 07-MAY-2003; 2003JP-00129554.
XX
PR 07-MAY-2003; 2003JP-00129554.
XX
PA (SERE-) SERESUTA REKISHIKO SCI KK.
XX
DR WPI; 2004-826797/82.
XX
DE Apparatus for producing antibody, has unit for acquiring information of
PT complementary determining and framework region of antibody, division
PT unit, search unit, mutation unit, activity determination unit, and
PT mutation determination unit.
XX
PS Disclosure; SEQ ID NO 16; 77pp; Japanese.
XX
CC The invention comprises an apparatus for producing an antibody. The
CC apparatus contains: an acquisition unit for acquiring information for an
CC antibody - information of complementarity determining and/or framework
CC region; a division unit; a unit for determining corresponding and similar
CC information of a predetermined antibody fragment; a unit for mutating
CC antibody fragment; and a unit for determining active maintenance factor of
CC the antibody; and a unit for determining mutated antibody. The apparatus
CC of the invention is useful for producing an antibody. The present amino
CC acid sequence represents a humanized mouse H chain protein.
XX
SQ Sequence 118 AA;
XX
Query Match 100.0%; Score 30; DB 8; Length 118;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 SYTYH 5
|||
31 SYTYH 35
DB
RESULT 28
ADU77883
ID ADU77883 standard; protein; 118 AA.
AC ADU77883;
XX
DT 10-FEB-2005 (first entry)
XX
DE Humanized mouse H chain protein - SEQ ID 20.
XX
KM antibody production; H chain; humanized protein.
XX
OS Mus sp.
XX Synthetic.
PN JP2004331569-A.
XX
PD 25-NOV-2004.
XX
PF 07-MAY-2003; 2003JP-00129554.
XX
PR 07-MAY-2003; 2003JP-00129554.
XX
PA (SERE-) SERESUTA REKISHIKO SCI KK.
XX
DR WPI; 2004-826797/82.
XX
DE Apparatus for producing antibody, has unit for acquiring information of
PT complementary determining and framework region of antibody, division
PT unit, search unit, mutation unit, activity determination unit, and
PT mutation determination unit.
XX
PS Disclosure; SEQ ID NO 20; 77pp; Japanese.
XX
CC The invention comprises an apparatus for producing an antibody. The
CC apparatus contains: an acquisition unit for acquiring information for an

CC antibody - information of complementarity determining and/or framework
CC region; a division unit; a unit for determining corresponding and similar
CC information of a predetermined antibody fragment; a unit for mutating
CC antibody fragment; a unit for determining active maintenance factor of
CC the antibody; and a unit for determining mutated antibody. The apparatus
CC of the invention is useful for producing an antibody. The present amino
CC acid sequence represents a humanized mouse H chain protein.

XX
SQ Sequence 118 AA;

Query Match 100.0%; Score 30; DB 8; Length 118;

Best Local Similarity 100.0%; Pred. No. 2.7e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYIYH 5
|||||

Db 31 SYIYH 35

RESULT 29

ADU77878 ID ADU77878 standard; protein; 118 AA.

XX AC ADU77878;

XX DT 10-FEB-2005 (first entry)

XX DE Mouse H chain protein - SEQ ID 15.

XX KM antibody production; H chain.

XX OS Mus sp.

XX PN JP2004331569-A.

XX PD 25-NOV-2004.

XX PF 07-MAY-2003; 2003JP-00129554.

XX PR 07-MAY-2003; 2003JP-00129554.

XX PA (SERE-) SERESUTA REKISHIKO SCI KK.

XX DR WPI; 2004-826797/82.

XX PT Apparatus for producing antibody, has unit for acquiring information of

XX PT complementary determining and framework region of antibody; division

XX PT unit; search unit; mutation unit; activity determination unit; and

XX PT mutation determination unit.

XX PS Disclosure; SEQ ID NO 15; 77pp; Japanese.

XX CC The invention comprises an apparatus for producing an antibody. The

XX CC apparatus contains: an acquisition unit for acquiring information for an

XX CC antibody - information of complementarity determining and/or framework

XX CC region; a division unit; a unit for determining corresponding and similar

XX CC information of a predetermined antibody fragment; a unit for mutating

XX CC antibody fragment; and a unit for determining active maintenance factor of

XX CC the antibody; and a unit for determining mutated antibody. The apparatus

XX CC of the invention is useful for producing an antibody. The present amino

XX CC acid sequence represents a mouse H chain protein.

XX SQ Sequence 118 AA;

Query Match 100.0%; Score 30; DB 8; Length 118;

Best Local Similarity 100.0%; Pred. No. 2.7e+02; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYIYH 5
|||||

Db 31 SYIYH 35

RESULT 30

ADU77867 ID ADU77867 standard; protein; 118 AA.

XX AC ADU77867;

XX DT 10-FEB-2005 (first entry)

XX DE Humanized mouse H chain protein - SEQ ID 4.

XX KM antibody production; H chain; humanized protein.

XX OS Mus sp.

XX OS Synthetic.

XX PN JP2004331569-A.

XX PD 25-NOV-2004.

XX PF 07-MAY-2003; 2003JP-00129554.

XX PR 07-MAY-2003; 2003JP-00129554.

XX PA (SERE-) SERESUTA REKISHIKO SCI KK.

XX DR WPI; 2004-826797/82.

XX PT Apparatus for producing antibody, has unit for acquiring information of

XX PT complementary determining and framework region of antibody; division

XX PT unit; search unit; mutation unit; activity determination unit; and

XX PT mutation determination unit.

XX PS Disclosure; SEQ ID NO 4; 77pp; Japanese.

XX CC The invention comprises an apparatus for producing an antibody. The

XX CC apparatus contains: an acquisition unit for acquiring information for an

XX CC antibody - information of complementarity determining and/or framework

XX CC region; a division unit; a unit for determining corresponding and similar

XX CC information of a predetermined antibody fragment; a unit for mutating

XX CC antibody fragment; and a unit for determining active maintenance factor of

XX CC the antibody; and a unit for determining mutated antibody. The apparatus

XX CC of the invention is useful for producing an antibody. The present amino

XX CC acid sequence represents a humanized mouse H chain protein.

XX SQ Sequence 118 AA;

Query Match 100.0%; Score 30; DB 8; Length 118;

Best Local Similarity 100.0%; Pred. No. 2.7e+02; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYIYH 5
|||||

Db 31 SYIYH 35

RESULT 31

ADU77871 ID ADU77871 standard; protein; 118 AA.

XX AC ADU77871;

XX DT 10-FEB-2005 (first entry)

XX DE Humanized mouse H chain protein - SEQ ID 8.

XX KM antibody production; H chain; humanized protein.

XX OS Mus sp.

XX OS Synthetic.

XX PN JP2004331569-A.

XX PD 25-NOV-2004.

XX 07-MAY-2003; 2003JP-00129554.
PF
XX 07-MAY-2003; 2003JP-00129554.
PR
XX (SERE-) SERESUTA REKISHIKO SCI KK.
PA
XX WPI; 2004-826797/82.
DR
XX Apparatus for producing antibody, has unit for acquiring information of
PT complementary determining and framework region of antibody, division
PT unit, search unit, mutation unit, activity determination unit, and
PT mutation determination unit.
XX
XX Disclosure; SEQ ID NO 8; 77pp; Japanese.
PS
XX The invention comprises an apparatus for producing an antibody. The
CC apparatus contains: an acquisition unit for acquiring information for an
CC antibody - information of complementarity determining and/or framework
CC region; a division unit; a unit for determining corresponding and similar
CC information of a predetermined antibody fragment; a unit for mutating
CC antibody fragment; a unit for determining active maintenance factor of
CC the antibody; and a unit for determining mutated antibody. The apparatus
CC of the invention is useful for producing an antibody. The present amino
CC acid sequence represents a humanized mouse H chain protein.
XX
SQ Sequence 118 AA;
Query Match 100.0%; Score 30; DB 8; Length 118;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SYTYH 5
Db 31 SYTYH 35
RESULT 32
ADU77874
ID ADU77874 standard; protein; 118 AA.
AC
XX ADU77874;
XX
DT 10-FEB-2005 (first entry)
XX
XX Humanized mouse H chain protein - SEQ ID 11.
DE
XX antibody production; H chain; humanized protein.
KM
XX
XX Mus sp.
OS
XX Synthetic.
OS
XX JP2004331569-A.
PN
XX 25-NOV-2004.
PD
XX 07-MAY-2003; 2003JP-00129554.
XX
XX 07-MAY-2003; 2003JP-00129554.
PR
XX (SERE-) SERESUTA REKISHIKO SCI KK.
PA
XX WPI; 2004-826797/82.
DR
XX Apparatus for producing antibody, has unit for acquiring information of
PT complementary determining and framework region of antibody, division
PT unit, search unit, mutation unit, activity determination unit, and
PT mutation determination unit.
XX
XX Disclosure; SEQ ID NO 11; 77pp; Japanese.
PS
XX The invention comprises an apparatus for producing an antibody. The
CC apparatus contains: an acquisition unit for acquiring information for an

CC antibody - information of complementarity determining and/or framework
CC region; a division unit; a unit for determining corresponding and similar
CC information of a predetermined antibody fragment; a unit for mutating
CC antibody fragment; a unit for determining active maintenance factor of
CC the antibody; and a unit for determining mutated antibody. The apparatus
CC of the invention is useful for producing an antibody. The present amino
CC acid sequence represents a humanized mouse H chain protein.
XX
SQ Sequence 118 AA;
Query Match 100.0%; Score 30; DB 8; Length 118;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SYTYH 5
Db 31 SYTYH 35
RESULT 33
ADU77866
ID ADU77866 standard; protein; 118 AA.
AC
XX ADU77866;
XX
DT 10-FEB-2005 (first entry)
XX
XX Mouse H chain protein - SEQ ID 3.
DE
XX antibody production; H chain.
KM
XX
XX Mus sp.
OS
XX JP2004331569-A.
PN
XX 25-NOV-2004.
PD
XX 07-MAY-2003; 2003JP-00129554.
XX
XX 07-MAY-2003; 2003JP-00129554.
PR
XX (SERE-) SERESUTA REKISHIKO SCI KK.
PA
XX WPI; 2004-826797/82.
DR
XX Apparatus for producing antibody, has unit for acquiring information of
PT complementary determining and framework region of antibody, division
PT unit, search unit, mutation unit, activity determination unit, and
PT mutation determination unit.
XX
XX Disclosure; SEQ ID NO 3; 77pp; Japanese.
PS
XX The invention comprises an apparatus for producing an antibody. The
CC apparatus contains: an acquisition unit for acquiring information for an
CC antibody - information of complementarity determining and/or framework
CC region; a division unit; a unit for determining corresponding and similar
CC information of a predetermined antibody fragment; a unit for mutating
CC antibody fragment; a unit for determining active maintenance factor of
CC the antibody; and a unit for determining mutated antibody. The apparatus
CC of the invention is useful for producing an antibody. The present amino
CC acid sequence represents a mouse H chain protein.
XX
SQ Sequence 118 AA;
Query Match 100.0%; Score 30; DB 8; Length 118;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SYTYH 5
Db 31 SYTYH 35


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RESULT 34
ADU77870
ID ADU77870 standard; protein; 118 AA.
XX
AC ADU77870;
XX
DT 10-FEB-2005 (first entry)
XX
DE Mouse H chain protein - SEQ ID 7.
XX
KM antibody production; H chain.
XX
OS Mus sp.
XX
PN JP200431569-A.
XX
PD 25-NOV-2004.
XX
PF 07-MAY-2003; 2003JP-00129554.
XX
PR 07-MAY-2003; 2003JP-00129554.
XX
PA (SERE-) SERESUTA REKISHIKO SCI KK.
XX
DR WPI; 2004-826797/82.
XX
PT Apparatus for producing antibody, has unit for acquiring information of
PT complementary determining and framework region of antibody, division
PT unit, search unit, mutation unit, activity determination unit, and
PT mutation determination unit.
XX
PS Disclosure; SEQ ID NO 7; 77pp; Japanese.
XX
CC The invention comprises an apparatus for producing an antibody. The
CC apparatus contains: an acquisition unit for acquiring information for an
CC antibody - information of complementarily determining and/or framework
CC region; a division unit; a unit for determining corresponding and similar
CC information of a predetermined antibody fragment; a unit for mutating
CC antibody fragment; a unit for determining active maintenance factor of
CC the antibody; and a unit for determining mutated antibody. The apparatus
CC of the invention is useful for producing an antibody. The present amino
CC acid sequence represents a mouse H chain protein.
XX
SQ Sequence 118' AA;

Query Match 100.0%; Score 30; DB 8; Length 118;
Best Local Similarity 100.0%; Pred. NO. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYVIH 5
Db 31 SYVIH 35

RESULT 35
ADQ91392
ID ADQ91392 standard; protein; 119 AA.
XX
AC ADQ91392;
XX
DT 23-SEP-2004 (first entry)
XX
DE Amino acid sequence of PD1-33 variable heavy chain (VH) domain.
XX
KM antibody; Programmed Death-1; PD-1; transmembrane receptor; IgG1; IgG4;
KM IgG1ambda; IgG1kappa; immune response; PD-1 receptor;
KM autoimmune disease; inflammatory disorder; allergy; transplant rejection;
KM cancer; immune cell; PDI-33.
XX
OS Homo sapiens.
XX
PN Key
XX Region 31. .35 Location/Qualifiers

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FT FT /note= "CDR1"
FT Region 50. .66
FT /note= "CDR2"
FT Region 99. .108
FT /note= "CDR3"
XX
PN WO2004056875-A1.
XX
PD 08-JUL-2004.
XX
PF 22-DEC-2003; 2003MO-IB006304.
XX
PR 23-DEC-2002; 2002US-0435354P.
XX
PA (AMHP ) WYETH.
XX (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Collins M, Wood C, Carreno B, Valge-Archer V, Luxenberg D;
PI Jussif J, Russell C, Carter LL, Bennett F, Andrews J;
XX
DR WPI; 2004-507701/48.
XX
DR N-PSDB; ADQ91391.
XX
PT New antibodies against Programmed Death-1 (PD-1) for modulating immune
PT responses regulated by the PD-1 receptor or for treating autoimmune
PT diseases, inflammatory disorders, allergies, transplant rejection or
PT cancer.
XX
PS Claim 2; SEQ ID NO 10; 96pp; English.
XX
CC The specification describes an antibody which is directed against
CC Programmed Death-1 (PD-1). PD-1 is a type I transmembrane receptor. The
CC antibody specifically binds to the extracellular domain of PD-1 with an
CC affinity constant greater than 107M-1, and inhibits the binding of PD-1
CC ligands to PD-1 with an IC50 of less than 10 nM. The antibody is IgG1 or
CC IgG4 of human origin, preferably IgG1ambda or IgG1kappa. Antibodies of
CC the invention are useful for modulating immune responses regulated by the
CC PD-1 receptor or for treating autoimmune diseases, inflammatory
CC disorders, allergies, transplant rejection or cancer. Antibodies of the
CC invention may also be used to detect PD-1, which, in turn, is correlated
CC with the activation status of immune cells. The present sequence
CC represents the variable heavy chain (VH) domain of antibody PDI-33, an
CC antibody of the invention.
XX
SQ Sequence 119 AA;

Query Match 100.0%; Score 30; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. NO. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYVIH 5
Db 31 SYVIH 35

RESULT 36
ABP59952
ID ABP59952 standard; protein; 120 AA.
XX
AC ABP59952;
XX
DT 28-AUG-2003 (first entry)
XX
DE Monoclonal antibody 5-11A humanised variable domain #2.
XX
KM CD28; receptor; human; C'-D loop; immunomodulatory; cytostatic; anti-HIV;
KM immunosuppressive; antiinflammatory; AIDS; leukemia; autoimmune disease;
KM inflammation.
XX
OS Unidentified.
XX Synthetic.
XX
PN WO2003048194-A2.

```

XX 12-JUN-2003.
PD 29-OCT-2002; 2002WO-DE004064.
XX
PF
XX 04-DEC-2001; 2001DE-01060516.
PR 10-JAN-2002; 2002DE-01000714.
XX
XX (TEGE-) TEGENERO AG.
XX
PI Huenig T, Luehder F, Hanke T;
XX
DR WPI; 2003-469080/44.
XX
XX New protein or peptide, useful for modulating T cell proliferation and
PT raising therapeutic antibodies, contains the C'-D loop of a CD28 protein
PT or its analog or mimic.
XX
PS Disclosure; Fig 10B; 63pp; German.
XX
CC The present invention relates to proteins and peptides containing the C'-
CC D loop of a member of the CD28 family, and its analogues and mimetics.
CC These can be used in the therapeutic modulation of T cell proliferation,
CC to prepare monoclonal antibodies (Mab) which modulate, proliferation of T
CC cells, of many (up to all) subtypes and to screen for compounds with
CC similar activity. Mab that bind these proteins are used to treat
CC disorders associated with reduced counts of CD4 T cells, especially AIDS,
CC for treatment, after stem cell transplants, following chemotherapy or
CC radiation therapy of leukaemia, for potentiation and/or qualitative
CC modification of the immune response after vaccination and for the
CC treatment of autoimmune-inflammatory diseases. The present sequence is a
CC protein shown in the exemplification of the invention
XX
SQ Sequence 120 AA;

Query March 100.0%; Score 30; DB 6; Length 120;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTTH 5
|||
|||
Db 31 SYTTH 35

RESULT 37
ABP59987
ID ABP59987 standard; protein; 120 AA.
XX
AC ABP59987;
XX
XX 28-AUG-2003 (first entry)
DT
XX
XX Antibody 5-11A heavy chain protein.
DE
XX
XX CD28; receptor; human; C'-D loop; immunomodulatory; cytostatic; anti-HIV;
KM immunosuppressive; antiinflammatory; AIDS; leukaemia; autoimmune disease;
KM inflammation;
XX
XX Unidentified.
OS
XX WO2003048194-A2.
PN
XX 12-JUN-2003.
PD
XX 29-OCT-2002; 2002WO-DE004064.
PF
XX 04-DEC-2001; 2001DE-01060516.
PR 10-JAN-2002; 2002DE-01000714.
XX
XX (TEGE-) TEGENERO AG.
PA
XX Huenig T, Luehder F, Hanke T;
PI
XX

DR WPI; 2003-469080/44.
DR N-PSDB; ACC59416.

PT New protein or peptide, useful for modulating T cell proliferation and
PT raising therapeutic antibodies, contains the C'-D loop of a CD28 protein
PT or its analog or mimic.
XX

PS Claim 11; Page 56-57; 63pp; German.

XX
CC The present invention relates to proteins and peptides containing the C'-
CC D loop of a member of the CD28 family, and its analogues and mimetics.
CC These can be used in the therapeutic modulation of T cell proliferation,
CC to prepare monoclonal antibodies (Mab) which modulate, proliferation of T
CC cells, of many (up to all) subtypes and to screen for compounds with
CC similar activity. Mab that bind these proteins are used to treat
CC disorders associated with reduced counts of CD4 T cells, especially AIDS,
CC for treatment, after stem cell transplants, following chemotherapy or
CC radiation therapy of leukaemia, for potentiation and/or qualitative
CC modification of the immune response after vaccination and for the
CC treatment of autoimmune-inflammatory diseases. The present sequence is a
CC protein shown in the exemplification of the invention
XX

SQ Sequence 120 AA;

Query March 100.0%; Score 30; DB 6; Length 120;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTTH 5
|||
|||
Db 31 SYTTH 35

RESULT 38
ADF69657
ID ADF69657 standard; protein; 120 AA.
XX
AC ADF69657;
XX
XX 12-FEB-2004 (first entry)
DT
XX
XX Humanised mAb 5.11A heavy chain variable region #2.
DE
XX
XX CD28; superagonistic; monoclonal antibody; Mab; regulatory T cell;
KM C'-D loop; Mab 9D7; Mab 5.11; immunosuppressive; antiinflammatory;
KM antidiabetic; neuroprotective; autoimmune disease; inflammatory reaction;
KM Guillain-Barre syndrome; chronic demyelinating polyneuropathy;
KM multiple sclerosis; type I diabetes; inflammatory bowel disease;
KM heavy chain; variable region.
XX
XX Synthetic.
OS
XX Unidentified.
XX
XX WO2003078468-A2.
PN
XX 25-SEP-2003.
PD
XX 13-MAR-2003; 2003WO-DE000890.
PF
XX 13-MAR-2002; 2002DE-01012108.
PR
XX (TEGE-) TEGENERO AG.
PA
XX
XX Huenig T;
PI
XX WPI; 2003-756995/71.
DR
XX Use of CD28-specific superagonistic antibodies, for treatment and
PT prevention of autoimmune or inflammatory diseases, by induction or
PT replication of regulatory T cells.
XX
XX Claim 7; SEQ ID NO 19; 72pp; German.
PS
XX

CC This invention describes a novel use of a CD28-specific superagonistic
 CC monoclonal antibody (Mab), or its mimics, to prepare a pharmaceutical
 CC composition for induction and/or replication of regulatory T cells, in
 CC vivo and/or in vitro. The monoclonal antibody is produced by immunising a
 CC non-human mammal with CD28 or its fragments, especially the C'-D loop,
 CC conventional preparation of hybridomas, then selection from presence of
 CC the required Mab in the culture supernatant. The selected hybridomas have
 CC been deposited as DSM ACC 2531 (Mab 9D7) and 2530 (Mab 5.11A). Mimics are
 CC identified from their ability to bind to CD28, or its fragments,
 CC optionally followed by assays to test superagonistic stimulation of at
 CC least one type of T cells. The products of the invention have
 CC immunosuppressive, antiinflammatory, antidiabetic and neuroprotective
 CC activity. Mab or their mimics are administered specifically by
 CC intravenous injection alternatively, cells are treated ex vivo then
 CC returned to the patient. The Mab and their mimics are used for treatment
 CC and/or prevention of autoimmune diseases and/or inflammatory reactions,
 CC specifically Guillain-Barre syndrome and chronic demyelinating
 CC polyneuropathy, multiple sclerosis, type I diabetes and inflammatory
 CC bowel disease. This sequence represents a humanised anti-CD28 monoclonal
 CC antibody 5.11A (mab 5.11A) heavy chain variable region.
 CC
 XX Sequence 120 AA;
 SQ

Query Match 100.0%; Score 30; DB 7; Length 120;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
 |||||
 Db 31 SYTH 35

RESULT 39

ADP69652
 ID ADP69652 standard; protein; 120 AA.

XX ADF69652;

DT 12-FEB-2004 (first entry)

XX Humanised mab 5.11A heavy chain variable region.

XX CD28; superagonistic; monoclonal antibody; Mab; regulatory T cell;
 KW C'-D loop; Mab 9D7; Mab 5.11; immunosuppressive; antiinflammatory;
 KW antidiabetic; neuroprotective; autoimmune disease; inflammatory reaction;
 KW Guillain-Barre syndrome; chronic demyelinating polyneuropathy;
 KW multiple sclerosis; type I diabetes; inflammatory bowel disease;
 KW heavy chain; variable region.
 XX
 XX Synthetic.
 OS Unidentified.
 XX
 XX WO2003078468-A2.
 XX
 XX 25-SEP-2003.
 PD
 XX 13-MAR-2003; 2003WO-DE000890.
 PF
 XX 13-MAR-2002; 2002DE-01012108.
 PR
 XX (TEGE-) TEGENERO AG.
 PA
 XX (TEGE-) TEGENERO AG.
 PA
 XX Huenig T;
 PI
 XX
 XX WPI; 2003-756995/71.
 DR N-PSDB; ADF69651.
 DR
 XX
 XX Use of CD28-specific superagonistic antibodies, for treatment and
 PT prevention of autoimmune or inflammatory diseases, by induction or
 PT replication of regulatory T cells.
 PT
 XX Claim 7; SEQ ID NO 14; 72pp; German.
 PS
 XX

CC This invention describes a novel use of a CD28-specific superagonistic
 CC monoclonal antibody (Mab), or its mimics, to prepare a pharmaceutical
 CC composition for induction and/or replication of regulatory T cells, in
 CC vivo and/or in vitro. The monoclonal antibody is produced by immunising a
 CC non-human mammal with CD28 or its fragments, especially the C'-D loop,
 CC conventional preparation of hybridomas, then selection from presence of
 CC the required Mab in the culture supernatant. The selected hybridomas have
 CC been deposited as DSM ACC 2531 (Mab 9D7) and 2530 (Mab 5.11A). Mimics are
 CC identified from their ability to bind to CD28, or its fragments,
 CC optionally followed by assays to test superagonistic stimulation of at
 CC least one type of T cells. The products of the invention have
 CC immunosuppressive, antiinflammatory, antidiabetic and neuroprotective
 CC activity. Mab or their mimics are administered specifically by
 CC intravenous injection alternatively, cells are treated ex vivo then
 CC returned to the patient. The Mab and their mimics are used for treatment
 CC and/or prevention of autoimmune diseases and/or inflammatory reactions,
 CC specifically Guillain-Barre syndrome and chronic demyelinating
 CC polyneuropathy, multiple sclerosis, type I diabetes and inflammatory
 CC bowel disease. This sequence represents the anti-CD28 monoclonal antibody
 CC 5.11A (mab 5.11A) heavy chain variable region.
 CC
 XX Sequence 120 AA;
 SQ

Query Match 100.0%; Score 30; DB 7; Length 120;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
 |||||
 Db 31 SYTH 35

RESULT 40

AEB03871
 ID AEB03871 standard; protein; 120 AA.

XX AEB03871;

DT 25-AUG-2005 (first entry)

XX B-CLL pharmaceutical composition-related antibody protein region Sequid14.

XX pharmaceutical; monoclonal antibody; T-lymphocyte; cytostatic;
 KW immunostimulant; antianemic; chronic lymphocytic leukemia;
 KW immune stimulation.
 XX
 XX Unidentified.
 OS
 XX DE10352900-A1.
 FN
 XX 16-JUN-2005.
 PD
 XX 11-NOV-2003; 2003DE-01052900.
 PF
 XX 11-NOV-2003; 2003DE-01052900.
 PR
 XX (TEGE-) TEGENERO AG.
 PA
 XX (TEGE-) TEGENERO AG.
 PA
 XX Hanke T;
 PI
 XX
 XX WPI; 2005-427538/44.
 DR N-PSDB; AEB03870.
 DR
 XX
 XX Method of making pharmaceutical composition for treatment of illnesses
 PT associated with deficient costimulation ability of T-cells, employs
 PT superagonistic monoclonal antibody.
 PT
 XX Claim 6; SEQ ID NO 14; 24pp; German.
 PS
 XX This invention relates to a novel method of making a pharmaceutical
 CC composition, comprising using a superagonistic monoclonal antibody (mab).
 CC This mab is specific for a natural costimulation receptor, which is
 CC expressed on T cells, or a mimic compound. The invention may be useful

CC for the development of compounds with a cytostatic, immunostimulant or
CC antianemic activity. The method yields a pharmaceutical composition, by
CC means of which chronic lymphocyte leukemia of the B-cell type (B-CLL) can
CC be treated. At the same time the immunosystem, weakened by illness,
CC especially the T-cell associated cellular immunity, is generally
CC reinforced. The present sequence is that of an antibody region which was
CC used in the development of the novel pharmaceutical of the invention.
XX
SQ Sequence 120 AA;

Query Match 100.0%; Score 30; DB 9; Length 120;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTYH 5
|||
Db 31 SYTYH 35

RESULT 41
AEB03876 standard; protein; 120 AA.
XX
AC AEB03876;
XX
DT 25-AUG-2005 (first entry)
XX
DE B-CLL pharmaceutical composition-related antibody protein region SeqID19.
XX
KW pharmaceutical; monoclonal antibody; t-Lymphocyte; cytostatic;
KW immunostimulant; antianemic; chronic lymphocytic leukemia;
KW immune stimulation.
XX
OS Unidentified.
XX
PN DE10352900-A1.
XX
PD 16-JUN-2005.
XX
PF 11-NOV-2003; 2003DE-01052900.
XX
PR 11-NOV-2003; 2003DE-01052900.
XX
PA (TEGE-) TEGENERO AG.
XX
PI Hanke T;
XX
DR WPI; 2005-427538/44.
XX
PT Method of making pharmaceutical composition for treatment of illnesses
PT associated with deficient costimulation ability of T-cells, employs
PT superagonistic monoclonal antibody.
XX
PS Claim 6; SEQ ID NO 19; 24pp; German.
XX
CC This invention relates to a novel method of making a pharmaceutical
CC composition, comprising using a superagonistic monoclonal antibody (mb).
CC This mb is specific for a natural costimulation receptor, which is
CC expressed on T cells, or a mimic compound. The invention may be useful
CC for the development of compounds with a cytostatic, immunostimulant or
CC antianemic activity. The method yields a pharmaceutical composition, by
CC means of which chronic lymphocyte leukemia of the B-cell type (B-CLL) can
CC be treated. At the same time the immunosystem, weakened by illness,
CC especially the T-cell associated cellular immunity, is generally
CC reinforced. The present sequence is that of an antibody region which was
CC used in the development of the novel pharmaceutical of the invention.
XX
SQ Sequence 120 AA;

Query Match 100.0%; Score 30; DB 9; Length 120;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTYH 5
|||
Db 31 SYTYH 35

RESULT 42
AEB21874 standard; protein; 120 AA.
XX
AC AEB21874;
XX
DT 08-SEP-2005 (first entry)
XX
DE Human DC-SIGN antibody, heavy chain, SEQ ID NO:30.
XX
KW antibody; DC-SIGN; dendritic cell-specific ICAM-3 grabbing non-integrin;
KW cancer; neoplasm; cytostatic; inflammation; antiinflammatory;
KW ectoparasite infection; antiparasitic; infection; viral infection;
KW bacterial infection; antibacterial; virucide; autoimmune disease;
KW immunosuppressive; immune disorder; allergy; antiallergic; immunotherapy;
KW transplant rejection; humanized antibody; single chain antibody;
KW heavy chain.
XX
OS Homo sapiens.
XX
PN WO2005058244-A2.
XX
PD 30-JUN-2005.
XX
PF 15-DEC-2004; 2004WO-US041788.
XX
PR 15-DEC-2003; 2003US-0529517P.
XX
PA (ALEX-) ALEXION PHARM INC.
XX
PI Bowdish KS, Kretz-Rommel A;
XX
DR WPI; 2005-506067/51.
XX
PT Novel antibody capable of binding or recognizing human dendritic cell-
PT specific intercellular adhesion molecule-3 grabbing non-integrin receptor
PT on cell, useful for treating cancer, and viral and bacterial infections.
XX
PS Example 5; SEQ ID NO 30; 44pp; English.
XX
CC The invention relates to an antibody (I) capable of binding human
CC Dendritic cell-specific intercellular adhesion molecule (ICAM)-3 grabbing
CC non-integrin (DC-SIGN) or recognizing a DC-SIGN receptor on a cell,
CC comprising an amino acid sequence having at least 80% homology to any one
CC of 18 fully defined 4-10 amino acid sequences (AEB21889 to AEB21906). An
CC antibody (I) capable of binding human DC-SIGN or recognizing a DC-SIGN
CC receptor on a cell, is chosen from: an antibody (A1) capable of binding
CC human DC-SIGN or recognizing a DC-SIGN receptor on a cell; and an
CC antibody (A4) capable of recognizing a DC-SIGN receptor on a cell. A4
CC effectively blocks binding of a virus to the cell, blocks infection of
CC the cell by a virus, and/or blocks transmission of a virus from the cell
CC to another cell, where the virus is chosen from HIV, hepatitis C virus
CC (HCV), Ebola, severe acute respiratory syndrome (SARS), cytomegalovirus
CC (CMV), Sindbis and Dengue; or effectively blocks binding of a bacteria or
CC parasite to the cell, blocks infection of the cell by a bacteria or
CC parasite, and/or blocks transmission of a bacteria or parasite from the
CC cell to another cell, where the bacteria is chosen from Helicobacter
CC pylori, Klebsiella pneumoniae, Mycobacterium tuberculosis and M. bovis,
CC and the parasite is chosen from Leishmania pifanoi and Schistosoma
CC mansoni. Also described are: a vaccine comprising A1; a composition
CC comprising A1 and a carrier; a diagnostic agent (II) for a tumor
CC characterized by increased DC-SIGN expression, comprising (I); a
CC diagnostic kit comprising (II); a therapeutic agent for treating a cancer
CC characterized by increased DC-SIGN expression, comprising A1; treating
CC (M1) a cancer, involves administering to a subject, a cancer cell killing
CC amount of a composition comprising A1; and treating (M2) an inflammatory
CC disease, which involves administering to a subject, a dendritic cell
CC killing amount of a composition comprising A1. A1 further comprises a

peptide attached to it. The peptide comprises an antigen, where the antigen comprises a cancer antigen. A1 is humanized antibody or an scFv. The amino acid sequence appears in the heavy chain CDR3 of the antibody or the light chain CDR3 of the antibody. A4 capable of blocking and transmitting virus, also binds to L-SIGN. (I) is useful in interfering with the interaction of DC-SIGN expressing cells and ICAM-expressing cells, which involves administering immune-modulating amount of (I), to a subject. (I) is useful for generating an immune response, which involves administering immune-modulating amount of (I), to a subject. It is useful for delivering an antigen to DC-SIGN expressing cells, which involves attaching the antigen to (I). (I) is useful for diagnosing cancer, which involves obtaining a tissue sample from a subject suspected of having cancer, and determining the degree to which the tissue sample binds with (I), where an increase in the degree of binding compared to corresponding normal tissue indicates the presence of cancer. The determining step involves staining for the presence of DC-SIGN. (I) is useful for treating cancer or inflammatory diseases. (I) is useful for blocking binding of a virus, bacteria or parasite to the cell, blocking infection of the cell by a virus, bacteria or parasite, and/or blocking transmission of a virus, bacteria or parasite from the cell to another cell, where the virus is chosen from HIV, HCV, Ebola, SARS, CMV, Sindbis and Dengue, the bacteria is chosen from H. pylori, K. pneumoniae, M. tuberculosis and M. bovis, and the parasite is chosen from L. pifanoi and S. mansoni. (I) is useful in treating autoimmune diseases (e.g., rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis), preventing transplant rejection, preventing and treating allergies, and to prevent, inhibit or at least delay T cell activation for slowing the onset and/or the progress of a viral disease such as HIV. (I) is useful in inducing tolerance, immunotherapy, and in diagnostic and research for studying dendritic cells and/or their function and interaction, studying immune system and for detecting dendritic cells and/or C-type lectins in biological samples. The present sequence represents a human DC-SIGN antibody, heavy chain, SEQ ID NO:30.

SO Sequence 120 AA;

Query Match 100.0%; Score 30; DB 9; Length 120;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
 ||||
 Db 31 SYTH 35

RESULT 43

AEB21876 AEB21876 standard; protein, 120 AA.

XX AEB21876;

DT 08-SEP-2005 (first entry)

DE Human DC-SIGN antibody, heavy chain, SEQ ID NO:32.

XX antibody; DC-SIGN; dendritic cell-specific ICAM-3 grabbing non-integrin;
 KM cancer; neoplasm; cytotoxic; inflammation; antiinflammatory;
 KM ectoparasite infection; antiparasitic; infection; viral infection;
 KM bacterial infection; antibacterial; virucide; autoimmune disease;
 KM immunosuppressive; immune disorder; allergy; antiallergic; immunotherapy;
 KM transplant rejection; humanized antibody; single chain antibody;
 XX heavy chain.

XX Homo sapiens.

XX WO2005058244-A2.

XX 30-JUN-2005.

XX 15-DEC-2004; 2004WO-US041788.

XX 15-DEC-2003; 2003US-0529517P.

XX

PA (ALEX-) ALEXION PHARM INC.

PI Bowdish KS, Kretz-Rommel A;

DR WPI: 2005-506067/51.

PT Novel antibody capable of binding or recognizing human dendritic cell-
 PT specific intercellular adhesion molecule-3 grabbing non-integrin receptor
 PT on cell, useful for treating cancer, and viral and bacterial infections.

PS Example 5; SEQ ID NO 32; 44pp; English.

XX The invention relates to an antibody (I) capable of binding human
 CC Dendritic cell-Specific intercellular adhesion molecule (ICAM)-3 grabbing
 CC non-integrin (DC-SIGN) or recognizing a DC-SIGN receptor on a cell.
 CC comprising an amino acid sequence having at least 80% homology to any one
 CC of 18 fully defined 4-10 amino acid sequences (AEB21889 to AEB21906). An
 CC antibody (I) capable of binding human DC-SIGN or recognizing a DC-SIGN
 CC receptor on a cell, is chosen from: an antibody (A1) capable of binding
 CC human DC-SIGN or recognizing a DC-SIGN receptor on a cell; and an
 CC antibody (A4) capable of recognizing a DC-SIGN receptor on a cell. A4
 CC effectively blocks binding of a virus to the cell, blocks infection of
 CC the cell by a virus, and/or blocks transmission of a virus from the cell
 CC to another cell, where the virus is chosen from HIV, hepatitis C virus
 CC (HCV), Ebola, severe acute respiratory syndrome (SARS), cytomegalovirus
 CC (CMV), Sindbis and Dengue; or effectively blocks binding of a bacteria or
 CC parasite to the cell, blocks infection of the cell by a bacteria or
 CC parasite, and/or blocks transmission of a bacteria or parasite from the
 CC cell to another cell, where the bacteria is chosen from Helicobacter
 CC pylori, Klebsiella pneumoniae, Mycobacterium tuberculosis and M. bovis,
 CC and the parasite is chosen from Leishmania pifanoi and Schistosoma
 CC mansoni. Also described are: a vaccine comprising A1; a composition
 CC comprising A1 and a carrier; a diagnostic agent (II) for a tumor
 CC characterized by increased DC-SIGN expression, comprising (I); a
 CC diagnostic kit comprising (II); a therapeutic agent for treating a cancer
 CC characterized by increased DC-SIGN expression, comprising A1; treating
 CC (M1) a cancer, involves administering to a subject, a cancer cell killing
 CC amount of a composition comprising A1; and treating (M2) an inflammatory
 CC disease, which involves administering to a subject, a dendritic cell
 CC killing amount of a composition comprising A1. A1 further comprises a
 CC peptide attached to it. The peptide comprises an antigen, where the
 CC antigen comprises a cancer antigen. A1 is humanized antibody or an scFv.
 CC The amino acid sequence appears in the heavy chain CDR3 of the antibody
 CC or the light chain CDR3 of the antibody. A4 capable of blocking and
 CC transmitting virus, also binds to L-SIGN. (I) is useful in interfering
 CC with the interaction of DC-SIGN expressing cells and ICAM-expressing
 CC cells, which involves administering immune-modulating amount of (I), to a
 CC subject. (I) is useful for generating an immune response, which involves
 CC administering immune-modulating amount of (I), to a subject. It is useful
 CC for delivering an antigen to DC-SIGN expressing cells, which involves
 CC attaching the antigen to (I). (I) is useful for diagnosing cancer, which
 CC involves obtaining a tissue sample from a subject suspected of having
 CC cancer, and determining the degree to which the tissue sample binds with
 CC (I), where an increase in the degree of binding compared to corresponding
 CC normal tissue indicates the presence of cancer. The determining step
 CC involves staining for the presence of DC-SIGN. (I) is useful for treating
 CC cancer or inflammatory diseases. (I) is useful for blocking binding of a
 CC virus, bacteria or parasite to the cell, blocking infection of the cell
 CC by a virus, bacteria or parasite, and/or blocking transmission of a
 CC virus, bacteria or parasite from the cell to another cell, where the
 CC virus is chosen from HIV, HCV, Ebola, SARS, CMV, Sindbis and Dengue, the
 CC bacteria is chosen from H. pylori, K. pneumoniae, M. tuberculosis and
 CC M. bovis, and the parasite is chosen from L. pifanoi and S. mansoni. (I) is
 CC useful in treating autoimmune diseases (e.g., rheumatoid arthritis,
 CC systemic lupus erythematosus, multiple sclerosis), preventing transplant
 CC rejection, preventing and treating allergies, and to prevent, inhibit or
 CC at least delay T cell activation for slowing the onset and/or the
 CC progress of a viral disease such as HIV. (I) is useful in inducing
 CC tolerance, immunotherapy, and in diagnostic and research for studying
 CC dendritic cells and/or their function and interaction, studying immune
 CC system and for detecting dendritic cells and/or C-type lectins in
 CC biological samples. The present sequence represents a human DC-SIGN
 CC antibody, heavy chain, SEQ ID NO:32.

XX Sequence 120 AA;
SQ Query Match 100.0%; Score 30; DB 9; Length 120;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYIYH 5
Db 31 SYIYH 35

RESULT 44
ADA89202
ID ADA89202 standard; protein; 128 AA.
XX ADA89202;
XX 20-NOV-2003 (first entry)
DT
XX Human antibody 2F1 heavy chain amino acid sequence SEQ ID NO:46.
DE
XX immunoglobulin; Ig; heavy chain variable domain;
KM light chain variable domain; major histocompatibility complex; MHC;
KM gp100; MUC1; TAX; hTERT; cytostatic; gene therapy; cancerous disorder;
KM cancer.
XX Synthetic.
OS Homo sapiens.
XX MO2003070752-A2.
XX
XX 28-AUG-2003.
PD
XX 20-FEB-2003; 2003WO-US005128.
PF
XX 20-FEB-2002; 2002US-0358994P.
PR
XX (DYAX-) DYAX CORP.
PA (TECR) TECHNION RES & DEV FOUND LTD.
XX Hoogenboom HRJM, Reiter Y;
XX
XX WPI: 2003-663847/62.
DR N-PSDB; ADA89201.
XX
PT New protein comprising an immunoglobulin heavy chain variable (VH) domain
PT and an immunoglobulin light chain variable (VL) domain, useful for
PT preparing a composition for treating or preventing a cancerous disorder.
XX
PS Disclosure; Fig 10B; 224pp; English.

XX The present invention describes a protein comprising an immunoglobulin
CC (Ig) heavy chain variable (VH) domain and an Ig light chain variable (VL)
CC domain. The protein binds a complex comprising a major histocompatibility
CC complex (MHC) and a peptide, does not substantially bind the MHC in the
CC absence of the bound peptide, and does not substantially bind the peptide
CC in the absence of the MHC. The peptide is a peptide fragment of gp100,
CC MUC1, TAX or hTERT. Also described: (1) a pharmaceutical composition
CC comprising the novel protein and a carrier; (2) a cytotoxic T cell
CC comprising one or more nucleic acids for expressing the Ig that binds a
CC complex having an MHC and a peptide, does not substantially bind the MHC
CC in the absence of the bound peptide, and does not substantially bind the
CC peptide in the absence of the MHC; (3) an isolated nucleic acid
CC comprising a first segment that encodes the Ig variable domain; (4) a
CC host cell comprising heterologous nucleic acid sequences that encodes the
CC novel protein; (5) a transgenic animal whose genome includes heterologous
CC nucleic acid sequences that encode the protein; (6) identifying the
CC protein that specifically binds the MHC-peptide complex; (7) expressing
CC an antigen-binding protein; (8) ablating or killing a target cell that
CC displays a peptide on a surface MHC molecule; (9) treating or preventing
CC a cancerous disorder in a subject; and (10) detecting an MHC-peptide
CC complex in a sample. A protein of the invention has cytostatic activity,

CC and can be used in gene therapy. The protein is useful for preparing a
CC composition for treating or preventing a cancerous disorder. The present
CC sequence represents the heavy chain of an antibody which binds to an MHC-
CC peptide complex where the peptide component in as peptide fragment of
CC gp100.
XX
SQ Sequence 128 AA;
Qy Query Match 100.0%; Score 30; DB 6; Length 128;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYIYH 5
Db 31 SYIYH 35

RESULT 45
AAR29016
ID AAR29016 standard; protein; 135 AA.
XX AAR29016;
XX
XX 25-MAR-2003 (revised)
DT 30-MAR-1993 (first entry)
DT
XX pUC-RVh-1220b.
DE
XX Human antibody; interleukin-6; receptor; IL-6R; CDR; PCR; mouse;
KM complementarity determining region; monoclonal; hybridoma; PCR; plasmid;
KM polymerase chain reaction; amplify.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH 1..19
FT /note= "Leader peptide"
FT 20..49
FT /label= FR1
FT 50..54
FT /label= CDR1
FT 55..68
FT /label= FR2
FT 69..85
FT /label= CDR2
FT 86..117
FT /label= FR3
FT 118..124
FT /label= CDR3
FT 125..135
FT /label= FR4
XX
XX WO9219759-A1.
XX
XX 12-NOV-1992.
PD
XX
XX 24-APR-1992; 92WO-JP000544.
PF
XX 25-APR-1991; 91JP-00095476.
PR 19-FEB-1992; 92JP-00032084.
XX
XX (CHUS) CHUGAI SEIYAKU KK.
XX
XX Tsuchiya M, Sato K, Bendig MM, Jones ST, Saldanha JW,
XX WPI: 1992-398882/48.
DR N-PSDB; AAQ31391.
XX
XX Reconstituted human antibody to human interleukin-6 receptor - has low
PT antigenicity and contains mouse V-region complementarily determining
PT regions.
XX
PS Disclosure; Page 157-8; 207pp; Japanese.

XX The sequences given in AAR29016-17 are portions of monoclonal antibodies
CC which were encoded by plasmids contained within the mouse hybridoma,
CC AUK12-20. The DNA encoding the complementarity determining regions,
CC (CDR's) was isolated by polymerase chain reaction. These antibodies
CC recognize human interleukin-6 receptor (IL-6R). The hybridoma cells were
CC transformed with plasmids containing fragments of the antibody gene which
CC caused the production of the antibody from the hybridoma cell line.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX

SO Sequence 135 AA;

Query Match 100.0%; Score 30; DB 2; Length 135;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYTH 5
|||
DB 50 SYTH 54

RESULT 46

AAR28669 ID AAR28669 standard; protein; 135 AA.

AC AAR28669;

DT 25-MAR-2003 (revised)
DT 30-MAR-1993 (first entry)

DE p12-h2.

XX Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; H;
KM heavy chain; variable region; mouse; monoclonal; hybridoma; AUK12-20;
KM plasmid; p12-k2; p12-h2.

XX Synthetic.

XX Key Location/Qualifiers
FT Peptide 1..19
FT /note= "Signal peptide"
FT Protein 20..135
FT /note= "Mature peptide"

PN WO9219759-A1.

XX 12-NOV-1992.

XX 24-APR-1992; 92WO-JP000544.

XX 25-APR-1991; 91JP-00095476.
PR 19-FEB-1992; 92JP-00032084.

PA (CHUS) CHUGAI SEIYAKU KK.

PI Tsuchiya M, Sato K, Bendig MM, Jones ST, Saldanha JW;

XX WPI: 1992-398882/48.

DR N-PSDB; AAQ30754.

XX Reconstituted human antibody to human interleukin-6 receptor - has low
PT antigenicity and contains mouse V-region complementarily determining
PT regions.

XX Disclosure; Page 119-20; 207pp; Japanese.

XX The sequences given in AAR28668-69 were encoded by plasmid sequences
CC which were used in example to illustrate the production of a human
CC antibody which recognizes human interleukin-6 receptor (IL-6R). The
CC antibody comprises light (L) chain and heavy (H) chain variable regions
CC which were derived from a mouse monoclonal antibody produced from the
CC hybridoma AUK12-20 which contained the plasmids p12-k2 and p12-h2.
CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 135 AA;

SO Query Match 100.0%; Score 30; DB 2; Length 135;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYTH 5
|||
DB 50 SYTH 54

RESULT 47

AAR29017 ID AAR29017 standard; protein; 135 AA.

AC AAR29017;

DT 25-MAR-2003 (revised)
DT 30-MAR-1993 (first entry)

DE pUC-RVh-1220d.

XX Human; antibody; interleukin-6; receptor; IL-6R; CDR; PCR; mouse;
KM complementarity determining region; monoclonal; hybridoma; PCR; plasmid;
KM polymerase chain reaction; amplify.

XX Synthetic.

XX Key Location/Qualifiers
FT Peptide 1..19
FT /note= "Leader peptide"
FT Region 20..49
FT /label= FR1
FT Region 50..54
FT /label= CDR1
FT Region 55..68
FT /label= FR2
FT Region 69..85
FT /label= CDR2
FT Region 86..117
FT /label= FR3
FT Region 118..124
FT /label= CDR3
FT Region 125..135
FT /label= FR4

PN WO9219759-A1.

XX 12-NOV-1992.

XX 24-APR-1992; 92WO-JP000544.

XX 25-APR-1991; 91JP-00095476.
PR 19-FEB-1992; 92JP-00032084.

PA (CHUS) CHUGAI SEIYAKU KK.

PI Tsuchiya M, Sato K, Bendig MM, Jones ST, Saldanha JW;

XX WPI: 1992-398882/48.

DR N-PSDB; AAQ31391.

XX Reconstituted human antibody to human interleukin-6 receptor - has low
PT antigenicity and contains mouse V-region complementarily determining
PT regions.

XX Disclosure; Page 159-60; 207pp; Japanese.

XX The sequences given in AAR29016-17 are portions of monoclonal antibodies
CC which were encoded by plasmids contained within the mouse hybridoma,
CC AUK12-20. The DNA encoding the complementarity determining regions
CC (CDR's) was isolated by polymerase chain reaction. These antibodies

CC recognise human interleukin-6 receptor (IL-6R). The hybridoma cells were
CC transformed with plasmids containing fragments of the antibody gene which
CC caused the production of the antibody from the hybridoma cell line.
CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 135 AA;

Query Match 100.0%; Score 30; DB 2; Length 135;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYIYH 5
|||||
DB 50 SYIYH 54

RESULT 48
ADG30439
ID ADG30439 standard; protein; 241 AA.

XX AC ADG30439;

XX DT 26-FEB-2004 (first entry)

XX DE Human GMBG646 scFv protein.

XX KM GMBG; VH; CDR; complementarity determining region; VL; scFv;
KM single chain antibody; antidiabetic; type II diabetes; human; GMBG646.

XX OS Homo sapiens.

XX PN WO2003085093-A2.

XX PD 16-OCT-2003.

XX PF 28-MAR-2003; 2003WO-US009625.

XX PR 01-APR-2002; 2002US-036813P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Baker KP, Albert VR, Chowdhury P;

XX DR WPI: 2003-804305/75.

XX DR N-PSDB; ADG30536.

XX PT New antibody that specifically binds to GMBD polypeptide, useful for
PT diagnosing, monitoring, treating, preventing or ameliorating type II
PT diabetes.

XX PS Claim 2; SEQ ID NO 72; 410pp; English.

XX CC The invention relates to a novel antibody that specifically binds to a
CC GMBD polypeptide comprising a first amino acid sequence that is at least
CC 95% identical to a second amino acid sequence of a VH CDR
CC (complementarity determining region) or VL CDR of an scFv (single chain
CC antibody molecule). The antibody of the invention demonstrates
CC antidiabetic activity and may be useful for diagnosing, monitoring,
CC treating, preventing or ameliorating type II diabetes. The current
CC sequence is that of the human scFv protein of the invention.

XX SQ Sequence 241 AA;

Query Match 100.0%; Score 30; DB 7; Length 241;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYIYH 5
|||||
DB 31 SYIYH 35

RESULT 49

ABP46078
ID ABP46078 standard; protein; 245 AA.

XX AC ABP46078;

XX DT 19-AUG-2002 (first entry)

XX DE Human Blys binding scFv SEQ ID 2089.

XX KM Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KM tumour necrosis factor; B cell proliferation; B cell differentiation;
KM immunosuppressive; immunostimulant; immunomodulatory; antineumatic;
KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KM common variable immunodeficiency; acquired immunodeficiency syndrome.

XX OS Homo sapiens.

XX PN WO200202641-A1.

XX PD 10-JAN-2002.

XX PF 15-JUN-2001; 2001WO-US019110.

XX PR 16-JUN-2000; 2000US-0212210P.

XX PR 17-OCT-2000; 2000US-0240816P.

XX PR 16-MAR-2001; 2001US-0276248P.

XX PR 21-MAR-2001; 2001US-0277379P.

XX PR 25-MAY-2001; 2001US-0293499P.

XX PA (HUMA-) HUMAN GENOME SCI INC.
XX (CMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

XX DR WPI: 2002-114799/15.

XX PT Antibodies against B lymphocyte Stimulating polypeptides, useful for the
PT diagnosis and treatment of cancers and immune disorders.

XX PS Claim 1; Page 2889-2890; 3148pp; English.

XX CC This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antineumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention

XX SQ Sequence 245 AA;

Query Match 100.0%; Score 30; DB 5; Length 245;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYIYH 5
|||||
DB 31 SYIYH 35

RESULT 50
ADG96905

ID ADG96905 standard; protein; 245 AA.
 XX
 AC ADG96905;
 XX
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE Single chain antibody that immunospecifically binds Blys SeqID 2089.
 XX
 KW antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;
 KW B cell proliferation; differentiation; scFv; myasthenia gravis;
 KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
 KW carcinoma; lymphoma; antirheumatic; antiallergic; neuroprotective;
 KW antiinflammatory; antiasthmatic; antiallergic; cytostatic.
 XX
 OS Unidentified.
 XX
 PN WO2003055979-A2.
 XX
 PD 10-JUL-2003.
 XX
 PF 14-NOV-2002; 2002WO-US036496.
 XX
 PR 16-NOV-2001; 2001US-0331469P.
 PR 19-DEC-2001; 2001US-0340817P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX
 PI Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;
 DR WPI; 2003-505530/47.
 XX
 PT Novel antibody that immunospecifically binds to a B lymphocyte stimulator
 PT (Blys), useful for detecting and treating diseases or disorders e.g.
 PT rheumatoid arthritis, asthma and leukemia.
 XX
 PS Example 1; SEQ ID NO 2089; 394pp; English.
 XX
 CC This invention relates to novel antibodies that immunospecifically bind
 CC to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
 CC chromosome 13q34 and encodes a protein that is a member of the tumour
 CC necrosis factor superfamily and induces both in vivo and in vitro B cell
 CC proliferation and differentiation. Specifically, it refers to single
 CC chain antibody molecules (scFvs) derived, preferably, from the variable
 CC heavy CDR3 region that immunospecifically bind to a polypeptide, or
 CC fragment thereof, of either human, murine, rat or monkey Blys. The
 CC present invention refers to the use of such antibodies in various methods
 CC for the detection, diagnosis and prognosis of diseases related to the
 CC aberrant expression or inappropriate function of Blys or its receptor. As
 CC such, these compositions are useful for identifying immune disorders
 CC including myasthenia gravis and multiple sclerosis, inflammatory
 CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
 CC as AIDS and proliferative disorders including leukaemia, carcinoma and
 CC lymphoma. Accordingly, they can be described as exhibiting various
 CC activities such as antirheumatic, antiallergic, neuroprotective,
 CC antiinflammatory, antiasthmatic, antiallergic and cytostatic. This
 CC polypeptide sequence is a single chain antibody that binds Blys of the
 CC invention. NOTE: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 245 AA;

Query Match 100.0%; Score 30; DB 7; Length 245;
 Best Local Similarity 100.0%; Pred. No. 5.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SYTTH 5
 |||||
 Db 31 SYTTH 35

Search completed: May 4, 2006, 12:58:51
 Job time : 82.4444 secs

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OM protein - protein search, using sw model

Run on: May 4, 2006, 13:00:03 ; Search time 7.14286 Seconds
(without alignments)
67.352 Million cell updates/sec

Title: US-10-700-632-1
Perfect score: 30
Sequence: 1 SYTH 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	100.0	104	2 S26466	Ig heavy chain V r
2	30	100.0	104	2 B71120	Ig heavy chain V r
3	30	100.0	112	2 S26473	Ig heavy chain V r
4	30	100.0	124	2 H30138	DNA transport mach
5	30	100.0	126	2 S58121	Ig heavy chain V r
6	30	100.0	135	2 S22591	hypothetical prote
7	30	100.0	135	2 S39212	gene C2 protein -
8	30	100.0	135	2 S39236	gene C2 protein -
9	30	100.0	138	2 S21810	Ig heavy chain V r
10	30	100.0	284	2 T20684	hypothetical prote
11	30	100.0	326	2 T40353	probable ribosomal
12	30	100.0	348	2 T02462	probable AT-hook D
13	30	100.0	384	2 S60948	MCT1 protein - yea
14	30	100.0	774	2 T39539	alpha-amylase homo
15	30	100.0	937	2 P00864	hypothetical prote
16	30	100.0	2105	1 A44059	genome polypeptid
17	29	96.7	115	2 S24653	Ig heavy chain V r
18	29	96.7	135	2 J02338	hypothetical prote
19	29	96.7	135	2 C83748	hypothetical prote
20	29	96.7	204	2 T29851	hypothetical prote
21	29	96.7	383	2 T30067	hypothetical prote
22	29	96.7	577	2 T06751	hypothetical prote
23	28	93.3	135	1 J01888	hypothetical prote
24	28	93.3	135	1 OOCVCA	Al2 protein - coma
25	28	93.3	135	2 S07593	hypothetical prote
26	28	93.3	135	2 B97251	spore protease GPR
27	28	93.3	280	2 D82017	hypothetical prote
28	28	93.3	288	2 D81002	conserved hypotet
29	28	93.3	299	2 C64397	hypothetical prote

30	28	93.3	317	2 H64037	hypothetical prote
31	28	93.3	347	2 T06584	probable DNA-bind
32	28	93.3	406	2 H89006	protein T22F3.11 l
33	28	93.3	453	2 T30985	hypothetical prote
34	28	93.3	482	2 T30983	hypothetical prote
35	28	93.3	521	2 F71009	probable sodium-de
36	28	93.3	527	2 A75122	sodium- and chlori
37	28	93.3	553	2 T45596	telomere repeat-bi
38	28	93.3	1817	2 H71611	protein secreted
39	28	93.3	2415	1 A33733	spectrin alpha cha
40	28	93.3	3898	1 GNMVHC	genome polypeptid
41	28	93.3	3898	1 GNMVHB	genome polypeptid
42	28	93.3	3898	1 S57437	genome polypeptid
43	28	93.3	3898	2 S58295	polypeptid - hog
44	27	90.0	80	2 S78706	protein YBR058C-a
45	27	90.0	98	2 S26920	Ig heavy chain V r
46	27	90.0	99	2 C48223	Ig heavy chain V r
47	27	90.0	115	2 A54378	Ig heavy chain V r
48	27	90.0	116	2 S22553	Ig heavy chain V r
49	27	90.0	117	1 HVH0HG	Ig heavy chain pre
50	27	90.0	117	2 S31680	Ig heavy chain V r
51	27	90.0	117	2 S09960	Ig heavy chain V-D
52	27	90.0	165	2 AH3295	acetyltransferase
53	27	90.0	197	2 B48290	hypothetical prote
54	27	90.0	216	2 B97312	hypothetical prote
55	27	90.0	241	2 S69131	Ig heavy chain (DO
56	27	90.0	292	2 S60950	probable membrane
57	27	90.0	312	2 D72451	hypothetical prote
58	27	90.0	354	2 T44109	conserved hypotet
59	27	90.0	397	2 AC2006	hypothetical prote
60	27	90.0	398	2 S76445	hypothetical prote
61	27	90.0	413	1 S39554	histidine decarbox
62	27	90.0	430	2 B71712	cell cycle protein
63	27	90.0	494	2 JC5320	cytochrome P450 mo
64	27	90.0	643	1 FOV2ZW	major core protein
65	27	90.0	644	1 FOV2SR	major core protein
66	27	90.0	644	2 T37390	major core protein
67	27	90.0	644	2 A72164	AA1 protein - vari
68	27	90.0	644	2 D36848	major core protein
69	27	90.0	644	2 T28545	hypothetical prote
70	27	90.0	667	2 T20799	hypothetical prote
71	27	90.0	742	2 C71983	endopeptidase C1P
72	27	90.0	984	1 DJNVCP	DNA-directed DNA p
73	27	90.0	985	2 T10339	DNA-directed DNA p
74	27	90.0	986	2 T41809	DNA polymerase orf
75	27	90.0	1013	2 J01920	DNA-directed DNA p
76	27	90.0	1014	2 T30431	DNA-directed DNA p
77	27	90.0	1884	1 A45553	genome polypeptid
78	27	90.0	1885	2 J02183	hypothetical 216.5
79	27	90.0	1968	1 PN0093	genome polypeptid
80	27	90.0	3135	2 A48584	transmission block
81	26	86.7	40	2 S33408	Ig heavy chain V r
82	26	86.7	41	2 T07570	hypothetical prote
83	26	86.7	79	2 G82811	hypothetical prote
84	26	86.7	98	2 PH0871	Ig heavy chain V r
85	26	86.7	104	2 S69899	Ig heavy chain V r
86	26	86.7	105	2 S67941	Ig heavy chain var
87	26	86.7	111	2 S64364	probable membrane
88	26	86.7	119	2 S24665	Ig heavy chain V r
89	26	86.7	120	2 S24664	Ig heavy chain V r
90	26	86.7	120	2 F28195	Ig heavy chain V r
91	26	86.7	120	2 A49982	Ig heavy chain V r
92	26	86.7	120	2 G28195	Ig heavy chain V r
93	26	86.7	125	2 E59106	hypothetical prote
94	26	86.7	130	2 F90278	conserved hypotet
95	26	86.7	130	2 A90230	conserved hypotet
96	26	86.7	130	2 C90363	conserved hypotet
97	26	86.7	145	2 T21691	hypothetical prote
98	26	86.7	150	2 S22328	gene D protein - p
99	26	86.7	152	1 ZDBBFA	gene D protein - p
100	26	86.7	152	1 ZDBBFA	gene D protein - p
101	26	86.7	152	2 US0454	gene D protein - p
102	26	86.7	152	2 D86648	ferrous ion transp

103	26	86.7	156	2	H71623	probable secreted
104	26	86.7	159	2	E69772	hypothetical prote
105	26	86.7	169	2	P84971	hypothetical prote
106	26	86.7	172	2	T26837	hypothetical prote
107	26	86.7	182	2	E70339	heat shock protein
108	26	86.7	192	2	C97315	uncharacterized pr
109	26	86.7	197	2	D82783	hypothetical prote
110	26	86.7	203	2	T29844	hypothetical prote
111	26	86.7	205	2	P82562	hypothetical prote
112	26	86.7	205	2	B82562	hypothetical prote
113	26	86.7	207	2	UQ0397	nods protein - Azo
114	26	86.7	210	2	B89958	hypothetical prote
115	26	86.7	210	2	G85729	hypothetical prote
116	26	86.7	215	2	E84966	adenylate kinase (
117	26	86.7	216	2	E82326	MSRA biogenesis pr
118	26	86.7	221	2	S46498	GTP-binding protei
119	26	86.7	222	2	B90888	hypothetical prote
120	26	86.7	230	2	T19437	hypothetical prote
121	26	86.7	231	2	D65217	D-allulose-6-phosp
122	26	86.7	232	2	T11072	cytochrome-c oxida
123	26	86.7	246	2	S38950	Ig gamma chain - m
124	26	86.7	251	2	H85781	hypothetical prote
125	26	86.7	251	2	D90933	hypothetical prote
126	26	86.7	258	2	H84204	copper transport A
127	26	86.7	259	2	E84125	hydrolase BH3805 I
128	26	86.7	284	2	AF1341	fructose-1,6-bipho
129	26	86.7	286	2	A95076	ribonuclease BN, p
130	26	86.7	291	2	P97943	conserved hypotet
131	26	86.7	296	2	AH0347	probable diacylgly
132	26	86.7	309	2	C81317	probable glycosylt
133	26	86.7	312	2	B89829	hypothetical prote
134	26	86.7	315	2	G70165	aldose reductase h
135	26	86.7	316	2	H90372	catechol 2,3-dioxy
136	26	86.7	325	2	G96718	unknown protein, 5
137	26	86.7	327	2	S48946	hypothetical prote
138	26	86.7	327	2	A81085	oxidoreductases ho
139	26	86.7	329	2	S28305	hypothetical prote
140	26	86.7	342	2	A10043	conserved hypotet
141	26	86.7	353	1	W2ML13	E2 protein - human
142	26	86.7	353	2	E84482	hypothetical prote
143	26	86.7	357	2	D69820	hypothetical prote
144	26	86.7	357	2	T40389	longevity assuranc
145	26	86.7	358	1	W2ML58	E2 protein - human
146	26	86.7	361	2	T38693	probable trna prot
147	26	86.7	362	2	T33092	hypothetical prote
148	26	86.7	369	2	A39157	probable RNA helic
149	26	86.7	372	2	A55262	protein kinase (EC
150	26	86.7	377	1	W2ML13	E2 protein - human
151	26	86.7	379	2	T52405	hypothetical prote
152	26	86.7	384	2	S36529	E2 protein - human
153	26	86.7	384	2	B64940	hypothetical prote
154	26	86.7	386	1	S49218	histidine decarbox
155	26	86.7	386	2	T04914	hypothetical prote
156	26	86.7	393	2	T15703	hypothetical prote
157	26	86.7	397	2	JW0075	cysteine-dependent
158	26	86.7	404	2	T19455	hypothetical prote
159	26	86.7	408	1	WMNVIA	immediate-early pr
160	26	86.7	408	2	A72869	early gene transac
161	26	86.7	409	2	S73724	ATP-dependent RNA
162	26	86.7	410	2	A64234	ATP-dependent meth
163	26	86.7	413	2	A69165	modification methy
164	26	86.7	416	2	T23383	hypothetical prote
165	26	86.7	425	2	S28295	hypothetical prote
166	26	86.7	430	2	JC3301	hypothetical 47.8K
167	26	86.7	433	2	AD1164	H+-transporting AT
168	26	86.7	433	2	AD1523	H+-transporting AT
169	26	86.7	437	2	JQ2015	nucleoprotein - ra
170	26	86.7	437	2	JQ2016	conserved hypotet
171	26	86.7	438	2	C64654	hypothetical prote
172	26	86.7	438	2	H71941	hypothetical prote
173	26	86.7	443	2	T19001	hypothetical prote
174	26	86.7	445	2	T20190	hypothetical prote
175	26	86.7	446	2	S40295	Ig gamma-2a chain
176	26	86.7	448	2	T30982	hypothetical prote
177	26	86.7	450	1	VHVNRY	nucleoprotein - ra
178	26	86.7	450	1	VHVNRY	nucleoprotein - ra
179	26	86.7	450	1	VHNSB	nucleoprotein N -
180	26	86.7	450	2	A46104	nucleoprotein N -
181	26	86.7	450	2	A58460	conserved hypotet
182	26	86.7	451	2	B82675	hypothetical prote
183	26	86.7	452	2	T28094	conserved hypotet
184	26	86.7	452	2	B90407	hypothetical prote
185	26	86.7	452	2	T34013	hypothetical prote
186	26	86.7	461	2	H90090	hypothetical prote
187	26	86.7	469	2	B90110	TATA box-binding p
188	26	86.7	473	1	XUBYRP	trans-pentaprenylt
189	26	86.7	476	2	T40330	hypothetical prote
190	26	86.7	491	2	AE1397	efflux transporter
191	26	86.7	491	2	AC1555	efflux transporter
192	26	86.7	498	2	AC1086	ATP synthase alpha
193	26	86.7	498	2	A11449	ATP synthase alpha
194	26	86.7	507	2	G01614	zinc finger protei
195	26	86.7	512	2	A53092	reduced folate car
196	26	86.7	517	2	T00980	hypothetical prote
197	26	86.7	534	2	A99316	hypothetical prote
198	26	86.7	537	2	T20746	hypothetical prote
199	26	86.7	541	2	G64559	arginine-tRNA lig
200	26	86.7	541	2	H71947	arginine-tRNA lig
201	26	86.7	548	2	A56353	MDI protein - Yea
202	26	86.7	587	2	AG3019	conserved hypotet
203	26	86.7	594	2	T06467	phosphoinositide-s
204	26	86.7	595	2	A35919	carotenoid biosynt
205	26	86.7	596	2	T19740	hypothetical prote
206	26	86.7	599	1	WMBP92	gene 9 protein - p
207	26	86.7	599	1	WMBP92	gene 9 protein - p
208	26	86.7	621	2	T20663	hypothetical prote
209	26	86.7	629	2	T51729	arginine-tRNA-prot
210	26	86.7	631	2	T20037	hypothetical prote
211	26	86.7	634	2	B98265	hypothetical prote
212	26	86.7	655	2	A70931	probable PPE prote
213	26	86.7	663	2	S55164	hypothetical prote
214	26	86.7	726	1	S73915	virulence-associat
215	26	86.7	737	2	B88551	adducin alpha cha
216	26	86.7	743	2	B88551	protein T23G5.2 [i
217	26	86.7	747	2	T16274	hypothetical prote
218	26	86.7	811	2	C86346	hypothetical prote
219	26	86.7	815	2	T15749	hypothetical prote
220	26	86.7	819	2	A47018	lectin-like adhesi
221	26	86.7	861	2	S51350	KAP9 protein - ye
222	26	86.7	892	2	T27005	hypothetical prote
223	26	86.7	897	2	S74225	leptin receptor, 1
224	26	86.7	995	2	S26426	type IV site-spect
225	26	86.7	997	2	I40805	collagenase - Clos
226	26	86.7	1021	2	G59436	KIAA1304 protein [
227	26	86.7	1051	2	S57450	protein-tyrosine k
228	26	86.7	1067	2	D82436	transporter, AcbB/
229	26	86.7	1075	2	G59434	KIAA0411 protein [
230	26	86.7	1095	2	C59437	KIAA0456 protein [
231	26	86.7	1138	2	E71615	probable amine tra
232	26	86.7	1146	2	A89922	conserved hypotet
233	26	86.7	1162	2	PC4184	leptin receptor, O
234	26	86.7	1167	1	A35066	streptococcal Csa
235	26	86.7	1188	2	G72734	hypothetical prote
236	26	86.7	1206	2	F72233	conserved hypotet
237	26	86.7	1265	2	T51314	probable CO--induc
238	26	86.7	1290	2	A55094	chromosomal protei
239	26	86.7	1320	2	E59092	hypothetical prote
240	26	86.7	1344	2	S67412	gene P2 protein -
241	26	86.7	1385	2	H88569	protein K03H1.5 [i
242	26	86.7	1389	2	T41230	hypothetical TPR d
243	26	86.7	1409	2	S41028	hypothetical prote
244	26	86.7	1423	2	A49206	exo-beta-D-fructos
245	26	86.7	1633	1	C3RT	complement C3 prec
246	26	86.7	1802	2	G71616	hypothetical prote
247	26	86.7	2322	2	T10542	hypothetical prote
248	26	86.7	2708	2	T09079	probable chloroqui

249	26	86.7	2819	2	T09080	probable chloroqui	322	25	83.3	287	2	T28540	hypothetical prote
250	26	86.7	2896	2	T30939	hemocyanin G-type	323	25	83.3	287	2	S12738	T-cell alloantigen
251	26	86.7	4572	2	S57908	hypothetical 527K	324	25	83.3	288	2	H70894	hypothetical prote
252	26	86.7	5369	2	T44807	myosubtilin synth	325	25	83.3	289	2	S42252	probable mRNA capp
253	25	83.3	50	2	S26941	Ig heavy chain v r	326	25	83.3	295	2	T30703	probable mRNA guan
254	25	83.3	71	2	PH136	Ig heavy chain v r	327	25	83.3	298	2	B75096	glycosyl transfera
255	25	83.3	72	2	S01837	nifT protein - Kle	328	25	83.3	302	2	B35961	hypothetical 21K p
256	25	83.3	90	2	G89871	hypothetical prote	329	25	83.3	306	2	D70681	probable esterase/
257	25	83.3	94	2	T18331	icm protein - Leg	330	25	83.3	310	2	S36581	E2 protein - human
258	25	83.3	98	2	PH111	Ig heavy chain v r	331	25	83.3	310	2	H69455	hypothetical prote
259	25	83.3	98	2	PH117	Ig heavy chain v r	332	25	83.3	310	2	B69755	ion channel homolo
260	25	83.3	100	2	B27144	larval serum prote	333	25	83.3	311	2	B69229	conserved hypotnet
261	25	83.3	108	2	PH0977	Ig heavy chain v r	334	25	83.3	312	2	B55461	NMD(P)-arginine AD
262	25	83.3	111	2	H97316	hypothetical prote	335	25	83.3	314	2	A69803	transcription regu
263	25	83.3	116	2	S22558	Ig heavy chain v r	336	25	83.3	315	2	T48797	hypothetical prote
264	25	83.3	142	1	P70437	nucleoside-diphosp	337	25	83.3	331	2	T26832	hypothetical prote
265	25	83.3	161	2	F70006	cysteine dioxygena	338	25	83.3	333	2	C37145	probable helvetic
266	25	83.3	169	2	S06580	finger protein (cl	339	25	83.3	335	2	T04029	hypothetical prote
267	25	83.3	175	2	S18882	prolactin - Americ	340	25	83.3	335	2	A86464	hypothetical prote
268	25	83.3	178	2	AD1156	hypothetical prote	341	25	83.3	335	2	T24540	hypothetical prote
269	25	83.3	178	2	AG1514	hypothetical prote	342	25	83.3	335	2	T33832	hypothetical prote
270	25	83.3	185	1	Z5BPT4	gene 55 protein -	343	25	83.3	337	2	T38500	interferon gamma r
271	25	83.3	185	2	T10151	hypothetical prote	344	25	83.3	340	2	S62584	probable oxidoredu
272	25	83.3	191	2	A95209	hypothetical prote	345	25	83.3	342	2	T09355	hypothetical prote
273	25	83.3	196	2	D83829	hypothetical prote	346	25	83.3	347	2	G82862	conjugal transfer
274	25	83.3	197	2	F72626	hypothetical prote	347	25	83.3	349	2	JE0202	paired-box-contain
275	25	83.3	198	1	A60620	prolactin - green	348	25	83.3	362	2	A84187	hypothetical prote
276	25	83.3	199	1	LCHO	prolactin - horse	349	25	83.3	365	1	W2WLS	E2 protein - human
277	25	83.3	199	2	H90206	amidoctransferase h	350	25	83.3	366	2	H96537	hypothetical prote
278	25	83.3	199	2	US0430	prolactin - elepha	351	25	83.3	367	1	W2WL35	E2 protein - human
279	25	83.3	199	2	PN0128	prolactin - sei wh	352	25	83.3	370	1	S36524	E2 protein - human
280	25	83.3	199	2	S15131	prolactin - Arabia	353	25	83.3	370	1	C69901	probable two-compo
281	25	83.3	203	2	G82535	superoxide dismuta	354	25	83.3	371	2	T19417	hypothetical prote
282	25	83.3	207	2	A60969	prolactin precursu	355	25	83.3	372	1	W2WL31	E2 protein - human
283	25	83.3	208	2	AP1145	amidoctransferases	356	25	83.3	373	2	T19419	hypothetical prote
284	25	83.3	208	2	AP1504	coat protein - Ind	357	25	83.3	374	2	T26200	hypothetical prote
285	25	83.3	208	2	S39338	conserved hypotnet	358	25	83.3	375	2	T40554	probable membrane
286	25	83.3	210	2	AD0906	hypothetical prote	359	25	83.3	375	2	S67302	E2 protein - Ba
287	25	83.3	211	2	T18799	hypothetical prote	360	25	83.3	375	2	S65312	probable membrane
288	25	83.3	212	2	C84007	negative regulator	361	25	83.3	378	2	S36506	E2 protein - human
289	25	83.3	213	2	UC6542	superoxide dismuta	362	25	83.3	378	2	T25626	hypothetical prote
290	25	83.3	219	2	F70474	conserved hypotnet	363	25	83.3	384	2	D90312	homogenitase oxyg
291	25	83.3	226	1	LCRT	prolactin precursu	364	25	83.3	389	2	D90498	acyl-CoA dehydroge
292	25	83.3	226	1	F85065	hypothetical prote	365	25	83.3	391	1	S15617	E2 protein - human
293	25	83.3	227	1	LCHU	prolactin precursu	366	25	83.3	391	2	T40029	hypothetical prote
294	25	83.3	228	1	LCMS	prolactin precursu	367	25	83.3	392	2	AI1341	Xaa-Pro dipeptidas
295	25	83.3	228	1	AC1402	prolactin precursu	368	25	83.3	392	2	C98146	Xaa-Pro dipeptidas
296	25	83.3	229	1	S54799	nitrile hydratase	369	25	83.3	393	2	D95894	probable hydrolase
297	25	83.3	229	1	S19713	prolactin precursu	370	25	83.3	394	2	D85256	hypothetical prote
298	25	83.3	229	1	LCBO	prolactin precursu	371	25	83.3	397	2	T23026	hypothetical prote
299	25	83.3	229	1	LCRG	prolactin precursu	372	25	83.3	402	2	G90254	conserved hypotnet
300	25	83.3	229	1	LCSH	prolactin precursu	373	25	83.3	404	2	E83851	N-acyl-L-amino aci
301	25	83.3	229	2	AC0972	prolactin precursu	374	25	83.3	406	2	C83867	Xaa-Pro dipeptidas
302	25	83.3	229	2	AC1133	prolactin precursu	375	25	83.3	409	2	T48967	hypothetical prote
303	25	83.3	229	2	UC4631	prolactin precursu	376	25	83.3	409	2	T40633	hypothetical prote
304	25	83.3	229	2	I83982	prolactin - goat	377	25	83.3	412	2	A69256	hypothetical prote
305	25	83.3	232	2	T16258	hypothetical prote	378	25	83.3	425	1	H69124	translation initia
306	25	83.3	234	2	AD2228	hypothetical prote	379	25	83.3	425	1	E86575	phosphate permease
307	25	83.3	241	2	S42436	proteasome endopap	380	25	83.3	426	2	D72049	phosphate permease
308	25	83.3	247	2	A57266	probable methane m	381	25	83.3	426	2	A97301	ATPase with chapar
309	25	83.3	248	2	T18962	hypothetical prote	382	25	83.3	430	2	E82583	threonine synthase
310	25	83.3	267	2	T37047	probable nitrate r	383	25	83.3	433	2	T14282	embryogenic callus
311	25	83.3	269	2	T49293	hypothetical prote	384	25	83.3	445	2	T49924	hypothetical prote
312	25	83.3	273	2	G83403	conserved hypotnet	385	25	83.3	447	2	F64706	UDP-MurNac-riptide
313	25	83.3	275	2	G83522	conserved hypotnet	386	25	83.3	449	2	S23158	nucleocapsid prote
314	25	83.3	278	2	S36387	probable protein k	387	25	83.3	449	2	T16259	hypothetical prote
315	25	83.3	278	2	T29904	hypothetical prote	388	25	83.3	450	1	WZBER4	49.2K membrane pro
316	25	83.3	279	2	T24606	mRNA capping enzym	389	25	83.3	450	2	T42595	envelope protein 5
317	25	83.3	287	1	OCV222	mRNA capping enzym	390	25	83.3	451	2	T24018	hypothetical prote
318	25	83.3	287	2	B42516	D12L protein - vac	391	25	83.3	454	2	AE1970	hypothetical prote
319	25	83.3	287	2	T37385	mRNA capping enzym	392	25	83.3	461	2	T25671	hypothetical prote
320	25	83.3	287	2	D72163	O2L protein - vari	393	25	83.3	463	2	T39004	probable histone a
321	25	83.3	287	2	I36847	N2L protein - vari	394	25	83.3	464	1	MNVDMC	nonstructural prot

395	25	83.3	465	2	T14997	hypotheical prote
396	25	83.3	466	2	T45880	hypotheical prote
397	25	83.3	466	2	T32280	hypotheical prote
398	25	83.3	467	1	KNVDM1	nonstructural prote
399	25	83.3	469	2	T26463	hypotheical prote
400	25	83.3	474	2	A40336	gamma-aminobutyric
401	25	83.3	474	2	B27142	gamma-aminobutyric
402	25	83.3	474	2	S53530	gamma-aminobutyric
403	25	83.3	474	2	B60039	gamma-aminobutyric
404	25	83.3	484	1	QOBER7	HULF3 protein - hu
405	25	83.3	499	2	C96976	exopolysphatase
406	25	83.3	501	2	I39360	IEP SSP 9502 - hum
407	25	83.3	505	2	S08598	hypotheical prote
408	25	83.3	505	2	S47451	hypotheical prote
409	25	83.3	505	2	AF2186	hypotheical prote
410	25	83.3	510	2	S35028	protein F82 precu
411	25	83.3	514	1	D70180	phosphotransferase
412	25	83.3	516	2	B75004	hypotheical prote
413	25	83.3	518	2	A53207	probable folate tr
414	25	83.3	523	2	B71985	hypotheical prote
415	25	83.3	526	2	H90554	xylose ABC transpo
416	25	83.3	529	2	A96536	hypotheical prote
417	25	83.3	529	2	D87995	protein K03D10.3 l
418	25	83.3	530	2	I38558	Mi-2 autoantigen 2
419	25	83.3	531	2	T21059	hypotheical prote
420	25	83.3	546	2	A84630	hypotheical prote
421	25	83.3	550	2	T23272	hypotheical prote
422	25	83.3	563	2	D84717	probable cysteinyl
423	25	83.3	565	2	H72253	DNA primase - Ther
424	25	83.3	567	2	JC4714	alpha-glucosidase
425	25	83.3	575	1	QOVZH5	H5 protein - vacci
426	25	83.3	577	2	H86414	F28N24.8 protein -
427	25	83.3	578	2	T51230	telomere repeat-bi
428	25	83.3	589	2	A55968	folate binding pro
429	25	83.3	590	2	JC2468	folate transporter
430	25	83.3	590	2	D84483	mutator-like trans
431	25	83.3	590	2	A26638	homeotic protein D
432	25	83.3	591	2	I38924	reduced folate car
433	25	83.3	591	2	I52728	reduced folate car
434	25	83.3	598	2	T20769	hypotheical prote
435	25	83.3	606	2	S43118	finger protein - m
436	25	83.3	622	2	T27155	hypotheical prote
437	25	83.3	634	2	I40217	glutaryl 7-ACA acy
438	25	83.3	637	2	AH3510	glycogen operon pr
439	25	83.3	656	2	D82388	hypotheical prote
440	25	83.3	656	2	B70766	probable pilinoma
441	25	83.3	657	2	D71351	hypotheical prote
442	25	83.3	659	2	T33557	exonuclease ABC c
443	25	83.3	662	2	B71731	collagen alpha 1(X
444	25	83.3	674	2	S13301	probable membrane
445	25	83.3	686	2	S61621	probable outer mem
446	25	83.3	695	2	B72129	probable outer mem
447	25	83.3	695	2	F86493	probable outer mem
448	25	83.3	697	2	H71525	conserved hypotet
449	25	83.3	700	2	B81682	conserved hypotet
450	25	83.3	704	2	C81542	origin recognition
451	25	83.3	707	2	T40070	hypotheical prote
452	25	83.3	721	2	T27570	vitulence-associat
453	25	83.3	725	1	B64211	hypotheical prote
454	25	83.3	729	2	T23769	hypotheical prote
455	25	83.3	746	2	G84605	probable transposo
456	25	83.3	769	2	F85077	ribonucleoside-dip
457	25	83.3	779	1	MMVZAL	H4L protein - vacc
458	25	83.3	795	1	QOVZHA	RAP 94 - vaccinia
459	25	83.3	795	2	T37370	H4L protein - vari
460	25	83.3	795	2	S31101	hypotheical prote
461	25	83.3	795	2	T28525	u4L protein - vari
462	25	83.3	795	2	E72161	probable membrane
463	25	83.3	823	2	T02812	probable secreted
464	25	83.3	865	2	T34584	leucyl-tRNA synthe
465	25	83.3	887	2	B82590	DNA mismatch repai
466	25	83.3	941	2	T37626	rho-GTPase-activat
467	25	83.3	946	2	I38100	
468	25	83.3	950	2	T09076	hypotheical prote
469	25	83.3	950	2	T28793	diacylglycerol kin
470	25	83.3	952	2	T28792	diacylglycerol kin
471	25	83.3	980	2	E90433	conserved hypotet
472	25	83.3	998	2	S77225	sensory transducti
473	25	83.3	1012	2	A84393	glycolate oxidase
474	25	83.3	1016	2	S30236	genome polypotein
475	25	83.3	1025	2	B54718	dihydropyrimidine
476	25	83.3	1025	2	A54718	dihydropyrimidine
477	25	83.3	1037	2	D96786	protein F10A5.15 l
478	25	83.3	1055	2	AD2499	hypotheical prote
479	25	83.3	1067	1	S62421	endopeptidase Va h
480	25	83.3	1083	2	H86921	probable arabinosy
481	25	83.3	1216	2	JW0105	synaptotjanin 2 alp
482	25	83.3	1245	2	T18211	delta endotoxin -
483	25	83.3	1256	2	G97902	alpha-amylase (EC
484	25	83.3	1260	2	A72603	probable nitrate r
485	25	83.3	1280	2	E95031	alkaline amylopull
486	25	83.3	1434	2	T32647	hypotheical prote
487	25	83.3	1497	2	S72250	sex-determining tr
488	25	83.3	1748	1	J01555	genome polypotein
489	25	83.3	1748	2	S42136	cnjB protein - Tet
490	25	83.3	1896	2	T01490	hypotheical prote
491	25	83.3	2102	2	T15626	hypotheical prote
492	25	83.3	2157	1	GNNY1B	genome polypotein
493	25	83.3	2164	1	GNNY89	genome polypotein
494	25	83.3	2291	2	S11238	polymrase - Berne
495	25	83.3	2359	2	T03094	A-kinase anchor pr
496	25	83.3	2559	2	T30850	fat facets protein
497	25	83.3	2685	2	T38755	hypotheical prote
498	25	83.3	3144	2	S64791	V5I3 protein - ye
499	25	83.3	3746	1	YGPLV3	alpha-aminoadipyl-
500	25	83.3	3770	2	A40889	alpha-aminoadipyl-
501	25	83.3	3791	1	YGPLV8	protein F14716.10
502	25	83.3	4056	2	H96599	polyketide synthas
503	25	83.3	4447	2	A69679	LDL-receptor-relat
504	25	83.3	4753	1	A47437	polyketide synthet
505	25	83.3	4930	2	B69679	microtubule-associ
506	25	83.3	5327	2	T13564	probable membrane
507	25	80.0	70	2	F97182	hypotheical prote
508	24	80.0	72	2	T28174	colicin 10 immunit
509	24	80.0	96	2	I41025	unknown protein [i
510	24	80.0	97	2	C96743	Ig heavy chain V r
511	24	80.0	103	2	S08462	Ig heavy chain V r
512	24	80.0	111	2	S25033	Ig heavy chain V r
513	24	80.0	111	2	S25034	Ig heavy chain V r
514	24	80.0	126	2	I44151	Ig heavy chain V r
515	24	80.0	128	2	S26430	hypotheical 14.5K
516	24	80.0	132	2	E59105	hypotheical prote
517	24	80.0	135	2	AF0184	probable membrane
518	24	80.0	136	2	B90443	hypotheical prote
519	24	80.0	136	2	B83730	transcription regu
520	24	80.0	137	2	D91067	hypotheical prote
521	24	80.0	142	2	A32483	Ig heavy chain V r
522	24	80.0	145	2	AD1215	hypotheical prote
523	24	80.0	145	2	AH1568	hypotheical prote
524	24	80.0	146	2	A90477	hypotheical prote
525	24	80.0	148	2	AD0077	hypotheical prote
526	24	80.0	151	2	G69014	conserved hypotet
527	24	80.0	151	2	H83041	conserved hypotet
528	24	80.0	156	2	B85911	hypotheical prote
529	24	80.0	159	2	F95001	transcription regu
530	24	80.0	159	2	H95234	transcription regu
531	24	80.0	159	2	B97873	hypotheical prote
532	24	80.0	159	2	A98099	hypotheical prote
533	24	80.0	179	2	H71367	conserved hypotet
534	24	80.0	180	2	S51966	probable membrane
535	24	80.0	182	2	AB1251	hypotheical prote
536	24	80.0	182	2	AF1613	hypotheical prote
537	24	80.0	184	2	T46711	hypotheical prote
538	24	80.0	186	2	A90334	hypotheical prote
539	24	80.0	191	2	U01999	hypotheical prote
540	24	80.0	191	2	AD2480	hypotheical prote

541	24	80.0	193	2	S38039	hypothetical prote
542	24	80.0	198	2	F72603	hypothetical prote
543	24	80.0	201	2	T33593	hypothetical prote
544	24	80.0	203	2	T33864	hypothetical prote
545	24	80.0	205	2	F64504	hypothetical prote
546	24	80.0	211	2	C69521	hypothetical prote
547	24	80.0	211	2	S54092	probable membrane
548	24	80.0	214	2	AH1962	hypothetical prote
549	24	80.0	217	2	AF3540	phosphoglycerate m
550	24	80.0	223	2	E66620	hypothetical prote
551	24	80.0	223	2	D72004	hypothetical prote
552	24	80.0	224	2	AC3181	two component reep
553	24	80.0	224	2	B72040	coenzyme pqg synth
554	24	80.0	224	2	G86585	Crf10 hypothetical
555	24	80.0	226	2	T24056	hypothetical prote
556	24	80.0	231	2	F71493	hypothetical prote
557	24	80.0	234	2	AG1167	hypothetical prote
558	24	80.0	234	2	AI1525	hypothetical prote
559	24	80.0	235	1	ASLJG4	vif protein - siml
560	24	80.0	236	2	A75530	cytochrome c-type
561	24	80.0	236	2	C90390	conserved hypotet
562	24	80.0	236	2	D81652	coenzyme PQ synth
563	24	80.0	237	2	T01359	fatty acid hydroxy
564	24	80.0	237	2	T10629	hypothetical prote
565	24	80.0	240	2	S75423	hypothetical prote
566	24	80.0	240	2	AD1950	hypothetical prote
567	24	80.0	242	2	B83738	hypothetical prote
568	24	80.0	244	2	T39339	hypothetical prote
569	24	80.0	246	2	AE1347	hypothetical prote
570	24	80.0	246	2	AI1717	hypothetical prote
571	24	80.0	263	2	S73129	hypothetical prote
572	24	80.0	266	2	AH2467	transcription regu
573	24	80.0	273	2	S11380	serine/threonine-s
574	24	80.0	274	2	D90814	probable beta-gluc
575	24	80.0	274	2	H85673	beta-glucosidase (
576	24	80.0	274	2	G64854	ycfN protein - Bsc
577	24	80.0	283	2	F66450	hypothetical prote
578	24	80.0	284	2	T06159	probable receptor-
579	24	80.0	290	2	G71304	probable translati
580	24	80.0	294	2	E70398	dihydrodipicolinat
581	24	80.0	296	2	T11062	hypothetical prote
582	24	80.0	296	2	D70314	heme O oxygenase -
583	24	80.0	304	2	T24846	hypothetical prote
584	24	80.0	304	2	T22697	hypothetical prote
585	24	80.0	309	2	G69796	lactose permease h
586	24	80.0	309	2	S52256	copper export prot
587	24	80.0	314	2	S69836	hypothetical prote
588	24	80.0	315	2	T12729	structural protein
589	24	80.0	316	2	B82907	conserved hypotet
590	24	80.0	316	2	T19435	hypothetical prote
591	24	80.0	316	2	F89791	peptidoglycan hydr
592	24	80.0	318	2	F83789	lactose transport
593	24	80.0	318	2	T12340	hypothetical prote
594	24	80.0	319	1	C71654	kpsF protein (kpsF
595	24	80.0	323	2	AE0563	acetyl esterase (E
596	24	80.0	327	2	E75296	aldo/keto reductas
597	24	80.0	333	2	H64429	probable xylogluc
598	24	80.0	338	2	B64148	hypothetical prote
599	24	80.0	338	2	E91190	probable regulator
600	24	80.0	338	2	F66037	hypothetical prote
601	24	80.0	338	2	T33200	hypothetical prote
602	24	80.0	340	2	G82047	conserved hypotet
603	24	80.0	340	2	D95045	choline binding pr
604	24	80.0	342	1	S63374	hypothetical 38.7k
605	24	80.0	342	2	AH1045	conserved hypotet
606	24	80.0	342	2	E86110	hypothetical prote
607	24	80.0	342	2	G91269	hypothetical prote
608	24	80.0	344	1	Q3ECTH	hypothetical 40.5K
609	24	80.0	344	2	A88023	protein T27A1.6 [i
610	24	80.0	345	2	A87338	L-lysine 2,3-amino
611	24	80.0	345	2	E71600	rtlin PFB1040w - m
612	24	80.0	345	2	F90461	hypothetical prote
613	24	80.0	347	2	H04608	probable RNA-bindi
614	24	80.0	348	2	H70549	probable pdhb prot
615	24	80.0	349	2	B86769	GMP cyclohydrolase
616	24	80.0	352	2	T39363	RNA binding protei
617	24	80.0	355	2	F90391	conserved hypotet
618	24	80.0	357	2	C62554	conserved hypotet
619	24	80.0	362	2	D82653	hypothetical prote
620	24	80.0	363	2	T49209	leucanthocyanidin
621	24	80.0	363	2	AB2890	L-lysine 2,3-amino
622	24	80.0	363	2	G97665	L-lysine 2,3-amino
623	24	80.0	366	2	UE0105	testicular serine
624	24	80.0	369	2	T08266	conserved hypotet
625	24	80.0	370	2	T50443	probable uroporph
626	24	80.0	370	2	S54297	protein phosphatas
627	24	80.0	371	2	B86489	protein T32E20.25
628	24	80.0	371	2	AE1348	a probable compete
629	24	80.0	371	2	AI1718	probable competent
630	24	80.0	373	2	H83891	spre germination
631	24	80.0	375	2	C83317	RNA methyltransfe
632	24	80.0	376	1	ZXBPH4	hoc protein - phag
633	24	80.0	377	2	S58009	PMF68 protein - mo
634	24	80.0	378	1	A25013	histidine decarbox
635	24	80.0	378	1	A40004	histidine decarbox
636	24	80.0	378	1	B40004	histidine decarbox
637	24	80.0	379	2	F82680	tRNA methyltransfe
638	24	80.0	380	2	A70073	hypothetical prote
639	24	80.0	381	2	T34015	hypothetical prote
640	24	80.0	382	2	T34127	hypothetical prote
641	24	80.0	383	2	E70156	lipopolysaccharide
642	24	80.0	387	2	G90359	conserved hypotet
643	24	80.0	389	2	D40785	hypothetical 46k p
644	24	80.0	397	2	UQ1030	beta-N-acetylgluco
645	24	80.0	398	1	S11336	glutamyL-tRNA redu
646	24	80.0	398	2	C84780	hypothetical prote
647	24	80.0	398	2	T47967	hypothetical prote
648	24	80.0	399	2	A33396	beta-N-acetylgluco
649	24	80.0	399	2	T21015	hypothetical prote
650	24	80.0	402	2	A72332	hypothetical prote
651	24	80.0	402	2	A72303	hypothetical prote
652	24	80.0	402	2	C72205	hypothetical prote
653	24	80.0	402	2	C72226	hypothetical prote
654	24	80.0	402	2	S05018	beta-N-acetylgluco
655	24	80.0	404	2	S66533	flavoprotein A - M
656	24	80.0	405	2	D72426	hypothetical prote
657	24	80.0	406	2	A36706	transcription acti
658	24	80.0	407	2	C64250	tyrosine-tRNA liga
659	24	80.0	408	2	T47585	hypothetical prote
660	24	80.0	408	2	T23285	hypothetical prote
661	24	80.0	411	2	AF1352	probable phosphoe
662	24	80.0	412	2	S23208	mRNA maturase b12
663	24	80.0	421	2	T44789	glutamate dehydrog
664	24	80.0	423	1	MRBY	mRNA maturase b13
665	24	80.0	423	1	C64927	probable membrane
666	24	80.0	423	2	S78662	mRNA maturase SCBI
667	24	80.0	423	2	F90928	probable amino aci
668	24	80.0	426	2	B85777	probable amino aci
669	24	80.0	426	2	H82239	conserved hypotet
670	24	80.0	433	2	C64917	terminator region
671	24	80.0	433	2	H85766	hypothetical prote
672	24	80.0	433	2	C90918	sensor histidine p
673	24	80.0	437	2	A64488	transposase (24) B
674	24	80.0	438	2	B84148	hypothetical prote
675	24	80.0	443	2	E71135	hypothetical prote
676	24	80.0	443	2	H84414	hypothetical prote
677	24	80.0	453	2	C86176	hypothetical prote
678	24	80.0	453	2	S57140	probable membrane
679	24	80.0	457	2	E96772	hypothetical prote
680	24	80.0	459	2	H85031	probable glycosylt
681	24	80.0	460	2	G85686	sensor protein Pho
682	24	80.0	460	2	T48061	alpha galactosyltr
683	24	80.0	461	2	T01300	hypothetical prote
684	24	80.0	463	2	AE1112	phospho-beta-gluc
685	24	80.0	463	2	AI1473	phospho-beta-gluc
686	24	80.0	463	2	E64685	fumarate hydratase

687	24	80.0	463	2	H71830	760	24	80.0	564	2	H75403	glycosyl hydrolase
688	24	80.0	467	2	S36559	761	24	80.0	570	2	A45249	alpha-glucosidase
689	24	80.0	468	2	S44815	762	24	80.0	587	2	S42358	alpha-glucosidase
690	24	80.0	469	2	AE3353	763	24	80.0	593	2	G71301	hypothetical prote
691	24	80.0	472	2	AE4576	764	24	80.0	597	2	UC7615	alpha-glucosidase
692	24	80.0	477	1	P2WLEP	765	24	80.0	603	2	JC1282	insulin-like growt
693	24	80.0	482	2	AB1421	766	24	80.0	605	2	AF1917	hypothetical prote
694	24	80.0	484	2	AD0199	767	24	80.0	605	2	AI2535	hypothetical prote
695	24	80.0	484	2	TI9300	768	24	80.0	609	2	S28283	hypothetical prote
696	24	80.0	486	1	B41966	769	24	80.0	620	2	B64379	hypothetical prote
697	24	80.0	486	1	A99829	770	24	80.0	626	2	E84432	hypothetical prote
698	24	80.0	487	1	VZE8PT	771	24	80.0	633	2	TI14612	hypothetical prote
699	24	80.0	487	2	AG0646	772	24	80.0	638	2	I139196	amiloride sensitiv
700	24	80.0	492	2	TP3349	773	24	80.0	642	2	E70683	probable helix-tur
701	24	80.0	493	1	P2WUDP	774	24	80.0	656	2	G85731	Rhs element associ
702	24	80.0	494	2	S36341	775	24	80.0	659	2	S20313	peroxisomal membra
703	24	80.0	495	2	TI24849	776	24	80.0	659	2	A35723	probable cellulose
704	24	80.0	498	2	S55362	777	24	80.0	664	2	A95889	hypothetical prote
705	24	80.0	507	2	S52469	778	24	80.0	666	2	H96723	endo-1,4-beta-mann
706	24	80.0	509	2	JO0535	779	24	80.0	669	2	D72278	collagen alpha 1(X
707	24	80.0	509	2	A55204	780	24	80.0	674	2	S23297	collagen alpha 1(X
708	24	80.0	510	2	A53802	781	24	80.0	680	1	CGHUID	collagen alpha 1(X
709	24	80.0	513	2	F86320	782	24	80.0	680	2	S31216	hypothetical prote
710	24	80.0	517	2	JC5875	783	24	80.0	683	2	A83674	excinuclease Abc s
711	24	80.0	520	2	G87343	784	24	80.0	698	2	E87082	probable uvrb prot
712	24	80.0	520	2	C71689	785	24	80.0	698	2	G70559	hypothetical prote
713	24	80.0	521	2	BE4181	786	24	80.0	715	2	E71073	hypothetical prote
714	24	80.0	522	2	S07253	787	24	80.0	725	2	G90555	vcbb-like (higell)
715	24	80.0	522	2	AH0591	788	24	80.0	741	2	T24768	sex-specific stora
716	24	80.0	522	2	F97756	789	24	80.0	747	2	S01918	basic juvenile hor
717	24	80.0	523	2	H90724	790	24	80.0	748	2	B45046	endopeptidase La (
718	24	80.0	523	2	DE4809	791	24	80.0	779	2	E97778	hypothetical prote
719	24	80.0	523	2	A85576	792	24	80.0	779	2	TI31732	hypothetical prote
720	24	80.0	529	2	JE0181	793	24	80.0	784	1	A71704	endopeptidase La (
721	24	80.0	529	2	AF3059	794	24	80.0	788	1	T25051	hypothetical prote
722	24	80.0	529	2	B98227	795	24	80.0	789	1	QAB132	gene cox1 intron 2
723	24	80.0	530	2	H82405	796	24	80.0	795	2	JC4234	gene fused protein
724	24	80.0	533	2	S36477	797	24	80.0	846	1	PNECA	penicillin amidase
725	24	80.0	533	2	S36594	798	24	80.0	854	1	S78644	gene cox1 intron 2
726	24	80.0	535	2	CE5040	799	24	80.0	865	2	T41909	hypothetical prote
727	24	80.0	535	2	F97910	800	24	80.0	867	2	D87320	hypothetical prote
728	24	80.0	536	2	A37231	801	24	80.0	925	2	T00781	probable alpha-gam
729	24	80.0	537	2	S39970	802	24	80.0	932	2	S65214	sasp protein - Cam
730	24	80.0	541	2	B95220	803	24	80.0	936	2	I40711	hypothetical prote
731	24	80.0	541	2	H80893	804	24	80.0	948	2	E82206	DnaK-related prote
732	24	80.0	541	2	B82149	805	24	80.0	953	2	T01093	lumidependens pr
733	24	80.0	546	2	DB9813	806	24	80.0	959	2	T25704	hypothetical prote
734	24	80.0	546	2	S56306	807	24	80.0	1012	2	TI24384	hypothetical prote
735	24	80.0	548	2	AF1231	808	24	80.0	1060	2	S06286	major merozoite su
736	24	80.0	548	2	AE1585	809	24	80.0	1086	2	S16752	major merozoite su
737	24	80.0	550	2	AE1058	810	24	80.0	1101	2	T20881	hypothetical prote
738	24	80.0	551	2	S56465	811	24	80.0	1136	2	T40355	hypothetical prote
739	24	80.0	551	2	H86121	812	24	80.0	1146	1	I64112	transcription/repa
740	24	80.0	551	2	H91280	813	24	80.0	1148	2	D83270	transcription-repa
741	24	80.0	551	2	P70684	814	24	80.0	1152	2	H86466	protein Ty1/copia-
742	24	80.0	552	2	P96769	815	24	80.0	1194	2	T03818	apoptotic proteina
743	24	80.0	553	2	AI1097	816	24	80.0	1216	2	A55620	apical endosomal p
744	24	80.0	553	2	AI1460	817	24	80.0	1315	2	T03167	hypothetical prote
745	24	80.0	553	2	AG3604	818	24	80.0	1322	2	H86196	hypothetical prote
746	24	80.0	553	2	H64494	819	24	80.0	1346	2	TI14849	cytochrome plink
747	24	80.0	554	2	H70011	820	24	80.0	1400	2	E90886	Rhs core protein
748	24	80.0	555	2	AH0449	821	24	80.0	1423	1	I37275	death-associated p
749	24	80.0	557	2	S77969	822	24	80.0	1485	2	S23756	CFPR protein - Afr
750	24	80.0	558	2	S13579	823	24	80.0	1489	2	G71406	probable retroviri
751	24	80.0	559	2	H83758	824	24	80.0	1701	2	A26868	major merozoite su
752	24	80.0	559	2	D83413	825	24	80.0	1701	2	A54498	major merozoite su
753	24	80.0	561	2	H69755	826	24	80.0	1726	1	SA2QGM	major merozoite su
754	24	80.0	561	2	B69725	827	24	80.0	1766	2	A45948	major merozoite su
755	24	80.0	561	2	D70034	828	24	80.0	5376	2	T42215	zonadhesin - mouse
756	24	80.0	561	2	G84012	829	23	76.7	44	2	AH1966	photovscem I 4.8K
757	24	80.0	561	2	CE4239	830	23	76.7	53	2	S61953	NCE1 protein - yea
758	24	80.0	562	2	A41707	831	23	76.7	77	2	S46465	Ig heavy chain V r
759	24	80.0	562	2	CE8263	832	23	76.7	80	2	T00184	hypothetical prote

833	23	76.7	82	2	G69987	hypothetical prote
834	23	76.7	83	2	E98230	exopolysaccharide
835	23	76.7	90	2	S24218	Ig kappa chain - m
836	23	76.7	90	2	D86690	hypothetical prote
837	23	76.7	91	1	MSML1	E5a protein - huma
838	23	76.7	91	2	A61055	E5a protein - huma
839	23	76.7	92	2	AH3055	exopolysaccharide
840	23	76.7	96	2	S78244	ribosomal protein
841	23	76.7	98	2	S26910	Ig heavy chain V r
842	23	76.7	98	2	S26909	Ig heavy chain V r
843	23	76.7	98	2	S26912	Ig heavy chain V r
844	23	76.7	98	2	S26938	Ig heavy chain V r
845	23	76.7	98	2	G47624	Ig heavy chain V-V
846	23	76.7	98	2	B95397	Ig heavy chain V-V
847	23	76.7	105	2	PH0978	protein [imported
848	23	76.7	107	2	S26320	Ig heavy chain V r
849	23	76.7	107	2	C72620	hypothetical prote
850	23	76.7	109	2	PH1668	Ig heavy chain V r
851	23	76.7	110	2	PH1669	Ig heavy chain V r
852	23	76.7	110	2	PH1000	Ig heavy chain V r
853	23	76.7	111	2	PS0074	Ig kappa chain V r
854	23	76.7	112	2	S37203	Ig kappa chain V r
855	23	76.7	113	2	E30560	Ig kappa chain V r
856	23	76.7	113	2	H30560	Ig kappa chain V r
857	23	76.7	114	2	PL0202	anti-DNA autoantib
858	23	76.7	114	2	S45800	probable membrane
859	23	76.7	114	2	T49634	dachshund isoform
860	23	76.7	116	2	S15672	Ig heavy chain V r
861	23	76.7	117	1	HYHU35	Ig heavy chain pre
862	23	76.7	117	2	S18551	Ig heavy chain V r
863	23	76.7	117	2	E33989	Ig heavy chain V-5
864	23	76.7	118	2	S36265	Ig heavy chain V r
865	23	76.7	121	2	S20783	Ig heavy chain V r
866	23	76.7	125	2	AD1817	hypothetical prote
867	23	76.7	127	2	A82324	hypothetical prote
868	23	76.7	129	2	S46393	Ig heavy chain V r
869	23	76.7	131	2	S08328	Ig heavy chain V r
870	23	76.7	132	2	B25912	Ig kappa chain pre
871	23	76.7	132	2	B24574	T-cell receptor ga
872	23	76.7	134	2	C81853	probable transposa
873	23	76.7	135	2	S49530	anti-Sm antibody V
874	23	76.7	136	1	RWHUGV	T-cell receptor ga
875	23	76.7	136	2	A31933	Ig heavy chain pre
876	23	76.7	137	2	C41287	Ig heavy chain pre
877	23	76.7	145	2	S06307	T-cell receptor ga
878	23	76.7	145	2	T34230	hypothetical prote
879	23	76.7	146	2	C64636	hypothetical prote
880	23	76.7	146	2	T02395	hypothetical prote
881	23	76.7	146	2	T33016	hypothetical prote
882	23	76.7	147	2	H82313	hypothetical prote
883	23	76.7	150	2	F69714	spore formation pr
884	23	76.7	150	2	G96906	hypothetical prote
885	23	76.7	151	2	E82011	probable transposa
886	23	76.7	151	2	D82030	probable IS1016 tr
887	23	76.7	151	2	F81986	probable transposa
888	23	76.7	151	2	D81818	insertion element
889	23	76.7	158	2	T09639	NMDH2 dehydrogenas
890	23	76.7	160	2	T07180	hypothetical prote
891	23	76.7	161	2	AE0981	probable acetyltera
892	23	76.7	173	2	A57049	hypothetical prote
893	23	76.7	177	2	A12177	hypothetical prote
894	23	76.7	178	2	A71512	hypothetical prote
895	23	76.7	191	2	F63251	probable acetyltera
896	23	76.7	193	2	G97238	uncharacterized me
897	23	76.7	196	2	T01982	tumor related prot
898	23	76.7	200	2	A61287	hypothetical prote
899	23	76.7	201	2	A10928	probable phage tai
900	23	76.7	201	2	A11035	probable phage tai
901	23	76.7	202	2	D87019	cytochrome-c oxida
902	23	76.7	203	2	B70784	cytochrome-c oxida
903	23	76.7	203	2	T20750	hypothetical prote
904	23	76.7	206	2	T35533	cytochrome-c oxida
905	23	76.7	206	2	AC2443	ototate phosphorib
906	23	76.7	206	2	T24037	hypothetical prote
907	23	76.7	212	2	S49807	hypothetical prote
908	23	76.7	212	2	A98328	hypothetical prote
909	23	76.7	213	2	AD2955	conserved hypotet
910	23	76.7	214	2	A90028	ureases accessory p
911	23	76.7	214	2	AC2022	hypothetical prote
912	23	76.7	219	2	A71879	hypothetical prote
913	23	76.7	223	2	S39688	ywcC protein - Bac
914	23	76.7	226	2	T38109	exoglucanase (EC 3
915	23	76.7	226	2	H90233	dUDP-4-dehydrotham
916	23	76.7	227	2	F36793	hypothetical prote
917	23	76.7	227	2	H82344	rIBT protein VC025
918	23	76.7	233	2	C90427	p33 specific singl
919	23	76.7	233	2	C90427	hypothetical prote
920	23	76.7	233	2	A71336	hypothetical prote
921	23	76.7	258	2	T56220	tyrase 2 - rat
922	23	76.7	260	2	B83713	dehydrogenase/redu
923	23	76.7	261	2	T22623	hypothetical prote
924	23	76.7	261	2	E72735	hypothetical prote
925	23	76.7	264	2	A81668	conserved hypotet
926	23	76.7	264	2	E71509	hypothetical prote
927	23	76.7	265	2	S40209	tubulin gamma chai
928	23	76.7	266	2	H71521	probable metal dep
929	23	76.7	268	2	F85756	hypothetical prote
930	23	76.7	268	2	C90862	hypothetical prote
931	23	76.7	268	2	E64877	peptide transport
932	23	76.7	268	2	S39589	peptide transport
933	23	76.7	268	2	AG0656	peptide transport
934	23	76.7	286	2	A42659	aerotype specific
935	23	76.7	286	2	S16969	O-antigen - Vibrio
936	23	76.7	288	2	S29690	Ig heavy chain VDJ
937	23	76.7	291	2	S22041	hypothetical prote
938	23	76.7	291	2	G81407	glycine N-methyltr
939	23	76.7	293	1	S00112	glycine N-methyltr
940	23	76.7	295	1	S42627	glycine N-methyltr
941	23	76.7	300	2	T10312	hypothetical prote
942	23	76.7	304	2	S04663	T-cell receptor ga
943	23	76.7	305	2	D97169	uncharacterized pr
944	23	76.7	306	2	B83705	ABC transporter (A
945	23	76.7	309	2	T27426	hypothetical prote
946	23	76.7	313	2	A36060	alpha-casein precu
947	23	76.7	316	1	WZB841	gene 41 protein -
948	23	76.7	317	2	B95113	competence protein
949	23	76.7	317	2	E86264	protein F3F19.7 [i
950	23	76.7	317	2	A97982	competence protein
951	23	76.7	320	2	T48408	hypothetical prote
952	23	76.7	320	2	A95872	hypothetical prote
953	23	76.7	323	2	S01895	T-cell receptor ga
954	23	76.7	328	2	C70075	penicillin amidase
955	23	76.7	332	2	T23307	hypothetical prote
956	23	76.7	333	2	H71703	hypothetical prote
957	23	76.7	334	2	T16708	probable threonine
958	23	76.7	334	2	T01789	hypothetical prote
959	23	76.7	334	2	U01789	Salp14R protein -
960	23	76.7	334	2	H42522	ASIR protein - vac
961	23	76.7	334	2	S46845	JSR protein - vari
962	23	76.7	334	2	T28596	27R protein - vari
963	23	76.7	335	2	B72171	KSR protein - vari
964	23	76.7	337	2	S50442	probable exported
965	23	76.7	338	2	T15263	hypothetical prote
966	23	76.7	340	2	AH0940	probable ABC trans
967	23	76.7	340	2	C90894	probable LACI-type
968	23	76.7	340	2	F85723	probable LACI-type
969	23	76.7	340	2	G64905	sugar-binding prot
970	23	76.7	343	2	D97778	threonine ammonta-
971	23	76.7	343	2	F95915	threonine sugar ABC
972	23	76.7	344	2	B85838	probable fibrinai
973	23	76.7	344	2	B90993	probable type-1 fi
974	23	76.7	344	2	C64978	hypothetical 36.9
975	23	76.7	345	2	C71046	hypothetical prote
976	23	76.7	346	2	T16074	hypothetical prote
977	23	76.7	346	2	A70144	hypothetical prote
978	23	76.7	349	2	A75169	probable iron (III

979 23 76.7 352 1 XYEBOT
980 23 76.7 353 2 AG0789
981 23 76.7 353 2 UA0123
982 23 76.7 353 2 A45859
983 23 76.7 354 2 AC0932
984 23 76.7 354 2 F66091
985 23 76.7 354 2 H65206
986 23 76.7 354 2 H91243
987 23 76.7 354 2 T18409
988 23 76.7 355 2 C66592
989 23 76.7 355 2 B72032
990 23 76.7 357 2 G84955
991 23 76.7 358 2 T22823
992 23 76.7 360 2 H97703
993 23 76.7 360 2 E71710
994 23 76.7 360 2 T27196
995 23 76.7 360 2 T27324
996 23 76.7 362 2 T52652
997 23 76.7 362 2 AB0135
998 23 76.7 363 2 T18100
999 23 76.7 368 2 F83785
1000 23 76.7 380 2 H81152

ALIGNMENTS

RESULT 1

S26466 Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C:Accession: S26466

R:Kavaler, J. submitted to the EMBL Data Library, April 1991

A:Reference number: S26459

A:Accession: S26466

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-104 <KAV>

A:Cross-references: UNIPARC:UPI0000115F6A; EMBL:X59116; NID:G51933; PIDN:CAA41842.1; PID

A:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:3-86/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 30; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 SYTH 5
Db 19 SYTH 23

RESULT 2

E71120 hypothetical protein PH0732 - Pyrococcus horikoshii

C:Species: Pyrococcus horikoshii

C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004

C:Accession: E71120

R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Hatahara, Y.; Hino, Y.; Yamamoto, S.; Sekit

M.; Ohnuki, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi

DNA Res. 5, 55-76, 1998

A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a

A:Reference number: A11000; MUID:98344137; PMID:9679194

A:Accession: E71120

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-104 <KAV>

A:Cross-references: UNIPROT:O58463; UNIPARC:UPI0000062BEC; GB:AP000003; NID:G3236130; PI

A:Experimental source: strain 073

A:Note: this accession replaces an interim accession for a sequence replaced by GenBank

A:Gene: PH0732

Query Match 100.0%; Score 30; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 SYTH 5
Db 67 SYTH 71

RESULT 3

S26473 Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C:Accession: S26473

R:Kavaler, J. submitted to the EMBL Data Library, April 1991

A:Reference number: S26459

A:Accession: S26473

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-112 <KAV>

A:Cross-references: UNIPARC:UPI0000115F65; EMBL:X59111; NID:G51955; PIDN:CAA41837.1; PID

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 30; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 SYTH 5
Db 31 SYTH 35

RESULT 4

H30338 DNA transport machinery protein comG - Bacillus subtilis

N:Alternate names: comG operon protein 7

C:Species: Bacillus subtilis

C:Date: 27-Feb-1990 #sequence_revision 27-Feb-1990 #text_change 31-Dec-2004

C:Accession: H30338; H69603

R:Albano, M.; Breitling, R.; Dubnau, D.A.

J. Bacteriol. 171, 5386-5404, 1989

A:Title: Nucleotide sequence and genetic organization of the Bacillus subtilis comG oper

A:Reference number: A30338; MUID:90008773; PMID:2507524

A:Accession: H30338

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-124 <AUB>

A:Cross-references: UNIPROT:P25959; UNIPARC:UPI000006070B; GB:M29691; GB:M22854; NID:G111

R:Kunst, F.; Ogasawara, N.; Moser, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertier

C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi

A.; Ehrlich, S.D.; Emmerston, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallert

lechy, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holtsappel, S.; Hosono, S.; Hullo, M.F.

Koester, P.; Konigsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,

A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel,

Y. M.; Ogawa, K.; Ogilwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetel,

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,

A:Authors: Schleich, S.; Schroeter, R.; Scottone, F.; Sekiguchi, J.; Sekowska, A.; Serot,

Akenuchi, M.; Tamakoshi, A.; Tanaka, T.; Terstila, P.; Tognoni, A.; Tosato, V.; Uchiyama,

T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K

A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.

A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A:Reference number: A69580; MUID:98044033; PMID:9384377

A:Accession: H69603

A:Status: nucleic acid sequence not shown; translation not shown

A;Residues: 1-124 <KUN>
 A;Cross-references: UNIPARC:UPI000006070B; GB:Z59116; GB:AL009126; NID:92634723; PIDN:CA
 A;Experimental source: strain 168
 C;Genetics:
 A;Gene: comCG

Query Match 100.0%; Score 30; DB 2; Length 124;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYTH 5
 |||||
 Db 80 SYTH 84

RESULT 5

S58121
 Ig heavy chain V region precursor - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 21-Jan-2000
 C;Accession: S58121
 R;Keywords: R
 submitted to the EMBL Data Library, July 1995
 A;Reference number: S58121
 A;Accession: S58121
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-126 <KUB>
 A;Cross-references: UNIPARC:UPI00001137B1; EMBL:X89595; NID:9929650; PIDN:CAA61756.1; PI
 C;Genetics:
 A;Intons: 9/1
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;27-110/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 30; DB 2; Length 126;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYTH 5
 |||||
 Db 43 SYTH 47

RESULT 6

S22591
 hypothetical protein C2 - tomato yellow leaf curl virus
 C;Species: tomato yellow leaf curl virus
 C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
 C;Accession: S22591
 R;Keywords: Pour, A.; Bendahmane, M.; Matveit, V.; Accotto, G.P.; Crespi, S.; Gronenborn, B.
 Nucleic Acids Res. 19, 6763-6769, 1991
 A;Title: tomato yellow leaf curl virus from Sardinia is a whitefly-transmitted monopartit
 A;Reference number: S22588; MUID:92107660; PMID:1840676
 A;Accession: S22591
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-135 <KHE>
 A;Cross-references: UNIPROT:P27263; UNIPARC:UPI00001380E1; EMBL:X61153; NID:962211; PIDN
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1991
 C;Superfamily: tomato golden mosaic virus AL2 protein

Query Match 100.0%; Score 30; DB 2; Length 135;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYTH 5
 |||||
 Db 40 SYTH 44

RESULT 7

S39212

gene C2 protein - tomato yellow leaf curl virus
 C;Species: tomato yellow leaf curl virus
 C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
 C;Accession: S39212
 R;Noris, E.; Hidalgo, E.; Accotto, G.; Moriones, E.
 submitted to the EMBL Data Library, August 1993
 A;Description: High similarity among the tomato yellow leaf curl virus isolates from the
 A;Reference number: S39209
 A;Accession: S39212
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-135 <NOR>
 A;Cross-references: UNIPROT:P38610; UNIPARC:UPI00001380E2; EMBL:Z25751; NID:9433655; PID
 C;Superfamily: tomato golden mosaic virus AL2 protein

Query Match 100.0%; Score 30; DB 2; Length 135;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYTH 5
 |||||
 Db 40 SYTH 44

RESULT 8

S39236
 gene C2 protein - tomato yellow leaf curl virus
 C;Species: tomato yellow leaf curl virus
 C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
 C;Accession: S39236
 R;Crespi, S.; Noris, E.; Valira, A.; Bosco, D.; Accotto, G.
 submitted to the EMBL Data Library, December 1993
 A;Description: A cloned DNA from a TYLCV isolate from Sicily showing low infectivity.
 A;Reference number: S39233
 A;Accession: S39236
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-135 <CRE>
 A;Cross-references: UNIPROT:Q88950; UNIPARC:UPI00001786FF; EMBL:Z28390; NID:91041671; PI
 C;Superfamily: tomato golden mosaic virus AL2 protein

Query Match 100.0%; Score 30; DB 2; Length 135;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYTH 5
 |||||
 Db 40 SYTH 44

RESULT 9

S21810
 Ig heavy chain V region - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
 C;Accession: S21810
 R;Ostermeyer, M.; Brack, C.H.; Trannecker, A.; Koehler, G.
 submitted to the EMBL Data Library, January 1991
 A;Description: Nucleotide sequence of a rearranged VDJ-region of a mouse Ig mu heavy cha
 A;Reference number: S21810
 A;Accession: S21810
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-138 <OST>
 A;Cross-references: UNIPARC:UPI0000115ED6; EMBL:X56936; NID:954163; PIDN:CAA40257.1; PID
 C;Genetics:
 A;Intons: 15/3
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 30; DB 2; Length 138;
 Best Local Similarity 100.0%; Pred. No. 24;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SYTH 5
 |||||
 Db 50 SYTH 54

RESULT 10

T02684 hypothetical protein F10A3.11 - *Caenorhabditis elegans*

C/Species: *Caenorhabditis elegans*

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C/Accession: T02684

R/Lloyd, C.

submitted to the EMBL Data Library, March 1997

A/Reference number: Z19309

A/Accession: T20684

A/Status: preliminary; translated from GB/EMBL/DDBJ

A/Molecule type: DNA

A/Residues: 1-284 <MTL>

A/Cross-references: UNIPROT:O45342; UNIPARC:UPI00000749C8; EMBL:Z92829; PIDD:CA807347.1;

A/Experimental source: clone F10A3

C/Genetics:

A/Gene: CESP:F10A3.11

A/Map position: 5

A/Introns: 56/3; 85/3; 186/1; 260/2

Query Match 100.0%; Score 30; DB 2; Length 284;

Best Local Similarity 100.0%; Pred. No. 49;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
 |||||

Db 58 SYTH 62

RESULT 11

T40353 probable ribosomal protein - fission yeast (*Schizosaccharomyces pombe*)

C/Species: *Schizosaccharomyces pombe*

C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C/Accession: T40353

R/Wood, V.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.

submitted to the EMBL Data Library, March 1997

A/Reference number: Z21922

A/Accession: T40353

A/Status: preliminary; translated from GB/EMBL/DDBJ

A/Molecule type: DNA

A/Residues: 1-126 <MOO>

A/Cross-references: UNIPROT:O43042; UNIPARC:UPI0000069941; EMBL:AL022070; PIDD:CAA17794.

A/Experimental source: strain 972h-; cosmid c3B9

C/Genetics:

A/Gene: SPDB:SPBC3B9.14C

A/Map position: 2

A/Introns: 188/3; 275/3

Query Match 100.0%; Score 30; DB 2; Length 326;

Best Local Similarity 100.0%; Pred. No. 56;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
 |||||

Db 283 SYTH 287

RESULT 12

T02462

probable AR-hook DNA-binding protein [imported] - *Arabidopsis thaliana*

N/Alternate names: DNA-binding protein homolog F4118.17

C/Species: *Arabidopsis thaliana* (mouse-ear cress)

C/Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 05-Oct-2004

C/Accession: T02462; F84895

R/Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul

submitted to the EMBL Data Library, August 1998

A/Description: *Arabidopsis thaliana* chromosome II BAC F4118 genomic sequence.

A/Reference number: Z14674

A/Accession: T02462

A/Status: translated from GB/EMBL/DDBJ

A/Molecule type: DNA

A/Residues: 1-348 <ROU>

A/Cross-references: UNIPROT:O80834; UNIPARC:UPI00000A2F18; EMBL:AC004665; NID:g3386593; I

A/Experimental source: cultivar Columbia

R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shee, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J

Nature 402, 761-768, 1999

A/Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.

A/Reference number: A84420; MUID:20083487; PMID:10617197

A/Accession: F84895

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-348 <STO>

A/Cross-references: UNIPARC:UPI00000A2F18; GB:AE002093; NID:g3386609; PIDD:AA028539.1; G

C/Genetics:

A/Gene: F4118.17; At2g45850

A/Map position: 2

A/Introns: 151/1; 173/3; 217/3; 271/3

C/Superfamily: DNA-binding protein PDI

Query Match 100.0%; Score 30; DB 2; Length 348;

Best Local Similarity 100.0%; Pred. No. 60;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
 |||||

Db 14 SYTH 18

RESULT 13

S60948 MCT1 protein - yeast (*Saccharomyces cerevisiae*)

N/Alternate names: protein O5058; protein YOR522c; protein YOR50-11

C/Species: *Saccharomyces cerevisiae*

C/Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004

C/Accession: S60948; S67114; S71723

R/Gallison, F.; Dujon, B.

submitted to the EMBL Data Library, October 1995

A/Description: Sequence and analysis of a 33 kb fragment from the right arm of chromosome

A/Reference number: S60938

A/Accession: S60948

A/Molecule type: DNA

A/Residues: 1-384 <GAL>

A/Cross-references: UNIPROT:Q12283; UNIPARC:UPI000006A526; EMBL:X92441; NID:g1050762; P

R/Boyer, J.; Fairhead, C.; Gallion, L.; Gallison, F.; Michaux, G.; Thierry, A.; Dujon, B

submitted to the Protein Sequence Database, July 1996

A/Reference number: S67104

A/Accession: S67114

A/Molecule type: DNA

A/Residues: 1-384 <BOY>

A/Cross-references: UNIPARC:UPI000006A526; EMBL:Z75129; NID:g1420511; PIDD:e252086; PIDD:g1

R/Gallison, F.; Dujon, B.

Yeast 12, 877-885, 1996

A/Title: Sequence and analysis of a 33 kb fragment from the right arm of chromosome XV of

A/Reference number: S71713; MUID:96437977; PMID:8840505

A/Accession: S71723

A/Status: nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-384 <GAM>

A/Cross-references: UNIPARC:UPI000006A526; EMBL:X92441; NID:g1050762; PIDD:CAA63184.1; P

A/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1995

C/Genetics:

A/Gene: SGD:MCT1; MCT1

A/Cross-references: SGD:S0005747

A/Map position: 15R

A/Introns: 32/1

Query Match 100.0%; Score 30; DB 2; Length 384;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTYH 5
|||||
Db 303 SYTYH 307

RESULT 14

T39539
alpha-amylase homolog - fission yeast (Schizosaccharomyces pombe)

C/Species: Schizosaccharomyces pombe
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C/Accession: T39539
R/Wood, V., Rajandream, M.A.; Barrell, B.G.; Beck, A.; Reinhardt, R.
submitted to the EMBL Data Library, February 1998

A/Reference number: 221862

A/Accession: T39539

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-774 <MO>

A/Cross-references: UNIPROT:O42918; UNIPARC:UPI0000125A55; EMBL:AL021748; PIDN:CAA16864.

A/Experimental source: strain 972h-; cosmid c16A3

C/Genetics:

A/Gene: SPDB:SPBC16A3.13

A/Map position: 2

Query Match 100.0%; Score 30; DB 2; Length 774;
Best Local Similarity 100.0%; Pred. No. 1,4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTYH 5
|||||
Db 668 SYTYH 672

RESULT 15

PQ0864
hypothetical protein 937 - citrus tatter leaf virus (fragment)

N/Alternate names: ORF1

C/Species: citrus tatter leaf virus

C/Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004

C/Accession: PQ0864

R/Yoshikawa, N.; Imaizumi, M.; Takahashi, T.; Inouye, N.

J. Gen. Virol. 74, 2743-2747, 1993

A/Title: Striking similarities between the nucleotide sequence and genome organization of

A/Reference number: PQ0864; PMID:8277280

A/Accession: PQ0864

A/Molecule type: hrNA

A/Residues: 1-937 <YOS>

A/Cross-references: UNIPROT:Q9YPI2; UNIPARC:UPI00000F95EB; DDBJ:D16368; NID:9464150; PID

A/Experimental source: strain Li-23

C/Superfamily: eggplant mosaic virus RNA-directed RNA polymerase

C/Keywords: ATP

Query Match 100.0%; Score 30; DB 2; Length 937;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTYH 5
|||||
Db 165 SYTYH 169

RESULT 16

A44059
genome polyprotein - apple stem grooving virus (strain P-209)

N/Alternate names: RNA nucleotidyltransferase (RNA-directed); RNA replicase

N/Contains: RNA-directed RNA polymerase (EC 2.7.7.48)

C/Species: apple stem grooving virus, ASGV

C/Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004

C/Accession: A44059
R/Yoshikawa, N.; Sasaki, E.; Kato, M.; Takahashi, T.

Virol. 191, 98-105, 1992

A/Title: The nucleotide sequence of apple stem grooving capillorvirus genome.

A/Reference number: A44059; PMID:1413530

A/Accession: A44059

A/Molecule type: genomic RNA

A/Residues: 1-2105 <YOS>

A/Cross-references: UNIPROT:P36309; UNIPARC:UPI000131EA4; GB:D14995; NID:9303496; PIDN:1

C/Superfamily: eggplant mosaic virus RNA-directed RNA polymerase

C/Keywords: ATP; nucleotide binding; nucleotidyltransferase; P-loop; RNA biosynthesis; R

F/781-788/Region: nucleotide-binding motif A (P-loop)

F/843-848/Region: nucleotide-binding motif B

F/787/Binding site: ATP (lys) #status predicted

Query Match 100.0%; Score 30; DB 1; Length 2105;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTYH 5
|||||
Db 1333 SYTYH 1337

RESULT 17

S24663
Ig heavy chain V region - horn shark

C/Species: Heterodontus francisci (horn shark)

C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Jan-2000

C/Accession: S24663

R/Litman, G.

submitted to the EMBL Data Library, March 1992

A/Reference number: S24653

A/Accession: S24663

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-115 <LIT>

A/Cross-references: UNIPARC:UPI0001163D5; EMBL:Z11790; NID:964006; PIDN:CAA77833.1; PID

C/Superfamily: immunoglobulin V region; immunoglobulin homology

F/15-96/Domain: immunoglobulin homology <IMV>

Query Match 96.7%; Score 29; DB 2; Length 115;
Best Local Similarity 80.0%; Pred. No. 32;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTYH 5
|||||
Db 31 SYTYH 35

RESULT 18

J02328
AL2 protein - Indian cassava mosaic virus

C/Species: Indian cassava mosaic virus

C/Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004

C/Accession: J02328; S35884

R/Hong, Y.G.; Robinson, D.J.; Harrison, B.D.

J. Gen. Virol. 74, 2437-2443, 1993

A/Title: Nucleotide sequence evidence for the occurrence of three distinct whitefly-trans

A/Reference number: J02326; PMID:9405670; PMID:8245859

A/Accession: J02328

A/Molecule type: DNA

A/Residues: 1-135 <HON>

A/Cross-references: UNIPROT:Q08589; UNIPARC:UPI0001380DE; EMBL:Z24758; NID:9395351; PID

C/Superfamily: tomato golden mosaic virus AL2 protein

Query Match 96.7%; Score 29; DB 2; Length 135;
Best Local Similarity 80.0%; Pred. No. 38;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTYH 5
|||||
Db 40 SYTYH 44

```
RESULT 19
C83748
hypothetical protein BH0787 [imported] - Bacillus halodurans (strain C-125)
C/Species: Bacillus halodurans
C/Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C/Accession: C83748
R/Takam, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hirai
Nucleic Acids Res. 28, 4317-4331, 2000
A/Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A/Reference number: A83650; MUID:20512582; PMID:11058132
A/Accession: C83748
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-204 <STO>
A/Cross-references: UNIPROT:Q9KER2; UNIPARC:UPI00000C39B5; GB:AP001509; GB:BA000004; NIT
C/Genetics:
A/Experimental source: strain C-125
C/Map position:
A/Status: preliminary
C/Superfamily: Bacillus subtilis conserved hypothetical protein yestl

Query Match          96.7%; Score 29; DB 2; Length 204;
Best Local Similarity 80.0%; Pred. No. 57;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
Db 129 SYTH 133

RESULT 20
T29851
hypothetical protein C49C8.2 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Dec-2004
C/Accession: T29851
R/Johnson, D.; Bradshaw, H.
Submitted to the EMBL Data Library, June 1996
A/Description: The sequence of C. elegans cosmid C49C8.
A/Reference number: Z20698
A/Accession: T29851
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-383 <JOH>
A/Cross-references: UNIPROT:Q18706; UNIPARC:UPI000007EF94; EMBL:U61945; PIDD:AA03127.1;
A/Experimental source: strain Bristol NZ; clone C49C8
C/Genetics:
A/Gene: CESP:C49C8.2
A/Map position: 4
A/Introns: 45/1; 171/3; 232/1

Query Match          96.7%; Score 29; DB 2; Length 383;
Best Local Similarity 80.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
Db 281 SYTH 285

RESULT 21
T30067
hypothetical protein C12D5.8 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C/Accession: T30067
R/Miller, N.; Stellyes, L.; Bradshaw, H.
Submitted to the EMBL Data Library, April 1996
A/Description: The sequence of C. elegans cosmid C12D5.
A/Reference number: Z20729
A/Accession: T30067
A/Status: preliminary; translated from GB/EMBL/DBJ
```

```
A/Molecule type: DNA
A/Residues: 1-577 <MTL>
A/Cross-references: UNIPARC:UPI000017B775; EMBL:U55365; PIDD:AA98572.1; GSPDB:GN00023;
A/Experimental source: strain Bristol NZ; clone C12D5
C/Genetics:
A/Gene: CESP:C12D5.8
A/Map position: 5
A/Introns: 11/1; 29/3; 77/3; 232/3; 260/2; 319/2; 371/1; 451/3; 523/3

Query Match          96.7%; Score 29; DB 2; Length 577;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
Db 153 SYTH 157

RESULT 22
T06751
hypothetical protein F15B8.120 - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C/Accession: T06751
R/Queller, F.; Benes, V.; Rechmann, S.; Borikova, D.; Ansoorge, W.; Salanoubat, M.; Mewes,
submitted to the Protein Sequence Database, April 1999
A/Reference number: Z15794
A/Accession: T06751
A/Molecule type: DNA
A/Residues: 1-61 <QDE>
A/Cross-references: UNIPROT:Q9SVY3; UNIPARC:UPI00009B4CB; EMBL:AL049660; GSPDB:GN00061;
A/Experimental source: cultivar Columbia; BAC clone F15B8
C/Genetics:
A/Gene: ATSP:F15B8.120
A/Map position: 3

Query Match          93.3%; Score 28; DB 2; Length 61;
Best Local Similarity 80.0%; Pred. No. 28;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
Db 57 SYTH 61

RESULT 23
JQ1888
AL2 protein - tomato yellow leaf curl virus (strain Australia)
N/Alternate names: C2 protein
C/Species: tomato yellow leaf curl virus
C/Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C/Accession: JQ1888
R/Dry, I.B.; Rigden, J.E.; Krake, L.R.; Mullineux, P.M.; Rezaian, M.A.
J. Gen. Virol. 74, 147-151, 1993
A/Title: Nucleotide sequence and genome organization of tomato leaf curl geminivirus.
A/Reference number: JQ1885; MUID:93139778; PMID:8423446
A/Accession: JQ1888
A/Status: translation not shown
A/Molecule type: DNA
A/Residues: 1-135 <DRY>
A/Cross-references: UNIPROT:P36280; UNIPARC:UPI000061A62; GB:S53251
C/Superfamily: tomato golden mosaic virus AL2 protein

Query Match          93.3%; Score 28; DB 1; Length 135;
Best Local Similarity 80.0%; Pred. No. 62;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
Db 40 SYTH 44

RESULT 24
```

Q0CWC4
AL2 protein - tomato yellow leaf curl virus
N:Alternate names: C2 protein
C:Species: tomato yellow leaf curl virus
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: C40779
R:Navot, N.; Pichersky, E.; Zeldan, M.; Zamir, D.; Czosnek, H.
Virology 185, 151-161, 1991
A:Title: Tomato yellow leaf curl virus: a whitefly-transmitted geminivirus with a single
A:Reference number: A40779; MUID:92024070; PMID:1926771
A:Accession: C40779
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-135 <NAV>
A:Cross-references: UNIPROT:P27262; UNIPARC:UPI00001380E3; GB:X15656; NID:G62204; PIDN:C
C:Superfamily: tomato golden mosaic virus AL2 protein

Query Match 93.3%; Score 28; DB 1; Length 135;
Best Local Similarity 80.0%; Pred. No. 62;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYTH 5
|||:-|
Db 40 SYTH 44

RESULT 25
S07593
hypothetical protein, 15.2K - cassava latent virus (Nigerian isolate)
C:Species: cassava latent virus
C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C:Accession: S07593
R:Morris, B.; Coates, L.; Lowe, S.; Richardson, K.; Eddy, P.
Nucleic Acids Res. 18, 197-198, 1990
A:Title: Nucleotide sequence of the infectious cloned DNA components of African cassava
A:Reference number: S07590; MUID:90174930; PMID:2308831
A:Accession: S07593
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-135 <MOR>
A:Cross-references: UNIPROT:P14968; UNIPARC:UPI00001380DD; EMBL:X17095; NID:G59371; PIDN:
C:Genetics:
A:Map position: segment DNA1
C:Superfamily: tomato golden mosaic virus AL2 protein

Query Match 93.3%; Score 28; DB 2; Length 135;
Best Local Similarity 80.0%; Pred. No. 62;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYTH 5
|||:-|
Db 40 SYTH 44

RESULT 26
E97251
spore protease GPR related protein, YYAC B. subtilis ortholog [imported] - Clostridium a
C:Species: Clostridium acetobutylicum
C>Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C:Accession: E97251
R:Nolling, J.; Bretton, G.; Omeichenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: E97251
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-188 <KUR>
A:Cross-references: UNIPROT:Q97F84; UNIPARC:UPI000000CA66A; GB:AE001437; PIDN:AAK0800.1;
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC2857

Query Match 93.3%; Score 28; DB 2; Length 188;
Best Local Similarity 80.0%; Pred. No. 86;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYTH 5
|||:-|
Db 168 SYTH 172

RESULT 27
D82017
hypothetical protein NMA0228 [imported] - Neisseria meningitidis (strain Z2491 serogroup
C:Species: Neisseria meningitidis
C>Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C:Accession: D82017
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jogle, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A:Reference number: A81775; MUID:20222556; PMID:10761919
A:Accession: D82017
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-280 <PAR>
A:Cross-references: UNIPROT:Q9JWV1; UNIPARC:UPI000000CA48FE; GB:AL162752; GB:AL157959; NID
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: NMA0228

Query Match 93.3%; Score 28; DB 2; Length 280;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYTH 5
|||:-|
Db 141 SYTH 145

RESULT 28
D81002
conserved hypothetical protein NMB2142 [imported] - Neisseria meningitidis (strain MC58
C:Species: Neisseria meningitidis
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: D81002
R:Tetzelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A
Hickey, E.K.; Hatt, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
Li, H.; Qiu, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Plaza, M.
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: A81000; MUID:20175755; PMID:10710307
A:Accession: D81002
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-288 <TEF>
A:Cross-references: UNIPROT:Q9JXB0; UNIPARC:UPI000000CA4883; GB:AE002562; GB:AE002098; NID
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB2142

Query Match 93.3%; Score 28; DB 2; Length 288;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYTH 5
|||:-|
Db 149 SYTH 153

RESULT 29
C64397
hypothetical protein MJ0779 - Methanococcus jannaschii

C:Species: *Methanococcus jannaschii*
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: C64387
R:Built, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R.; Bult, C.J.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Tsom, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Bordovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.
A:Title: Complete genome sequence of the methanogenic archaeon, *Methanococcus jannaschii*
A:Reference number: A64300; MUID:96337999; PMID:8688087
A:Accession: C64397
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-299 <BUI>
A:Cross-references: UNIPROT:Q58189; UNIPARC:UPI0000139CB0; GB:U67522; GB:L77117; NID:928
C:Genetics:
A:Map position: REV700511-699612

Query Match 93.3%; Score 28; DB 2; Length 299;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYTH 5
|||:
47 SYTH 51

Db 47 SYTH 51

RESULT 30
H64037
hypothetical protein H11600 - Haemophilus influenzae (strain Rd KW20)
C:Species: *Haemophilus influenzae*
C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C:Accession: H64037
R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhmann, J.L.; Geoghegan, N.S.M.
Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.; Title: Whole-genome random sequencing and assembly of *Haemophilus influenzae* Rd.
A:Reference number: A64000; MUID:95350630; PMID:7542800
A:Accession: H64037
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-317 <TTGR>
A:Cross-references: UNIPROT:P44268; UNIPARC:UPI000013AF06; GB:U32834; GB:L42023; NID:915

Query Match 93.3%; Score 28; DB 2; Length 317;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYTH 5
|||:
152 SYTH 156

Db 152 SYTH 156

RESULT 31
T06584
probable DNA-binding protein - garden pea
C:Species: *Pisum sativum* (garden pea)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-Oct-2004
C:Accession: T06584; T06582
R:Sato, N.; Kazuno, A.A.; Ohna, N.; Ohshima, K.
submitted to the EMBL Data Library, June 1996
A:Description: Identification of a novel family of DNA-binding proteins with two AT-hook
A:Reference number: Z15774
A:Accession: T06584
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-347 <SAT>
A:Cross-references: UNIPROT:O04696; UNIPARC:UPI00000A9995; EMBL:X98738; PIDN:CAA67290.1
A:Accession: T06582
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA

A:Residues: 1-114,'S',116-334 <SA2>
A:Cross-references: UNIPARC:UPI00000A8CE8; EMBL:X98739; PIDN:CAA67291.1
A:Experimental source: cv. Alaska
C:Superfamily: DNA-binding protein PDI
C:Keywords: DNA binding

Query Match 93.3%; Score 28; DB 2; Length 347;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYTH 5
|||:
15 SYTH 19

Db 15 SYTH 19

RESULT 32
H89006
protein T22F3.11 [imported] - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C:Accession: H89006
R:Anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode *C. elegans*: a platform for investigating biology
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genome.msl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C.eleg
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: H89006
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-406 <STO>
A:Cross-references: UNIPARC:UPI000017A6A; GB:chr_V; PIDN:AB18313.1; PID:G1658348; GSPDF
C:Genetics:
A:Gene: T22F3.11
A:Map position: 5

Query Match 93.3%; Score 28; DB 2; Length 406;
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYTH 5
|||:
139 SYTH 143

Db 139 SYTH 143

RESULT 33
T30985
hypothetical protein T22F3.11 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C:Accession: T30985
R:Wu, X.
submitted to the EMBL Data Library, September 1999
A:Description: The sequence of *C. elegans* cosmid T22F3.
A:Reference number: Z20950
A:Accession: T30985
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-453 <WUX>
A:Cross-references: UNIPROT:Q94307; UNIPARC:UPI000007BD17; EMBL:U64844; PIDN:AAD56301.1
A:Experimental source: strain Bristol N2
C:Genetics:
A:Map position: V
A:Introns: 10/2; 51/3; 241/3; 375/2
A:Note: T22F3.11

Query Match 93.3%; Score 28; DB 2; Length 453;
Best Local Similarity 80.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYTH 5
|||:
186 SYTH 190

Db 186 SYTH 190

RESULT 34
T30983
hypothetical protein T22F3.8 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C:Accession: T30983
R:Wu, X.
submitted to the EMBL Data Library, September 1999
A:Description: The sequence of C. elegans cosmid T22F3.
A:Reference number: Z20950
A:Accession: T30983
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-482 <MIX>
A:Cross-references: UNIPROT:Q94305; UNIPARC:UPI000007DCE; EMBL:U64844; PIDN:AAB18311.1
A:Experimental source: strain Bristol N2
C:Genetics:
A:Map position: V
A:Introns: 40/2; 81/3; 122/2; 157/3; 271/3; 341/2; 405/2; 456/3
A:Note: T22F3.8

Query Match 93.3%; Score 28; DB 2; Length 482;
Best Local Similarity 80.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
|||:
216 SYTH 220

RESULT 35
F71009
probable sodium-dependent transporter - *Pyrococcus horikoshii*
C:Species: *Pyrococcus horikoshii*
C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
C:Accession: F71009
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Halkawa, Y.; Hino, Y.; Yamamoto, S.; Sekit
M.; Ohfuku, Y.; Punahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A:Reference number: A71000; MUID:98344137; PMID:9679194
A:Accession: F71009
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-521 <KAM>
A:Cross-references: UNIPROT:O50080; UNIPARC:UPI000006678E; GB:AP000006; NID:g3236133; PI
A:Experimental source: strain OT3
A:Note: this accession replaces an interim accession for a sequence replaced by GenBank
C:Genetics:
A:Gene: PH1372

Query Match 93.3%; Score 28; DB 2; Length 521;
Best Local Similarity 80.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
|||:
Db 115 SYTH 119

RESULT 36
A75122
sodium- and chloride-dependent transporter PAB1850 - *Pyrococcus abyssi* (strain Orey)

C:Species: *Pyrococcus abyssi*
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: A75122
R:anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A:Description: *Pyrococcus abyssi* genome sequence: insights into archaeal chromosome stru
A:Reference number: A75001
A:Accession: A75122

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-527 <KAM>
A:Cross-references: UNIPROT:Q9V0L3; UNIPARC:UPI000003464C; GB:AJ248285; GB:AL036836; NID
C:Genetics:
A:Experimental source: strain Orey
C:Gene: PAB1850
A:Superfamily: gamma-aminobutyric acid transporter

Query Match 93.3%; Score 28; DB 2; Length 527;
Best Local Similarity 80.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
|||:
Db 120 SYTH 124

RESULT 37
T45596
telomere repeat-binding protein homolog - *Arabidopsis thaliana*
N:Alternate names: protein F12A12.110
C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 31-Dec-2004
C:Accession: T45596
R:Choinsne, N.; Robert, C.; Brotier, P.; Winkler, P.; Catolico, L.; Artiguenave, F.; Sa
submitted to the Protein Sequence Database, December 1999
A:Reference number: Z23008
A:Accession: T45596
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-553 <CHO>
A:Cross-references: UNIPROT:Q9SNB9; UNIPARC:UPI0000A855A; EMBL:AL133314
C:Genetics:
A:Map position: 3
A:Introns: 27/3; 216/1; 264/1; 285/1; 311/3; 377/2; 475/2; 496/3
A:Note: F12A12.110
C:Superfamily: MYB-like DNA-binding protein

Query Match 93.3%; Score 28; DB 2; Length 553;
Best Local Similarity 80.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
|||:
Db 226 SYTH 230

RESULT 38
H71611
probable secreted protein PRB0565w - malaria parasite (*Plasmodium falciparum*)
C:Species: *Plasmodium falciparum*
C:Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004
C:Accession: H71611
R:Gardner, M.J.; Tetteh, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;
; Pertea, M.; Salzberg, S.; Zhou, L.; Sutch, G.G.; Clayton, R.; White, O.; Smith, H.O.
Science 282, 1126-1132, 1998
A:Title: Chromosome 2 sequence of the human malaria parasite *Plasmodium falciparum*.
A:Reference number: A71600; MUID:99021743; PMID:9804551
A:Accession: H71611
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1817 <GAR>
A:Cross-references: UNIPROT:Q96205; UNIPARC:UPI000017862F; GB:AE001403; GB:AE001362; NID
A:Experimental source: clone 307
C:Genetics:
A:Gene: PRB0565w

Query Match 93.3%; Score 28; DB 2; Length 1817;
Best Local Similarity 80.0%; Pred. No. 8.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYTH 5
 Db 1075 SYTH 1079

RESULT 39

spectrin alpha chain - fruit fly (Drosophila melanogaster)
 A33733
 C/Species: Drosophila melanogaster
 C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C/Accession: A33733; A49468; B49468
 F/Dbireuil, R.R.; Byers, T.J.; Sillman, A.L.; Bar-Zvi, D.; Goldstein, L.S.B.; Branton, D.
 J. Cell Biol. 109, 2197-2205, 1989
 A/Title: The complete sequence of Drosophila alpha-spectrin: conservation of structural
 A/Reference number: A33733; MUID:90037215; PMID:2808524
 A/Accession: A33733
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-2415 <DUB>
 A/Cross-references: UNIPROT:P13395; UNIPARC:UPI000016BD82; GB:M26400; NID:G158488; PIDN:
 R;Lee, J.K.; Coyne, R.S.; Dubreuil, R.R.; Goldstein, L.S.; Branton, D.
 J. Cell Biol. 123, 1797-1809, 1993
 A/Title: Cell shape and interaction defects in alpha-spectrin mutants of Drosophila mela
 A/Reference number: A49468; MUID:94103334; PMID:8276898
 A/Accession: A49468
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-150 <LEB>
 A/Cross-references: UNIPARC:UPI0000173DB4; GB:S67765; NID:G544666; PIDN:AA529441.1; PID:
 A/Note: sequence extracted from NCBI backbone (NCBIN:141786, NCBIN:141790, NCBI:P.141792)
 A/Accession: B49468
 A/Status: preliminary; not compared with conceptual translation
 A/Molecule type: DNA
 A/Residues: 2192-2415 <LE2>
 A/Cross-references: UNIPARC:UPI000016C014; GB:S67765; NID:G544666; PIDN:AA529442.1; PID:
 C/Genetics:
 A/Note: sequence extracted from NCBI backbone (NCBI:P.141794)
 C/Accession:
 A/Status: preliminary
 A/Residues: 1-3898 <MOO>
 A/Cross-references: UNIPROT:P21530; UNIPARC:UPI0000131B1B; GB:M31768; NID:G325460; PIDN:
 C/Comment: The cleavage sites of this polypeptide have not been determined.
 C/Superfamily: spectrin alpha chain; calmodulin repeat homology; SH3 homology; spectrin/
 C/Keywords: actin binding; cytoskeleton; EF hand
 F/46-150/Domain: spectrin/dystrophin repeat homology <SP1>
 F/151-256/Domain: spectrin/dystrophin repeat homology <SP2>
 F/257-362/Domain: spectrin/dystrophin repeat homology <SP3>
 F/363-468/Domain: spectrin/dystrophin repeat homology <SP4>
 F/469-574/Domain: spectrin/dystrophin repeat homology <SP5>
 F/575-679/Domain: spectrin/dystrophin repeat homology <SP6>
 F/680-781/Domain: spectrin/dystrophin repeat homology <SP7>
 F/782-891/Domain: spectrin/dystrophin repeat homology <SP8>
 F/892-976/Domain: spectrin/dystrophin repeat homology #status atypical <SP9>
 F/977-1024/Domain: SH3 homology <SH3>
 F/1072-1179/Domain: spectrin/dystrophin repeat homology <SP10>
 F/1180-1285/Domain: spectrin/dystrophin repeat homology <SP11>
 F/1286-1391/Domain: spectrin/dystrophin repeat homology <SP12>
 F/1392-1497/Domain: spectrin/dystrophin repeat homology <SP13>
 F/1498-1604/Domain: spectrin/dystrophin repeat homology <SP14>
 F/1605-1710/Domain: spectrin/dystrophin repeat homology <SP15>
 F/1711-1816/Domain: spectrin/dystrophin repeat homology <SP16>
 F/1817-1922/Domain: spectrin/dystrophin repeat homology <SP17>
 F/1923-2029/Domain: spectrin/dystrophin repeat homology <SP18>
 F/2038-2143/Domain: spectrin/dystrophin repeat homology <SP19>
 F/2152-2252/Domain: spectrin/dystrophin repeat homology <SP20>
 F/2265-2297/Domain: calmodulin repeat homology <EF1>
 F/2308-2340/Domain: calmodulin repeat homology <EF2>

Query Match 93.3%; Score 28; DB 1; Length 2415;
 Best Local Similarity 80.0%; Pred. No. 1.1e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYTH 5
 Db 363 SYTH 367

RESULT 40
 GNMVHC
 genome polypeptide - hog cholera virus (strain Alfort)

C/Species: hog cholera virus
 C/Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 19-Jan-2001
 C/Accession: A34037
 R;Meyers, G.; Ruemampf, T.; Thiel, H.J.
 Virology 171, 555-567, 1989
 A/Title: Molecular cloning and nucleotide sequence of the genome of hog cholera virus.
 A/Reference number: A34037; MUID:89348014; PMID:2763466
 A/Accession: A34037
 A/Molecule type: genomic RNA
 A/Residues: 1-3898 <MEY>
 A/Cross-references: UNIPARC:UPI00002FPA84; GB:J04358; NID:G325462; PIDN:AAA43844.1; PID:
 C/Superfamily: pestivirus genome polypeptide
 C/Keywords: ATP; glycoprotein; nucleotide binding; P-loop; polypeptide; transmembrane pr
 F/2-231/Product: viral proteinase p20 #status predicted <VPT>
 F/545-1111/Product: major envelope glycoprotein gp55 #status predicted <EGP>
 F/1815-1822/Region: nucleotide-binding motif A (P-loop)
 F/1906-1911/Region: nucleotide-binding motif B
 F/1910-1913/Region: DEXH motif
 F/157,269,274,278,293,362,367,410,425,500,594,805,810,918,949,986,1713,2134,2217,2494,276

Query Match 93.3%; Score 28; DB 1; Length 3898;
 Best Local Similarity 80.0%; Pred. No. 1.8e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYTH 5
 Db 1390 SYTH 1394

RESULT 41
 GNMVHB
 genome polypeptide - hog cholera virus (strain Brescia)
 C/Species: hog cholera virus
 C/Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
 C/Accession: A35317
 R;Moormann, R.J.M.; Warner, P.A.M.; Van Der Meer, B.; Schaper, W.M.M.; Wensvoort, G.,
 Virology 177, 184-198, 1990
 A/Title: Molecular cloning and nucleotide sequence of hog cholera virus strain Brescia ar
 A/Reference number: A35317; MUID:90281581; PMID:2162104
 A/Accession: A35317
 A/Molecule type: genomic RNA
 A/Residues: 1-3898 <MOO>
 A/Cross-references: UNIPROT:P21530; UNIPARC:UPI0000131B1B; GB:M31768; NID:G325460; PIDN:
 C/Comment: The cleavage sites of this polypeptide have not been determined.
 C/Superfamily: pestivirus genome polypeptide
 C/Keywords: ATP; glycoprotein; nucleotide binding; P-loop; polypeptide; transmembrane pr
 F/2-231/Product: viral proteinase p20 #status predicted <VPT>
 F/545-1111/Product: major envelope glycoprotein gp55 #status predicted <EGP>
 F/1031-1052/Domain: transmembrane #status predicted <TMN>
 F/1815-1822/Region: nucleotide-binding motif A (P-loop)
 F/1906-1911/Region: nucleotide-binding motif B
 F/1910-1913/Region: DEXH motif
 F/157,269,278,332,362,410,425,500,513,594,805,810,874,918,949,1713,2134,2217,2419,2494,276

Query Match 93.3%; Score 28; DB 1; Length 3898;
 Best Local Similarity 80.0%; Pred. No. 1.8e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYTH 5
 Db 1390 SYTH 1394

RESULT 42
 S57437
 genome polypeptide - hog cholera virus
 C/Species: hog cholera virus
 C/Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
 C/Accession: S57437

R.Ruggli, N.; Hofmann, M.A.; Tratschin, J.D.
submitted to the EMBL Data Library, June 1995
A:Description: Complete nucleotide sequence of classical swine fever virus strain allfort
A:Reference number: S57437
A:Accession: S57437
A:Status: Preliminary
A:Molecule type: genomic RNA
A:Residues: 1-3898 <RUG>
A:Cross-references: UNIPROT:068871; UNIPARC:UPI00000F9C5D; EMBL:X87939; NID:ig871250; PID
C:Superfamily: peptidyl transferase
C:Keywords: ATP; nucleotide binding; P-loop; polypeptide
F:1815-1822/Region: nucleotide-binding motif A (P-loop)
F:1906-1911/Region: nucleotide-binding motif B
F:1910-1913/Region: DEXH motif

Query Match 93.3%; Score 28; DB 2; Length 3898;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYTH 5
|||:
1390 SYTH 1394

Db 1390 SYTH 1394

RESULT 43
S58295
polyprotein - hog cholera virus
C:Species: hog cholera virus
C:Date: 14-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 31-Dec-2004
C:Accession: S58295
R:Moormann, H.G.P.; Miedema, G.R.W.; Hulst, P.A.
submitted to the EMBL Data Library, October 1994
A:Description: Infectious RNA transcribed from a full-length DNA copy of the genome of
A:Reference number: S58295
A:Accession: S58295
A:Status: Preliminary
A:Molecule type: genomic RNA
A:Residues: 1-3898 <MOO>
A:Cross-references: UNIPROT:092364; UNIPROT:068534; UNIPROT:Q8JPF7; UNIPROT:Q96891; UNIF
C:Keywords: ATP; nucleotide binding; P-loop; polypeptide
F:1815-1822/Region: nucleotide-binding motif A (P-loop)
F:1906-1911/Region: nucleotide-binding motif B
F:1910-1913/Region: DEXH motif

Query Match 93.3%; Score 28; DB 2; Length 3898;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYTH 5
|||:
1390 SYTH 1394

Db 1390 SYTH 1394

RESULT 44
S78706
protein YBR058c-a - yeast (*Saccharomyces cerevisiae*)
C:Species: *Saccharomyces cerevisiae*
C:Date: 15-Jan-1999 #sequence_revision 15-Jan-1999 #text_change 15-Jan-1999
C:Accession: S78706
R:Aljinovic, G.; Pohl, F.M.; Pohl, T.M.
submitted to the Protein Sequence Database, August 1994
A:Reference number: S45906
A:Accession: S78706
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-80 <ALT>
A:Cross-references: UNIPARC:UPI00001682BE; EMBL:Z35925; MIPS:YBR058c-a
C:Genetics:
A:Experimental source: strain S288C
A:Map position: 2R

Query Match 90.0%; Score 27; DB 2; Length 80;
Best Local Similarity 80.0%; Pred. No. 59;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYTH 5
|||:
41 TYTH 45

Db 41 TYTH 45

RESULT 45
S26920
Ig heavy chain V region (DP-7) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S26920
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline VH sequences reveals about fifty groups of V
A:Reference number: S26885; MUID:9302117; PMID:1404388
A:Accession: S26920
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-98 <TOM>
A:Cross-references: UNIPARC:UPI00001163FE; EMBL:Z12309; NID:932958; PIDN:CAA78179.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 90.0%; Score 27; DB 2; Length 98;
Best Local Similarity 80.0%; Pred. No. 73;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYTH 5
|||:
31 SYVMH 35

Db 31 SYVMH 35

RESULT 46
C48223
Ig heavy chain V region (15022) - coelacanth
C:Species: *Latimeria chalumnae* (coelacanth)
C:Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 07-May-1999
C:Accession: C48223
R:Amemiya, C.T.; Ohta, Y.; Litman, R.T.; Raaf, J.P.; Haire, R.N.; Litman, G.W.
Proc. Natl. Acad. Sci. U.S.A. 90, 6661-6665, 1993
A:Title: V-H gene organization in a relict species, the coelacanth *Latimeria chalumnae*:
A:Reference number: A48223; MUID:93342050; PMID:8341683
A:Accession: C48223
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-99 <AME>
A:Cross-references: UNIPARC:UPI0000176E69; DB:X57356
C:Genetics:
A:Gene: VH
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immune response; immunoglobulin
F:15-99/Domain: immunoglobulin homology <IMM>

Query Match 90.0%; Score 27; DB 2; Length 99;
Best Local Similarity 80.0%; Pred. No. 74;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYTH 5
|||:
31 SYVMH 35

Db 31 SYVMH 35

RESULT 47
A54378
Ig heavy chain V region anti-triplex DNA - mouse (fragment)
C:Species: *Mus musculus* (house mouse)
C:Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C:Accession: A54378
R:Agazie, Y.M.; Lee, J.S.; Burkholder, G.D.
J. Biol. Chem. 269, 7019-7023, 1994

A;Title: Characterization of a new monoclonal antibody to triplex DNA and immunofluorescent
A;Reference number: A54378; MUID:94165109; PMID:7509814
A;Accession: A54378
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-115 <AGN>
A;Cross-references: UNIPARC:UPI0000176E3F; GB:S68981; NID:9545744; PIDN:AAB30095.1; PID:
A;Experimental source: spleen and myeloma cell line MOPC 315.43
A;Note: sequence inconsistent with nucleotide translation
A;Note: sequence extracted from NCBI Backbone (NCBIN:144172, NCBI:P.144173)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 90.0%; Score 27; DB 2; Length 115;
Best Local Similarity 80.0%; Pred. No. 86;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYTYH 5
|||:
31 TYTYH 35

RESULT 48
S22553
Ig heavy chain V region (family XI) - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S22553
R;Haire, R.N.; Ohba, Y.; Litman, R.T.; Amemiya, C.T.; Litman, G.W.
Nucleic Acids Res. 19, 3061-3066, 1991
A;Title: The genomic organization of immunoglobulin V(H) genes in Xenopus laevis shows e
A;Reference number: S22552; MUID:91279463; PMID:1905399
A;Accession: S22553
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-116 <HAI>
A;Cross-references: UNIPARC:UPI0000116E6E; EMBL:X56865; NID:964813; PIDN:CAA0191.1; PID:
A;Note: this sequence was submitted to the EMBL Data Library, December 1990
C;Genetics:
A;Intons: 15/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;33-116/Domain: immunoglobulin homology <IMM>

Query Match 90.0%; Score 27; DB 2; Length 116;
Best Local Similarity 80.0%; Pred. No. 86;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYTYH 5
|||:
49 SYTYH 53

RESULT 49
HVHUNG
Ig heavy chain precursor V-I region (HG3) - human
C;Species: Homo sapiens (man)
C;Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 09-Jul-2004
C;Accession: A02024
R;Rechavi, G.; Ram, D.; Glazer, L.; Zakut, R.; Givol, D.
Proc. Natl. Acad. Sci. U.S.A. 80, 855-859, 1983
A;Title: Evolutionary aspects of immunoglobulin heavy chain variable region (V-H) gene e
A;Reference number: A02024; MUID:83144028; PMID:6298778
A;Accession: A02024
A;Molecule type: DNA
A;Residues: 1-117 <REC>
A;Cross-references: UNIPROT:P01743; UNIPARC:UPI000012CEB1
A;Note: the sequence was determined from the germ-line gene
C;Genetics:
A;Gene: GDB:IGHV@
A;Cross-references: GDB:128528; OMTM:147070
A;Map position: 14q32.33-14q32.33

A;Intons: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-117/Product: Ig heavy chain V-I region (HG3) #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 90.0%; Score 27; DB 1; Length 117;
Best Local Similarity 80.0%; Pred. No. 87;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYTYH 5
|||:
50 SYTYH 54

RESULT 50
S31680
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31680
R;Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the e
A;Reference number: S31585
A;Accession: S31680
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-117 <CU>
A;Cross-references: UNIPARC:UPI000011647D; EMBL:Z14213; NID:937795; PIDN:CAAY8582.1; PID:
C;Genetics:
A;Intons: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 90.0%; Score 27; DB 2; Length 117;
Best Local Similarity 80.0%; Pred. No. 87;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYTYH 5
|||:
50 SYTYH 54

Search completed: May 4, 2006, 13:09:26
Job time : 18.1429 secs

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OM protein - protein search, using sw model

Run on: May 4, 2006, 12:46:39 ; Search time 46.8254 Seconds
(without alignments)
75.336 Million cell updates/sec

Title: US-10-700-632-1
Perfect score: 30
Sequence: 1 SYTH 5

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	68	2 Q4YV5_PLABE	Q4YV5 plasmodium
2	30	100.0	104	2 O58463_PYRHO	O58463 pyrococcus
3	30	100.0	104	2 O8V590_TYLCs	O8V590 tomato yell
4	30	100.0	104	2 O8V593_TYLCs	O8V593 tomato yell
5	30	100.0	104	2 O8V596_TYLCs	O8V596 tomato yell
6	30	100.0	104	2 O8V599_TYLCs	O8V599 tomato yell
7	30	100.0	104	2 O8V5A2_TYLCs	O8V5A2 tomato yell
8	30	100.0	104	2 O8V5A5_TYLCs	O8V5A5 tomato yell
9	30	100.0	124	1 COMGG_BACSU	P25959 bacillus su
10	30	100.0	135	1 VAL2_TYLCs	P27263 tomato yell
11	30	100.0	135	1 VAL2_TYLCU	P36610 tomato yell
12	30	100.0	135	2 O91596_GGEMI	O91596 mungbean ye
13	30	100.0	135	2 O66UV8_TYLCs	O66UV8 tomato yell
14	30	100.0	135	2 O67619_TYLCs	O67619 tomato yell
15	30	100.0	135	2 O6WRU8_GGEMI	O6WRU8 mungbean ye
16	30	100.0	135	2 O701P9_GGEMI	O701P9 horseggram y
17	30	100.0	135	2 Q7TLD7_GGEMI	Q7TLD7 mungbean ye
18	30	100.0	135	2 O808T6_GGEMI	O808T6 mungbean ye
19	30	100.0	135	2 O88950_TYLCs	O88950 tomato yell
20	30	100.0	135	2 O8B6S6_TYLCs	O8B6S6 tomato yell
21	30	100.0	135	2 O8UYT7_GGEMI	O8UYT7 mungbean ye
22	30	100.0	135	2 O91M69_GGEMI	O91M69 tobacco lea
23	30	100.0	135	2 O99DR6_GGEMI	O99DR6 mungbean ye
24	30	100.0	135	2 O9YPS3_GGEMI	O9YPS3 mungbean ye
25	30	100.0	135	2 O534Y0_GGEMI	O534Y0 mungbean ye
26	30	100.0	136	2 O8JXP4_GGEMI	O8JXP4 mungbean ye
27	30	100.0	136	2 O913F0_GGEMI	O913F0 mungbean ye
28	30	100.0	136	2 O917N2_GGEMI	O917N2 mungbean ye
29	30	100.0	136	2 O9WH23_GGEMI	O9WH23 mungbean ye
30	30	100.0	136	2 O535C4_GGEMI	O535C4 mungbean ye
31	30	100.0	142	2 O86MX5_DICTDI	O86MX5 dictyosteli

32	30	100.0	146	2 Q91N71_GGEMI	Q91N71 mungbean ye
33	30	100.0	150	2 O5YA42_GGEMI	O5YA42 cowpea gold
34	30	100.0	150	2 Q7TLD3_GGEMI	Q7TLD3 mungbean ye
35	30	100.0	150	2 O808U2_GGEMI	O808U2 mungbean ye
36	30	100.0	150	2 O808V0_GGEMI	O808V0 mungbean ye
37	30	100.0	150	2 O80P53_GGEMI	O80P53 legume yell
38	30	100.0	150	2 O80P59_GGEMI	O80P59 legume yell
39	30	100.0	150	2 O80P64_GGEMI	O80P64 legume yell
40	30	100.0	150	2 O910Y8_GGEMI	O910Y8 mungbean ye
41	30	100.0	150	2 O52UQ4_GGEMI	O52UQ4 mungbean ye
42	30	100.0	150	2 O6QDA7_GGEMI	O6QDA7_GGEMI
43	30	100.0	157	2 O95978_HUMAN	O95978 homo sapien
44	30	100.0	195	2 O9CUG6_MOUSE	O9CUG6 mus musculu
45	30	100.0	214	2 O50NV4_ENTHI	O50NV4 entamoeba h
46	30	100.0	223	2 Q7VTZ4_BORPE	Q7VTZ4 bordetella
47	30	100.0	231	2 O8RE63_TUSN	O8RE63 fusobacteri
48	30	100.0	251	2 O8CDS7_MOUSE	O8CDS7 mus musculu
49	30	100.0	253	2 O4MGN2_BACCE	O4MGN2 bacillus ce
50	30	100.0	284	2 O45342_CAEBL	O45342 caenorhabdi
51	30	100.0	289	2 O5CEB1_CRYHO	O5CEB1 cryospori
52	30	100.0	326	2 O43042_SCHPO	O43042 schistosach
53	30	100.0	348	2 O80834_ARATH	O80834 arabidopsis
54	30	100.0	384	2 Q12283_YEAST	Q12283 saccharomyc
55	30	100.0	385	2 Q74LR5_LACJO	Q74LR5 lactobacill
56	30	100.0	437	2 O5CVM9_CRYPV	O5CVM9 cryospori
57	30	100.0	437	2 O6FLJ3_MESPL	O6FLJ3 mesoplasma
58	30	100.0	460	2 Q91WT1_MOUSE	Q91WT1 mus musculu
59	30	100.0	678	1 NTP2_MTXVL	NTP2 myxoma vltro
60	30	100.0	678	1 NTP2_SFVKA	Q99G2 myxoma vltro
61	30	100.0	774	1 AMY2_SCHPO ;	Q9927 schizo fibro
62	30	100.0	792	2 O5CUT2_CRYPV	O5CUT2 schistosach
63	30	100.0	870	2 O87585_VIRU	O87585 citrus talt
64	30	100.0	918	2 Q7TA21_VIRU	Q7TA21 apple stem
65	30	100.0	937	2 Q9YPI2_VIRU	Q9YPI2 citrus talt
66	30	100.0	1244	2 Q4QI12_LEIMA	Q4QI12 leishmania
67	30	100.0	1344	2 O93419_CHICK	O93419 gallus gall
68	30	100.0	1546	2 Q4UEB1_THEAN	Q4UEB1 theileria a
69	30	100.0	1560	2 Q4NAV2_THERPA	Q4NAV2 theileria p
70	30	100.0	1706	2 O54TS2_DICTDI	O54TS2 dictyosteli
71	30	100.0	1956	2 Q7OSU1_GIATA	Q7OSU1 giardia lam
72	30	100.0	2105	1 POLR_ASGBP	P63109 apple stem
73	30	100.0	2105	2 O618X5_VIRU	O618X5 citrus talt
74	30	100.0	2105	2 O6PLS1_VIRU	O6PLS1 pear black
75	30	100.0	2105	2 O91R74_VIRU	Q91R74 apple stem
76	30	100.0	2604	2 O50T90_ENTHI	O50T90 entamoeba h
77	30	100.0	3946	2 Q4PA92_USTMA	Q4PA92 ustilago ma
78	30	100.0	4564	2 Q77075_DROXY	Q77075 drosophiila
79	30	100.0	133	2 O817M3_CAEBL	O817M3 caenorhabdi
80	29	96.7	135	2 O5CAN1_MANS	O5CAN1 manihot esc
81	29	96.7	135	2 O5CAN1_GGEMI	O5CAN1 sri lankan
82	29	96.7	135	2 O709N8_GGEMI	Q709N8 sri lankan
83	29	96.7	135	2 Q776F0_GGEMI	Q776F0 sri lankan
84	29	96.7	135	2 O8UYX0_GGEMI	O8UYX0 sri lankan
85	29	96.7	135	2 O8UZS6_ICMV	O8UZS6 indian cass
86	29	96.7	135	2 O534X6_ICMV	O534X6 indian cass
87	29	96.7	135	2 O5CAN7_GGEMI	O5CAN7 sri lankan
88	29	96.7	135	2 O643X7_ICMV	O643X7 indian cass
89	29	96.7	135	2 Q7TLE3_GGEMI	Q7TLE3 mungbean ye
90	29	96.7	150	2 O80P48_GGEMI	O80P48 legume yell
91	29	96.7	150	2 O528I9_MAGGR	O528I9 magnaporthe
92	29	96.7	165	2 O6YSS1_ORYDA	O6YSS1 oryza sativ
93	29	96.7	176	2 Q4TZU8_GCAID	Q4TZU8 enterobacte
94	29	96.7	182	2 O8LIW6_GRIK	O8LIW6 wolbachia e
95	29	96.7	204	2 O9KER2_BACD	O9KER2 bacillus ha
96	29	96.7	208	2 O8G7C0_BIFLO	O8G7C0 bifidobacte
97	29	96.7	219	2 Q71106_ADEB3	Q71106 bovine aden
98	29	96.7	236	2 O4LOK1_9BURI	O4LOK1 bacteroides
99	29	96.7	236	2 O519K7_BACNR	O519K7 bacteroides
100	29	96.7	236	2 O64PUS_BACR	O64PUS bacteroides
101	29	96.7	236	2 Q7S1G3_SALSA	Q7S1G3 salmo salar
102	29	96.7	273	2 O9GTC5_CAEBL	O9GTC5 caenorhabdi
103	29	96.7			
104	29	96.7			

105	29	96.7	297	2	OSW3K6_YVIRU	05w3k6 toxoneuron	178	28	93.3	135	2	OS8WK2_9GEMI	058wk2 african cas
106	29	96.7	321	2	Q6UD13_9HERP	Q6ud13 pelteacid h	179	28	93.3	135	2	OSDV80_9GEMI	OSDV80 9GEMI
107	29	96.7	327	2	Q6ZR60_HUMAN	Q6zr60 homo sapien	180	28	93.3	135	2	OSDV85_9GEMI	OSDV85 tomato leaf
108	29	96.7	338	2	Q817M4_CAEEL	Q817m4 caenorhabd	181	28	93.3	135	2	OSDVCL_9GEMI	OSDVCL tomato leaf
109	29	96.7	351	2	Q4UBJ7_TREAN	Q4ubj7 theileria a	182	28	93.3	135	2	OSDVCL_9GEMI	OSDVCL tomato leaf
110	29	96.7	356	2	Q73149_TREDE	Q73149 treponema d	183	28	93.3	135	2	OSDV86_TREDE	OSDV86 tomato leaf
111	29	96.7	379	2	Q74150_LACJO	Q74150 lactobacill	184	28	93.3	144	2	Q7MNA9_VIBVY	Q7mna9 vibrio vuln
112	29	96.7	421	2	Q51L59_SILPO	Q51l59 silicobacte	185	28	93.3	156	2	Q559G1_DICDI	Q559g1 dictyosceli
113	29	96.7	443	2	Q8EM10_OCEIH	Q8em10 oceanobacti	186	28	93.3	188	2	Q97P84_CIOAB	Q97p84 clostridum
114	29	96.7	529	2	Q7S284_NEUCR	Q7s284 neurospora	187	28	93.3	230	2	Q8TRF2_METAC	Q8trf2 methanobac
115	29	96.7	598	1	VQ9_BPB03	Q37890 bacterioph	188	28	93.3	242	2	Q57WS1_9TRYP	Q57ws1 typhlosoem
116	29	96.7	660	2	Q4P3E3_USJTA	Q4p3e3 ussiliago m	189	28	93.3	249	2	Q5SGN0_THET8	Q5sgn0 thermus th
117	29	96.7	660	2	Q4P3E3_USJTA	Q4p3e3 ussiliago m	190	28	93.3	249	2	Q5SGN0_THET8	Q5sgn0 thermus th
118	29	96.7	758	2	Q6RSNO_CANGA	Q6rsno candida gla	191	28	93.3	265	2	Q5HPZ5_STABO	Q5hpz5 staphylococ
119	29	96.7	796	2	Q8KW22_9HROE	Q8kw22 ruegeria sp	192	28	93.3	269	2	Q8RPS5_OCEIH	Q8rps5 oceanobacti
120	29	96.7	870	2	Q8XNBS_CLOPE	Q8xnbs clostridium	193	28	93.3	280	1	Y2142_NEIMB	Y2142 neisseria m
121	29	96.7	871	2	Q4SCX8_TETNG	Q4scx8 tetraodon n	194	28	93.3	280	1	Y228_NEIMA	Q9jwv1 neisseria m
122	29	96.7	894	2	Q6BUFE_DEBHA	Q6bufe debaryomyce	195	28	93.3	280	2	Q5F5H9_NEIG1	Q5f5h9 neisseria g
123	29	96.7	902	2	Q9Q8X9_9PROX	Q9q8x9 rabbit fibr	196	28	93.3	293	2	Q7OLP6_PASMU	Q7olp6 pasteurella
124	29	96.7	902	2	Q5ONDI_ENTMT	Q5ond1 entamoeba h	197	28	93.3	299	1	Y779_METJA	Q58p22 haemophilus
125	29	96.7	1150	2	Q5ONDI_ENTMT	Q5ond1 entamoeba h	198	28	93.3	307	1	Y211_PASMU	Q58p22 haemophilus
126	29	96.7	1223	1	Q4YK14_HUMAN	Q4y14 homo sapien	199	28	93.3	307	1	Y211_PASMU	Q58p22 haemophilus
127	29	96.7	1223	1	Q5T4G0_HUMAN	Q5t4g0 homo sapien	200	28	93.3	310	2	Q5KYE2_GEOXA	Q5kye2 geobacillus
128	29	96.7	1226	2	Q5T4G1_HUMAN	Q5t4g1 homo sapien	201	28	93.3	312	2	Q8W4L7_ARATH	Q8w4l7 arabidopsis
129	29	96.7	1377	2	Q4MZG4_THEPA	Q4mzg4 theileria p	202	28	93.3	316	2	Q5DBY1_SCHJA	Q5dbyl schistosoma
129	29	96.7	2238	2	Q5S152_CRYNE	Q5s152 cryptococcu	203	28	93.3	317	2	Q4QL35_HAE18	Q4ql35 haemophilus
130	29	96.7	2238	2	Q5KAC9_CRYNE	Q5kac9 cryptococcu	204	28	93.3	324	2	Q4T214_TETNG	Q4t214 tetraodon n
131	29	96.7	3525	2	Q815W5_PLA7F	Q815w5 plasmodium	205	28	93.3	328	2	Q8UGU1_CHICK	Q8ugu1 gallus gall
132	28	93.3	38	2	Q7R901_PLA7O	Q7r901 plasmodium	206	28	93.3	328	2	Q7TOL4_CHICK	Q7tol4 gallus gall
133	28	93.3	52	2	Q4YK15_PLABH	Q4yk15 plasmodium	207	28	93.3	332	2	Q61E97_CAEER	Q61e97 caenorhabd
134	28	93.3	61	2	Q8S2W4_PLABH	Q8s2w4 arabidopsis	208	28	93.3	334	2	Q04695_PEA	Q04695 pisum sativ
135	28	93.3	61	2	Q9SVY3_ARATH	Q9svy3 arabidopsis	209	28	93.3	345	2	Q5KZE0_GEOXA	Q5kze0 geobacillus
136	28	93.3	63	2	Q4YMH1_PLABH	Q4ymh1 plasmodium	210	28	93.3	347	2	Q97OR8_SULFO	Q97or8 sulfobobus
137	28	93.3	122	2	Q37881_TYLAV	Q37881 tomato yell	211	28	93.3	347	2	Q04696_PEA	Q04696 pisum sativ
138	28	93.3	131	2	Q4Y2X5_PLACH	Q4y2x5 plasmodium	212	28	93.3	372	2	Q5U1V7_PYRKO	Q5u1v7 pyrococcus
139	28	93.3	135	1	VAL2_CLVN	Q14976 caesava lat	213	28	93.3	375	2	Q6WJF6_TRIVA	Q6wjf6 trichomonas
140	28	93.3	135	1	VAL2_CLVN	Q14968 caesava lat	214	28	93.3	375	2	Q86NCO_CAEEL	Q86nc0 caenorhabd
141	28	93.3	135	1	VAL2_TYLCA	P32262 tomato yell	215	28	93.3	413	2	Q5TIN3_9ROSI	Q5tin3 gossypium r
142	28	93.3	135	1	VAL2_TYLCA	P32262 tomato yell	216	28	93.3	413	2	Q7PPV4_ANOGA	Q7ppv4 anopheles g
143	28	93.3	135	2	Q38543_TYLAV	Q38543 tomato yell	217	28	93.3	437	2	Q61E59_CAEER	Q61e59 caenorhabd
144	28	93.3	135	2	Q6BMH3_9GEMI	Q6bmh3 african cas	218	28	93.3	443	2	Q5RIQ7_BRARE	Q5riq7 brachydanio
145	28	93.3	135	2	Q6PMS4_TYLAV	Q6pms4 tomato yell	219	28	93.3	450	2	Q61E94_CAEER	Q61e94 caenorhabd
146	28	93.3	135	2	Q6P6P1_TYLAV	Q6p6p1 tomato yell	220	28	93.3	450	2	Q5TIM6_NICBE	Q5tim6 nicotiana b
147	28	93.3	135	2	Q6RCU1_9GEMI	Q6rcu1 tomato leaf	221	28	93.3	453	2	Q94307_CAEEL	Q94307 caenorhabd
148	28	93.3	135	2	Q6RCU1_9GEMI	Q6rcu1 tomato leaf	222	28	93.3	467	2	Q4MZ45_THRPA	Q4mz45 theileria p
149	28	93.3	135	2	Q6RCU1_9GEMI	Q6rcu1 tomato yell	223	28	93.3	474	2	Q5TIM7_SOLTU	Q5tim7 solanum tub
150	28	93.3	135	2	Q764F3_TYLAV	Q764f3 tomato yell	224	28	93.3	479	2	Q861O8_DICDI	Q861o8 dictyosceli
151	28	93.3	135	2	Q764F9_TYLAV	Q764f9 tomato yell	225	28	93.3	480	2	Q6H765_ORYSA	Q6h765 oryza sativ
152	28	93.3	135	2	Q764H7_TYLAV	Q764h7 tomato yell	226	28	93.3	482	2	Q94305_CAEEL	Q94305 caenorhabd
153	28	93.3	135	2	Q76C59_TYLAV	Q76c59 tomato yell	227	28	93.3	485	2	Q4FPE5_9RICK	Q4fpe5 candidatus
154	28	93.3	135	2	Q76C68_TYLAV	Q76c68 tomato yell	228	28	93.3	493	2	Q61PP8_CAEER	Q61pp8 caenorhabd
155	28	93.3	135	2	Q77B82_TYLAV	Q77b82 tomato yell	229	28	93.3	508	2	Q6H559_ORYSA	Q6h559 oryza sativ
156	28	93.3	135	2	Q88943_TYLAV	Q88943 tomato yell	230	28	93.3	519	2	Q5UDK2_PYRKO	Q5udk2 pyrococcus
157	28	93.3	135	2	Q8B2Y3_TYLAV	Q8b2y3 tomato yell	231	28	93.3	521	2	Q5O080_PYRHO	Q5o080 pyrococcus
158	28	93.3	135	2	Q8B656_9GEMI	Q8b656 african cas	232	28	93.3	525	2	Q81H81_DROME	Q81h81 drosophila
159	28	93.3	135	2	Q8BA62_TYLAV	Q8ba62 tomato yell	233	28	93.3	525	2	Q81N45_DROME	Q81n45 drosophila
160	28	93.3	135	2	Q84JTB_TYLAV	Q84jtb tomato yell	234	28	93.3	527	2	Q9V0L3_PYRAB	Q9v0l3 pyrococcus
161	28	93.3	135	2	Q84JTB_TYLAV	Q84jtb tomato yell	235	28	93.3	547	2	Q93N56_COXBU	Q93n56 coxiella bu
162	28	93.3	135	2	Q84JTB_TYLAV	Q84jtb tomato yell	236	28	93.3	552	2	Q700E9_ARATH	Q700e9 arabidopsis
163	28	93.3	135	2	Q84JTB_TYLAV	Q84jtb tomato yell	237	28	93.3	553	2	Q9SNB9_ARATH	Q9snb9 arabidopsis
164	28	93.3	135	2	Q84JTB_TYLAV	Q84jtb tomato yell	238	28	93.3	563	2	Q753F3_ASHGO	Q753f3 ashbya goss
165	28	93.3	135	2	Q84JTB_TYLAV	Q84jtb tomato yell	239	28	93.3	571	2	Q7QRL1_GIALA	Q7qrl1 campylobact
166	28	93.3	135	2	Q84JTB_TYLAV	Q84jtb tomato yell	240	28	93.3	572	2	Q93PC2_9SPHT	Q93pc2 microscilla
167	28	93.3	135	2	Q84JTB_TYLAV	Q84jtb tomato yell	241	28	93.3	578	2	Q8U1F4_PYRRT	Q8u1f4 pyrococcus
168	28	93.3	135	2	Q84JTB_TYLAV	Q84jtb tomato yell	242	28	93.3	581	2	Q96XHO_SULTO	Q96xho sulfobobus
169	28	93.3	135	2	Q84JTB_TYLAV	Q84jtb tomato yell	243	28	93.3	601	2	Q61H01_CAEER	Q61h01 caenorhabd
170	28	93.3	135	2	Q84JTB_TYLAV	Q84jtb tomato yell	244	28	93.3	602	2	Q96P88_CAEEL	Q96p88 caenorhabd
171	28	93.3	135	2	Q84JTB_TYLAV	Q84jtb tomato yell	245	28	93.3	605	2	Q5HT71_CAMUR	Q5ht71 campylobact
172	28	93.3	135	2	Q84JTB_TYLAV	Q84jtb tomato yell	246	28	93.3	621	2	Q4UP92_THRAN	Q4up92 theileria a
173	28	93.3	135	2	Q84JTB_TYLAV	Q84jtb tomato yell	247	28	93.3	624	2	Q6MAS3_PARUN	Q6mas3 parachlamy
174	28	93.3	135	2	Q84JTB_TYLAV	Q84jtb tomato yell	248	28	93.3	637	2	Q8T0V7_DROME	Q8t0v7 drosophila
175	28	93.3	135	2	Q84JTB_TYLAV	Q84jtb tomato yell	249	28	93.3	657	2	Q8D842_VIBVU	Q8d842 vibrio vuln
176	28	93.3	135	2	Q84JTB_TYLAV	Q84jtb tomato yell	250	28	93.3	657	2	Q7MMD2_VIBVY	Q7mmd2 vibrio vuln
177	28	93.3	135	2	Q84JTB_TYLAV	Q84jtb tomato yell	250	28	93.3	657	2	Q7MMD2_VIBVY	Q7mmd2 vibrio vuln

251	28	93.3	658	2	061E88_CABER	061e88 caenorhabdi	324	27	90.0	96	2	08V3A7_VIRU	08V3a7 apple chlor
252	28	93.3	661	1	PACC_CANAL	08V3a7 candida alb	325	27	90.0	96	2	08V3A8_VIRU	08V3a8 apple chlor
253	28	93.3	666	1	PACC_CANU	08V3y3 candida dub	326	27	90.0	96	2	08V3A9_VIRU	08V3a9 apple chlor
254	28	93.3	666	2	017479_HYACE	017479 hyalophora	327	27	90.0	96	2	08V3B0_VIRU	08V3b0 apple chlor
255	28	93.3	725	2	08D5T3_VIBRV	08D5t3 vibrio vuln	328	27	90.0	96	2	08V3B1_VIRU	08V3b1 apple chlor
256	28	93.3	725	2	Q7MCU9_VIBVY	Q7mcu9 vibrio vuln	329	27	90.0	96	2	08V3B3_VIRU	08V3b3 apple chlor
257	28	93.3	744	2	06K688_9CAUD	06K688 bacterioph	330	27	90.0	96	2	08V3B5_VIRU	08V3b5 apple chlor
258	28	93.3	744	2	04Z6H6_PLABE	04Z6h6 plasmodium	331	27	90.0	96	2	08V3B6_VIRU	08V3b6 apple chlor
259	28	93.3	748	2	Q7R153_PLAYO	Q7r153 plasmodium	332	27	90.0	96	2	08V3B7_VIRU	08V3b7 apple chlor
260	28	93.3	751	2	Q7AGM6_GEOSL	Q7agm6 geobacter s	333	27	90.0	96	2	08V3B8_VIRU	08V3b8 apple chlor
261	28	93.3	773	2	Q4FZ25_LEIMA	Q4fz25 leishmania	334	27	90.0	96	2	08V3B9_VIRU	08V3b9 apple chlor
262	28	93.3	804	2	0817C5_DICDI	0817c5 dictyosteli	335	27	90.0	96	2	08V3C0_VIRU	08V3c0 apple chlor
263	28	93.3	804	2	054X55_DICDI	054x55 dictyosteli	336	27	90.0	96	2	08V3C1_VIRU	08V3c1 apple chlor
264	28	93.3	871	2	08A1H5_SIVCZ	08a1h5 chimpazee	337	27	90.0	96	2	08V3C2_VIRU	08V3c2 apple chlor
265	28	93.3	956	2	Q4N0F2_THEPA	Q4n0f2 thelateria p	338	27	90.0	96	2	08V3C3_VIRU	08V3c3 apple chlor
266	28	93.3	986	2	Q75JG4_DICDI	Q75jg4 dictyosteli	339	27	90.0	96	2	08V3C4_VIRU	08V3c4 apple chlor
267	28	93.3	1038	2	Q54EH0_DICDI	Q54eh0 dictyosteli	340	27	90.0	96	2	08V3C5_VIRU	08V3c5 apple chlor
268	28	93.3	1114	2	Q679P5_MOUSE	Q679p5 mus musculu	341	27	90.0	96	2	08V3C6_VIRU	08V3c6 apple chlor
269	28	93.3	1122	2	08GVQ8_ORYSA	08gvq8 oryza sativ	342	27	90.0	96	2	08V3C7_VIRU	08V3c7 apple chlor
270	28	93.3	1171	2	Q97BJ7_THIEVO	Q97bj7 thermoplasm	343	27	90.0	96	2	08V3C8_VIRU	08V3c8 apple chlor
271	28	93.3	1205	2	Q5YL88_MOUSE	Q5yl88 mus musculu	344	27	90.0	96	2	08V3D0_VIRU	08V3d0 apple chlor
272	28	93.3	1222	2	Q4T4E0_TETNG	Q4t4e0 tetraodon n	345	27	90.0	96	2	08V3D1_VIRU	08V3d1 apple chlor
273	28	93.3	1248	2	Q6GND6_XENLA	Q6gnd6 xenopus lae	346	27	90.0	96	2	08V3D2_VIRU	08V3d2 apple chlor
274	28	93.3	1300	2	Q7PTD0_ANOGA	Q7ptd0 anopheles g	347	27	90.0	96	2	08V3D4_VIRU	08V3d4 apple chlor
275	28	93.3	1435	2	Q8GVF4_GREOV	Q8gvf4 eyach virus	348	27	90.0	101	2	08JPE0_VIRU	08Jpe0 apple chlor
276	28	93.3	1540	2	Q6XZL8_MOUSE	Q6xzl8 mus musculu	349	27	90.0	108	2	Q7YN64_EIMTE	Q7yn64 elmeria ten
277	28	93.3	1565	2	Q571B8_MOUSE	Q571b8 mus musculu	350	27	90.0	117	1	HV1B_HUMAN	PO1743 homo sapien
278	28	93.3	1607	2	Q8RH77_FUSNN	Q8rh77 fusobacteri	351	27	90.0	120	1	05H1T0_VIRU	05h1t0 homo sapien
279	28	93.3	1640	2	Q8JNK9_9LIDO	Q8jnk9 gill-associ	352	27	90.0	120	2	05S8T0_VIRU	05s8t0 cherry gree
280	28	93.3	1666	2	Q8ON15_9NIDO	Q8on15 yellow head	353	27	90.0	121	2	05S8T3_CRYNE	05s8t3 cryptococcu
281	28	93.3	1739	1	DOT1L_HUMAN	Q8ek12 homo sapien	354	27	90.0	121	2	0566S2_VIRU	0566s2 apple chlor
282	28	93.3	1751	2	Q54T12_DICDI	Q54t12 dictyosteli	355	27	90.0	124	2	Q9UL92_HUMAN	Q9ul92 homo sapien
283	28	93.3	1848	1	DOT1L_DROME	Q8mr12 drosophila	356	27	90.0	125	2	Q8E5H6_STRA3	Q8e5h6 streptococc
284	28	93.3	2415	1	SPTCA_DROME	P13395 drosophila	357	27	90.0	152	2	Q8XPD1_CLOJE	Q8xpd1 clostridium
285	28	93.3	2837	1	Q52PA6_SDELT	Q52pab angiococcus	358	27	90.0	165	2	Q8Y1U2_BRUME	Q8y1u2 brucella me
286	28	93.3	3895	2	Q65464_9PLAV	Q65464 border dise	359	27	90.0	169	2	Q57BU6_BRUBA	Q57bu6 brucella ab
287	28	93.3	3895	2	Q9PZ97_9PLAV	Q9pzz97 pestivirus	360	27	90.0	199	2	Q8FZ19_BRUBA	Q8fz19 brucella su
288	28	93.3	3896	2	P87514_9PLAV	P87514 border dise	361	27	90.0	178	2	Q4ZSR6_PLABE	Q4zsr6 plasmodium
289	28	93.3	3897	2	Q98Y26_9PLAV	Q98y26 classical s	362	27	90.0	201	2	Q6MYX0_ASPTU	Q6myx0 aspergillus
290	28	93.3	3898	1	POLG_HCVA	P11712 h genome po	363	27	90.0	216	2	Q97DW7_CLOAB	Q97dw7 clostridum
291	28	93.3	3898	1	POLG_HCVA	P21560 h genome po	364	27	90.0	221	2	Q4WSU0_ASPTU	Q4wsu0 aspergillus
292	28	93.3	3898	2	Q92366_9PLAV	Q92366 classical s	365	27	90.0	222	2	Q9FLQ3_ARATH	Q9flq3 arabidopsis
293	28	93.3	3898	2	Q592M3_9PLAV	Q592m3 classical s	366	27	90.0	223	2	Q9YPM5_VIRU	Q9ypm5 sugarcane s
294	28	93.3	3898	2	Q5JOW4_9PLAV	Q5jow4 classical s	367	27	90.0	227	2	Q8DZS7_STRA5	Q8dzs7 streptococc
295	28	93.3	3898	2	Q5J1KO_9PLAV	Q5j1ko classical s	368	27	90.0	228	2	Q9UEF4_PLAFA	Q9uef4 plasmodium
296	28	93.3	3898	2	Q5RLU0_9PLAV	Q5rlu0 classical s	369	27	90.0	234	2	Q9UCF5_PLAFA	Q9ucf5 plasmodium
297	28	93.3	3898	2	Q5U8X5_9PLAV	Q5u8x5 classical s	370	27	90.0	237	2	Q6MS64_MYCMS	Q6ms64 mycoplasma
298	28	93.3	3898	2	Q6BDP6_9PLAV	Q6bdp6 classical s	371	27	90.0	279	2	Q4URF4_THEAN	Q4urf4 theileria a
299	28	93.3	3898	2	Q6TY14_9PLAV	Q6ty14 classical s	372	27	90.0	292	2	Q648F1_9ARCH	Q648f1 uncultured
300	28	93.3	3898	2	Q6UKZ9_9PLAV	Q6ukz9 classical s	373	27	90.0	292	2	Q12015_YEARF	Q12015 saccharomyc
301	28	93.3	3898	2	Q6OBBO_9PLAV	Q6obbo classical s	374	27	90.0	293	2	Q7SDM8_NEUCR	Q7sdm8 neurospora
302	28	93.3	3898	2	Q8UZK1_9PLAV	Q8uzk1 classical s	375	27	90.0	301	2	Q51UD4_VIRU	Q51ud4 banana viru
303	28	93.3	3898	2	Q91BS9_9PLAV	Q91bs9 classical s	376	27	90.0	312	2	Q9Y9N2_AERPE	Q9y9n2 aeropyrum p
304	28	93.3	3898	2	Q991S8_9PLAV	Q991s8 classical s	377	27	90.0	315	2	Q4RHX9_TETNG	Q4rhx9 tetradodon n
305	28	93.3	3898	2	Q99BK1_9PLAV	Q99bk1 classical s	378	27	90.0	316	2	Q8Z2P5_PYRAE	Q8z2p5 pyrobaculum
306	28	93.3	3898	2	Q9YRM6_9PLAV	Q9yrm6 classical s	379	27	90.0	328	2	Q4NBS9_THIEPA	Q4nbs9 theileria p
307	28	93.3	3898	2	Q9YX30_9PLAV	Q9yx30 classical s	380	27	90.0	328	2	Q8E8F5_OCRTH	Q8e8f5 oenococcu
308	28	93.3	3898	2	Q99710_9PLAV	Q99710 classical s	381	27	90.0	331	2	Q9RGJ3_BACFR	Q9rgj3 bacteroides
309	28	93.3	3898	2	Q92364_9PLAV	Q92364 classical s	382	27	90.0	339	2	Q41FN0_GIBBE	Q41fn0 gibberella
310	28	93.3	3898	2	Q68534_9PLAV	Q68534 classical s	383	27	90.0	353	2	Q8TNU4_METAC	Q8tnu4 methanosaer
311	28	93.3	3898	2	Q68535_9PLAV	Q68535 classical s	384	27	90.0	354	2	Q4JF96_STANU	Q4jfe6 staphylococ
312	28	93.3	3898	2	Q68871_9PLAV	Q68871 classical s	385	27	90.0	354	2	Q9XB85_STANU	Q9xb85 staphylococ
313	28	93.3	3898	2	Q68872_9PLAV	Q68872 classical s	386	27	90.0	354	2	Q7V6B4_BROMN	Q7v6b4 streptococo
314	28	93.3	3898	2	Q68964_9PLAV	Q68964 classical s	387	27	90.0	354	2	Q6GKQ3_STAR	Q6gkq3 staphylococ
315	28	93.3	3898	2	Q68965_9PLAV	Q68965 classical s	388	27	90.0	354	2	Q5HK36_STANU	Q5hk36 staphylococ
316	28	93.3	3898	2	Q8JP77_9PLAV	Q8jp77 classical s	389	27	90.0	354	2	Q7A3O3_STANU	Q7a3o3 staphylococ
317	28	93.3	3898	2	Q96891_9PLAV	Q96891 classical s	390	27	90.0	354	2	Q7A8C3_STANU	Q7a8c3 staphylococ
318	28	93.3	3990	2	Q96205_PLAFA	Q96205 classical s	391	27	90.0	362	2	Q9MJ80_PHYPO	Q9mj80 physearum po
319	27	90.0	30	2	Q7RNM7_PLAYO	Q7rnm7 plasmodium	392	27	90.0	363	2	Q4XXW0_PLACH	Q4xxw0 vibrio vuln
320	27	90.0	61	2	Q9XBY8_BRACM	Q9xyb8 bractisica ca	393	27	90.0	367	2	Q8DAU7_VIBVY	Q8dau7 vibrio vuln
321	27	90.0	76	2	Q52OB3_NOCFA	Q52ob3 nocardia fa	394	27	90.0	367	2	Q7MGF1_VIBVY	Q7mgf1 vibrio vuln
322	27	90.0	96	2	Q8V3A5_VIRU	Q8v3a5 apple chlor	395	27	90.0	374	2	Q961V2_DROME	Q961v2 drosophila
323	27	90.0	96	2	Q8V3A6_VIRU	Q8v3a6 apple chlor	396	27	90.0	383	2	Q6PUC9_HUMAN	Q6pje9 homo sapien

397	27	90.0	384	2	05FMW9_LACAC	05fmw9_lactobacilli
398	27	90.0	387	2	Q7ROP5_PLAYO	Q7rop5_plasmodium
399	27	90.0	389	2	081W89_BACAN	081w89_bacillus an
400	27	90.0	397	1	Y1601_ANASP	P46015 anabesna sp
401	27	90.0	398	2	P74473_SYNEJ3	064473 synechocyst
402	27	90.0	398	2	08DHV0_SYNEL	08dhv0_synechococc
403	27	90.0	402	2	04TN39_9SPHN	04tn39_eylthrobact
404	27	90.0	404	2	06HND3_BACAN	06hnd3_bacillus an
405	27	90.0	413	1	DCH5_LYCRS	P54772 lycopersico
406	27	90.0	422	2	Q7UI66_RHOBA	Q7ui66_rhodospirilli
407	27	90.0	426	2	Q7MY72_PHOLA	Q7my72_photorehabdu
408	27	90.0	430	1	TILS_RICPR	09zeas_rickettsia
409	27	90.0	437	2	089253_VAVR	089253_variella vir
410	27	90.0	451	2	Q4J4A1_SULAC	Q4j4a1_sulfolobus
411	27	90.0	453	2	Q97582_SULTO	Q97582_sulfolobus
412	27	90.0	453	2	Q6MTD9_MYCMS	Q6mtd9_mycoplasm
413	27	90.0	465	2	Q7SA07_NEUCR	Q7sa07_neutrospora
414	27	90.0	478	2	Q4QR71_RAT	Q4qr71_rattus norv
415	27	90.0	486	2	Q97BU0_THEVO	Q97bu0_thermoplasm
416	27	90.0	494	2	Q6J3R0_DROME	06j3r0_drosophila
417	27	90.0	494	2	Q6WEO0_ORISA	Q6wEO0_oryza sativ
418	27	90.0	506	1	CP6A8_DROME	Q27593 drosophila
419	27	90.0	514	2	Q8IS17_PLAFA	Q8is17_plasmodium
420	27	90.0	514	2	Q81IR7_PLAF7	Q81ir7_plasmodium
421	27	90.0	517	1	MATK_LYCCR	054873 lycopodiell
422	27	90.0	519	2	OSLDZ4_BACFN	05ldz4_bacteroides
423	27	90.0	519	2	Q64V31_BACFR	Q64v31_bacteroides
424	27	90.0	531	2	Q5APU6_CANAL	Q5apj6_candida alb
425	27	90.0	555	2	Q8RTF7_OENOE	Q8rtf7_oenococcus
426	27	90.0	571	2	Q9LI98_ARATH	Q9li98_arabidopsi
427	27	90.0	574	2	Q569W2_MOUSE	Q569w2_mus musc
428	27	90.0	584	2	Q70207_ANOGA	Q702g7_anopheles g
429	27	90.0	595	2	Q66KX6_DICDI	Q66kx6_dicyosteli
430	27	90.0	596	2	Q6ZNO5_HUMAN	Q6zn05_homo sapien
431	27	90.0	643	1	VP4B_VACCV	P06440 vaccinia vi
432	27	90.0	644	1	VP4B_VACCC	P20643 vaccinia vi
433	27	90.0	644	1	VP4B_VARV	P31818 variola vir
434	27	90.0	644	2	Q93121_9POXV	Q93121_vaccinia vi
435	27	90.0	644	2	Q6RZ10_9POXV	Q6rzi0_rabbitpox v
436	27	90.0	644	2	Q76PZ6_VAVR	Q76pze_variella min
437	27	90.0	644	2	Q76ZRO_9POXV	Q76zr0_vaccinia vi
438	27	90.0	644	2	Q77582_CAMPS	Q77582_campeliox vi
439	27	90.0	644	2	Q8OMU6_COMPX	Q8omu6_cowpox viru
440	27	90.0	644	2	Q8V202_CAMPM	Q8v202_campeliox vi
441	27	90.0	644	2	Q8V4X2_MONPV	Q8v4x2_monkeypox v
442	27	90.0	644	2	Q9JF95_VACCT	Q9jf95_vaccinia vi
443	27	90.0	644	2	Q80DW7_COMPX	Q80dw7_cowpox viru
444	27	90.0	654	2	Q8JLA9_9POXV	Q8jla9_ectromella
445	27	90.0	654	2	Q616A5_CABBR	Q616a5_caenorhabdi
446	27	90.0	661	2	Q8JTS7_LSDV	Q8jts7_lumpy skin
447	27	90.0	661	2	Q91MR9_LSDV	Q91mr9_lumpy skin
448	27	90.0	667	2	Q19367_CABEL	Q19367_caenorhabdi
449	27	90.0	672	2	Q8QHN9_COMPX	Q8qhn9_cowpox viru
450	27	90.0	707	2	Q5NGM7_FRATT	Q5ngm7_francisella
451	27	90.0	717	2	Q614N7_ORISA	Q614n7_oryza sativ
452	27	90.0	722	2	Q782S9_9ALPH	Q782s9_gallid hepd
453	27	90.0	722	2	Q9QTC7_9ALPH	Q9qtc7_marek's dis
454	27	90.0	729	2	Q5R112_IDILO	Q5r112_idiomarina
455	27	90.0	735	2	Q8EBQ4_SHEON	Q8ebq4_sheanella
456	27	90.0	742	2	Q9ZN31_HBLPJ	Q9zn31_helicobacte
457	27	90.0	757	2	Q5CT46_CRYPV	Q5ct46_cryptospori
458	27	90.0	758	2	Q5CK44_CRYHO	Q5ck44_cryptospori
459	27	90.0	796	2	Q81S26_9BACU	Q81s26_phthorimeae
460	27	90.0	811	2	Q8S7P4_ORYSA	Q8s7p4_oryza sativ
461	27	90.0	829	2	Q6WNV6_9REOV	Q6wnv6_avian rotav
462	27	90.0	868	2	Q4YV14_PLABE	Q4yv14_plasmodium
463	27	90.0	873	2	Q510S9_ENTHI	Q510s9_enteomeba h
464	27	90.0	876	2	Q66H85_RAT	Q66h85_rattus norv
465	27	90.0	924	2	Q41313_GTBZE	Q41313_gliberella
466	27	90.0	933	2	Q5TS61_ANOGA	Q5ts61_anopheles g
467	27	90.0	960	2	Q91GJ3_NPEVP	Q91gj3_epiphyas po
468	27	90.0	984	1	DPOL_NPVOP	P18131 autographa
469	27	90.0	985	1	DPOL_NPVOP	Q83948 oryia pseu

689	26	86.7	192	1	Y3379_CLOAB	O97du2_clostridium	762	26	86.7	226	2	O69XM7_ORYSA	O69xm7_oryza sativ
690	26	86.7	192	2	OSUO21_MIMIV	OSuq21_mimivirus	763	26	86.7	228	2	O4UR90_XANCP	O4ur90_xanthomonas
691	26	86.7	194	2	O5C217_SCHUA	O5c217_schistosoma	764	26	86.7	228	2	O8PAD5_XANCP	O8pad5_xanthomonas
692	26	86.7	194	2	Q4TDx4_TETNG	Q4tdx4_tetradodon n	765	26	86.7	229	2	O81595_PLAF7	O81595_plasmodium
693	26	86.7	195	2	Q4EY3_PLABE	Q4ey3_plasmodium	766	26	86.7	229	2	O4HTA9_CAMUP	O4hta9_campylobact
694	26	86.7	196	2	O8SR4_PYRAE	O8sr4_pyrobaculum	767	26	86.7	230	2	O7RIV6_PLAYO	O7riv6_plasmodium
695	26	86.7	197	2	O9PP4_XYLFA	O9pp4_xylella fas	768	26	86.7	230	2	O17593_CAEEL	O17593_caenorhabdi
696	26	86.7	197	2	O7UG4_RHOBA	O7ug4_rhodopirell	769	26	86.7	230	2	O8VUP5_STRSU	O8vup5_streptococc
697	26	86.7	199	2	O64EM4_PARCH	O64em4_uncultured	770	26	86.7	231	1	ALSE_ECOLI	ALse_ecoli
698	26	86.7	199	2	Q4YIC2_PLABE	Q4yic2_plasmodium	771	26	86.7	231	2	O67FM1_PASPA	O67fm1_hyacinthus
699	26	86.7	199	2	O87BB8_XYLFT	O87bb8_xylella fas	772	26	86.7	232	2	O47580_ONCVO	O47580_onchocerca
700	26	86.7	201	2	O8AAS1_BACTN	O8aas1_bacteroides	773	26	86.7	232	2	O70UR8_DIRIM	O70ur8_dirofilaria
701	26	86.7	203	1	SEL9_CAEEL	O17528_caenorhabdi	774	26	86.7	233	2	O8FAM7_ECOL6	O8fam7_escherichia
702	26	86.7	203	2	O9VEF4_SULTO	O9vef4_sulfolobus	775	26	86.7	233	2	O4RPE1_TETNG	O4rpe1_tetradodon n
703	26	86.7	203	2	O61GB4_CAEER	O61gb4_caenorhabdi	776	26	86.7	236	2	O83VD1_9GANM	O83vd1_photobacter
704	26	86.7	203	2	O7Q4R1_ANOGA	O7q4r1_anopheles g	777	26	86.7	236	2	O83VD2_9GANM	O83vd2_photobacter
705	26	86.7	204	2	O5ENL8_HETTR	O5enl8_heterocapsa	778	26	86.7	236	2	O83VD3_PHOTO	O83vd3_photobacter
706	26	86.7	204	2	O83VP3_STRSU	O83vp3_streptococc	779	26	86.7	243	2	O8SCM3_9CAUD	O8scm3_pseudomonas
707	26	86.7	205	2	O83VNS_STRSU	O83vns_streptococc	780	26	86.7	246	2	O5V516_HALMA	O5v516_haloaercula
708	26	86.7	205	2	O87BM4_XYLFT	O87bm4_xylella fas	781	26	86.7	246	2	O4XL41_PLACH	O4xl41_plasmodium
709	26	86.7	205	2	O87BN0_XYLFT	O87bn0_xylella fas	782	26	86.7	246	2	O4Z3W9_PLABE	O4z3w9_plasmodium
710	26	86.7	205	2	O9PAT9_XYLFA	O9pat9_xylella fas	783	26	86.7	246	2	O6EDZ3_LACCA	O6edz3_lactobacilli
711	26	86.7	205	2	O9PAU3_XYLFA	O9pau3_xylella fas	784	26	86.7	247	2	O5WHZ4_BACSK	O5whz4_bacillus c1
712	26	86.7	206	2	O65297_9VIRU	O65297_anapari_vir	785	26	86.7	251	2	O8XE14_ECO57	O8xe14_escherichia
713	26	86.7	207	1	NODS_AZOCA	O07758_azornitrobiu	786	26	86.7	251	2	O5PCU8_RAT	O5pcu8_rattus norv
714	26	86.7	208	2	O893A6_CLOTE	O893a6_clostridium	787	26	86.7	252	2	O75CC09_ASHGO	O75cc09_ashya goss
715	26	86.7	209	1	RANIA_LORJA	P54765_lotus japon	788	26	86.7	252	2	O4YNE8_PLABE	O4yne8_plasmodium
716	26	86.7	209	1	RANIB_LORJA	P54766_lotus japon	789	26	86.7	252	2	O4XA41_PSER5	O4xa41_pseudomonas
717	26	86.7	210	2	O84MP2_ORYSA	O84mp2_oryza sativ	790	26	86.7	253	2	O4Z7F1_PLABE	O4z7f1_plasmodium
718	26	86.7	210	2	O6G8U3_STRAS	O6g8u3_staphylococ	791	26	86.7	255	2	O941B9_ARATH	O941b9_arabidopsis
719	26	86.7	210	2	O6GFx4_STRAC	O6gfxx4_staphylococ	792	26	86.7	257	2	O9U259_CAEEL	O9u259_caenorhabdi
720	26	86.7	210	2	O5HP40_STRAC	O5hpf40_staphylococ	793	26	86.7	258	2	O9HS04_HALSA	O9hs04_haloactereri
721	26	86.7	210	2	O7AS34_STRAM	O7as34_staphylococ	794	26	86.7	259	2	O5AR05_EMENI	O5ar05_aspergillus
722	26	86.7	210	2	O8NM35_STRAM	O8nm35_staphylococ	795	26	86.7	259	2	O9K6C4_BACND	O9k6c4_bacillus ha
723	26	86.7	210	2	O99TD0_STRAM	O99td0_staphylococ	796	26	86.7	260	2	O6VU49_MANSE	O6vu49_manduca sex
724	26	86.7	210	2	O8XAR9_ECO57	O8xar9_escherichia	797	26	86.7	261	2	O7RXZ5_NEUCR	O7rxz5_neutrospora
725	26	86.7	212	2	O5E7Z4_VIBF1	O5e7z4_vibrio fisc	798	26	86.7	261	2	O7QBZ2_ANOGA	O7qbz2_anopheles g
726	26	86.7	213	2	O83VN9_STRSU	O83vn9_streptococc	799	26	86.7	261	2	O7OB05_ANOGA	O7qb05_anopheles g
727	26	86.7	214	2	O9LIL4_ARATH	O9lil4_arabidopsis	800	26	86.7	262	2	O58CR5_BOVIN	O58cr5_bos taurus
728	26	86.7	215	1	KAD_BUCAT	P55556_buchnera ap	801	26	86.7	264	2	O7P2B8_FUSNV	O7p2b8_fusobacteri
729	26	86.7	215	2	O73M60_TREDE	O73m60_trepomema d	802	26	86.7	266	2	O4YZ14_PLABE	O4yz14_plasmodium
730	26	86.7	216	2	O96F25_HUMAN	O96f25_homo sapien	803	26	86.7	266	2	O8KU37_ENTRA	O8ku37_enterococcu
731	26	86.7	216	2	O41GW7_9BURK	O41gw7_burkholderi	804	26	86.7	270	2	O57U0A_9TRYP	O57u0a_trypanosoma
732	26	86.7	216	2	O56671_VIBCH	O56671_vibrio chol	805	26	86.7	270	2	O4UBB4_THEAM	O4ubb4_thellexia a
733	26	86.7	216	2	O65CZ1_BACLD	O65cz1_bacillus li	806	26	86.7	272	2	O6CMZ8_KLULA	O6cmz8_kluyveromyc
734	26	86.7	220	2	O6SL21_9MAXI	O6sl21_argulus ame	807	26	86.7	275	2	O5JA25_9LABR	O5ja25_scarus dimi
735	26	86.7	220	1	RANI_ARATH	P41916_arabidopsis	808	26	86.7	276	2	O61OU1_BACAN	O61ou1_bacillus an
736	26	86.7	221	1	RANI_LYCES	P38546_lycopersico	809	26	86.7	276	2	O4MT41_BACCE	O4mt41_bacillus ce
737	26	86.7	221	1	RAN2_ARATH	P41917_arabidopsis	810	26	86.7	276	2	O63DD2_BACCE	O63dd2_bacillus ce
738	26	86.7	221	1	RAN2_LYCES	P38547_lycopersico	811	26	86.7	276	2	O6HKU4_BACCH	O6hku4_bacillus ch
739	26	86.7	221	1	RANAI_TOBAC	P41918_nicotiana t	812	26	86.7	276	2	O73AP1_BACC1	O73ap1_bacillus ce
740	26	86.7	221	1	RANBI_TOBAC	P41919_nicotiana t	813	26	86.7	276	2	O81FH3_BACCR	O81fh3_bacillus ce
741	26	86.7	221	1	RAN_VICPA	P38548_vicia faba	814	26	86.7	276	2	O81SK7_BACAN	O81sk7_bacillus an
742	26	86.7	221	2	O04148_ARATH	O04148_arabidopsis	815	26	86.7	278	2	O5FH23_EHRNG	O5fh23_entrichia r
743	26	86.7	221	2	O22495_ARATH	O22495_arabidopsis	816	26	86.7	278	2	O6SUD0_9RHOB	O6sud0_marine alph
744	26	86.7	221	2	O6J9G2_NICSY	O6j9g2_nicotiana s	817	26	86.7	278	2	O6TFB6_CLOTE	O6tfb6_clostridium
745	26	86.7	221	2	O7F717_ORYSA	O7f717_oryza sativ	818	26	86.7	278	2	O5XDA2_STRP6	O5xda2_streptococc
746	26	86.7	221	2	O7GD79_ORYSA	O7gd79_oryza sativ	819	26	86.7	278	2	O9A101_STRPY	O9a101_streptococc
747	26	86.7	221	2	O8H156_ARATH	O8h156_arabidopsis	820	26	86.7	278	2	O7CNG5_STRP8	O7cng5_streptococc
748	26	86.7	221	2	O8S227_HELAN	O8s227_helianthus	821	26	86.7	278	2	O7CFD0_STRP3	O7cfd0_streptococc
749	26	86.7	221	2	O944C6_WHEAT	O944c6_triticum ae	822	26	86.7	278	2	O5HBB8_EHRMW	O5hbb8_entrichia r
750	26	86.7	221	2	O9FSZ5_CICAR	O9fsz5_cicer ariet	823	26	86.7	282	2	O6L201_PICVO	O6l201_picrophilus
751	26	86.7	221	2	O9XJ44_ORYSA	O9xj44_oryza sativ	824	26	86.7	282	2	O81I65_PLAF7	O81i65_plasmodium
752	26	86.7	221	2	O9XJ45_ORYSA	O9xj45_oryza sativ	825	26	86.7	284	2	O8Y5D1_LISMO	O8y5d1_listeria mo
753	26	86.7	221	2	O04664_ARATH	O04664_arabidopsis	826	26	86.7	285	2	O6VZC5_CNPV	O6vzc5_canarypox v
754	26	86.7	222	2	O7AE34_ECO57	O7ae34_escherichia	827	26	86.7	286	2	O64S03_BACFR	O64s03_bacteroides
755	26	86.7	222	2	O5LCY0_BACFN	O5lcy0_bacteroides	828	26	86.7	286	2	O97RX6_STRPN	O97rx6_streptococc
756	26	86.7	222	2	O64U40_BACFR	O64u40_bacteroides	829	26	86.7	290	2	O6H050_BACAN	O6h050_bacillus an
757	26	86.7	223	2	O8DXX1_SYNEL	O8dxx1_synechococc	830	26	86.7	291	2	O8DOP1_STRR6	O8dop1_streptococc
758	26	86.7	223	2	O6SNC1_TRAAU	O6snc1_trachypithe	831	26	86.7	292	2	O81JK7_BACAN	O81jk7_bacillus an
759	26	86.7	223	2	O7WK92_BORBR	O7wk92_bordecella	832	26	86.7	293	2	O4MLM4_BACCE	O4mlm4_bacillus ce
760	26	86.7	225	2	O17602_CAEEL	O17602_caenorhabdi	833	26	86.7	293	2	O6HA19_BACCK	O6ha19_bacillus th
761	26	86.7	226	2	O54V65_DICDI	O54v65_dicyosteli	834	26	86.7	293	2	O72WZ8_BACCI	O72wz8_bacillus ce


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981 26 86.7 382 2 06C0A8_YARLI 06C0A8_Yarlowia_1i
982 26 86.7 383 2 076HJ4_ACTIBA 076HJ4_actinobact
983 26 86.7 384 1 VHZ_HPV3 076HJ4_actinobact
984 26 86.7 384 1 VHXF_SCHPO 059735_schizosacch
985 26 86.7 384 2 08FGV8_ECOL6 08FGV8_escherichia
986 26 86.7 386 1 DCHS_VIBAN 056581_vibrioangu
987 26 86.7 386 2 049638_ARATH 049638_arabidopsi
988 26 86.7 386 2 079JY8_VIBAN 079JY8_vibrioangu
989 26 86.7 387 2 07T5M8_GYCL 07T5M8_cryptophleb
990 26 86.7 388 2 07UNA9_RKROA 07UNA9_rhodospirill
991 26 86.7 389 1 GR68A_DROME 09VTN0_drosophila
992 26 86.7 389 2 04JY04_SYRPN 04JY04_streptococc
993 26 86.7 390 2 04J862_SULAC 04J862_sulfolobus
994 26 86.7 390 2 09J235_PLAF7 09J235_plasmodium
995 26 86.7 390 2 04XHT8_PLACH 04XHT8_plasmodium
996 26 86.7 393 2 06CUS0_KULUA 06CUS0_kluveromyc
997 26 86.7 393 2 062IA3_CAEBR 062IA3_caenorhabdi
998 26 86.7 393 2 018315_CAEEL 018315_caenorhabdi
999 26 86.7 393 2 07T315_BRARE 07T315_brachydantio
1000 26 86.7 394 2 07XYS8_9ASTR 07XYS8_atentisia t

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ALIGNMENTS

RESULT 1

Q4YV5_PLABE PRELIMINARY; PRT; 68 AA.

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ID Q4YV5_PLABE PRELIMINARY; PRT; 68 AA.
AC Q4YV5;
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=PB104018.00.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NC NCB1_TaxID=5821;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlson J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen G.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell J.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Jaise C.J., Barrett B., Turner C.M.R., Waters A.P., Sinden R.S.;
RA "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC preliminary data.
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
DR EMBL; CAAT01001634; CAH96793.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 68 AA; 8555 MW; F1E7C9675526DBBC CRC64;

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Query Match 100.0%; Score 30; DB 2; Length 68;
 Best Local Similarity 100.0%; Pred. No. 74;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
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 Db 5 SYTH 9

RESULT 2

058463_PYRHO PRELIMINARY; PRT; 104 AA.

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ID 058463_PYRHO PRELIMINARY; PRT; 104 AA.
AC 058463;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Hypothetical protein PH0732.
GN OrderedLocusNames=PH0732;

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OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
NC NCB1_TaxID=53953;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=OT3;
RX MEDLINE=98344137; PubMed=9679194;
RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA Yamamoto S., Sekine W., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuchi Y., Shitaya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
RL DNA Res. 5:55-76(1998).
DR EMBL; BA000001; BAA29823.1; -; Genomic_DNA.
DR PIR; E71120.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 104 AA; 12464 MW; BC41918F6F570DB3 CRC64;

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Query Match 100.0%; Score 30; DB 2; Length 104;
 Best Local Similarity 100.0%; Pred. No. 11e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
 |||||
 Db 67 SYTH 71

RESULT 3

Q8V590_TYLCs PRELIMINARY; PRT; 104 AA.

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ID Q8V590_TYLCs PRELIMINARY; PRT; 104 AA.
AC Q8V590;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE C2 protein TrAP (Fragment).
OS Tomato yellow leaf curl Sardinia virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
NC NCB1_TaxID=123735;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Navas-Castillo J., Sanchez-Campos S., Moriones E.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF376007; ALU57259.1; -; Genomic_DNA.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR000942; Gemin1 AL2.
DR Pfam; PF01440; Gemin1 AL2; I.
DR PRINTS; PR00230; GEMCONTAL2.
DR ProDom; PD001117; Gemin1_AL2; 1.
FT NON TER 1
FT NON TER 104
SQ SEQUENCE 104 AA; 12100 MW; A91792747F9B5639 CRC64;

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Query Match 100.0%; Score 30; DB 2; Length 104;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
 |||||
 Db 34 SYTH 38

RESULT 4

Q8V593_TYLCs PRELIMINARY; PRT; 104 AA.

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ID Q8V593_TYLCs PRELIMINARY; PRT; 104 AA.
AC Q8V593;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

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DE C2 protein TrAP (Fragment).
OS Tomato yellow leaf curl Sardinia virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=123735;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Navas-Castillo J., Sanchez-Campos S., Moriones E.;
  Submitted (MAY-2001) to the EMBL/Genbank/DBJ databases.
RL EMBL; AF376006; AAL57256.1; -; Genomic_DNA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000942; Gemini_AL2; 1.
DR Pfam; PF01440; Gemini_AL2; 1.
DR PRINTS; PR00230; GEMCOATAL2.
DR ProDom; PD001117; Gemini_AL2; 1.
FT NON_TER 1
FT NON_TER 104
SQ SEQUENCE 104 AA; 12147 MW; B71672747F9B5639 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
Db 34 SYTH 38

RESULT 5
Q8V596 TYLCS
ID Q8V596 TYLCS PRELIMINARY; PRT; 104 AA.
AC Q8V596;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE C2 protein TrAP (Fragment).
OS Tomato yellow leaf curl Sardinia virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=123735;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Navas-Castillo J., Sanchez-Campos S., Moriones E.;
  Submitted (MAY-2001) to the EMBL/Genbank/DBJ databases.
RL EMBL; AF376005; AAL57253.1; -; Genomic_DNA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000942; Gemini_AL2.
DR Pfam; PF01440; Gemini_AL2; 1.
DR PRINTS; PR00230; GEMCOATAL2.
DR ProDom; PD001117; Gemini_AL2; 1.
FT NON_TER 1
FT NON_TER 104
SQ SEQUENCE 104 AA; 12144 MW; AAD672747F91P696 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
Db 34 SYTH 38

RESULT 6
Q8V599 TYLCS
ID Q8V599 TYLCS PRELIMINARY; PRT; 104 AA.
AC Q8V599;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE C2 protein TrAP (Fragment).
OS Tomato yellow leaf curl Sardinia virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
```

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OX NCBI_TaxID=123735;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Navas-Castillo J., Sanchez-Campos S., Moriones E.;
  Submitted (MAY-2001) to the EMBL/Genbank/DBJ databases.
RL EMBL; AF376004; AAL57250.1; -; Genomic_DNA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000942; Gemini_AL2.
DR Pfam; PF01440; Gemini_AL2; 1.
DR PRINTS; PR00230; GEMCOATAL2.
DR ProDom; PD001117; Gemini_AL2; 1.
FT NON_TER 1
FT NON_TER 104
SQ SEQUENCE 104 AA; 12147 MW; B711050478EC2639 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
Db 34 SYTH 38

RESULT 7
Q8V5A2 TYLCS
ID Q8V5A2 TYLCS PRELIMINARY; PRT; 104 AA.
AC Q8V5A2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE C2 protein TrAP (Fragment).
OS Tomato yellow leaf curl Sardinia virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=123735;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Navas-Castillo J., Sanchez-Campos S., Moriones E.;
  Submitted (MAY-2001) to the EMBL/Genbank/DBJ databases.
RL EMBL; AF376003; AAL57247.1; -; Genomic_DNA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000942; Gemini_AL2.
DR Pfam; PF01440; Gemini_AL2; 1.
DR PRINTS; PR00230; GEMCOATAL2.
DR ProDom; PD001117; Gemini_AL2; 1.
FT NON_TER 1
FT NON_TER 104
SQ SEQUENCE 104 AA; 12207 MW; 2837A060D46FE972 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
Db 34 SYTH 38

RESULT 8
Q8V5A5 TYLCS
ID Q8V5A5 TYLCS PRELIMINARY; PRT; 104 AA.
AC Q8V5A5;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE C2 protein TrAP (Fragment).
OS Tomato yellow leaf curl Sardinia virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=123735;
RN [1]
RP NUCLEOTIDE SEQUENCE.
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RA Navas-Castillo J., Sanchez-Campos S., Moriones E.;
RL Submitted (May-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF376002; AAU57244.1; -; Genomic_DNA.
DR GO; GO:0019028; C:Viral capsid, IEA.
DR GO; GO:0005198; F:Structural molecule activity, IEA.
DR InterPro; IPR000942; Gemini AL2.
DR Pfam; PF01440; Gemini AL2; 1.
DR PRINTS; PR00230; GEMICADAL2.
DR ProDom; PD001117; Gemini AL2; 1.
FT NON_TER
FT 1
SQ SEQUENCE 104 AA; 12147 MW; B71672747F9B5639 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. NO. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
Db 34 SYTH 38

RESULT 9
COMG BACSU STANDARD; PRT; 124 AA.
ID COMG BACSU STANDARD; PRT; 124 AA.
AC P25959;
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Comg operon protein 7 precursor.
GN Name=comG; Synonyms=comG7; OrderedLocNames=BSU24670;
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
CX NCBI_TaxID=1423;
CX [1]
RX NUCLEOTIDE SEQUENCE.
RX MEDLINE=90006773; PubMed=2507524;
RA Albano M., Breitling R., Dubnau D.A.;
RT "Nucleotide sequence and genetic organization of the Bacillus subtilis
RT comg operon." 171:5386-5404(1989).
RL J. Bacteriol. 171:5386-5404(1989).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RP STRAIN=168 / JH642;
RC MEDLINE=97124195; PubMed=8969508;
RX Mićuno M., Masuda S., Takemaru K.-I., Hosono S., Sato T., Takeuchi M.,
RA Kodayashi Y.;
RT "Systematic sequencing of the 283 kb 210 degrees-232 degrees region of
RT the Bacillus subtilis genome containing the skin element and many
RT sporulation genes."
RL Microbiology 142:3103-3111(1996).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=168;
RC MEDLINE=98044033; PubMed=9384377; DOI=10.1038/36786;
RX Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bartiro M.G., Bessieres P., Bolotin A., Borchert S.,
RA Boudreau R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.-K., Codani J.-J., Conerton I.F., Cummings N.J., Daniel R.A.,
RA Denicot F., Devine K.M., Duesterhoeft A., Ehrlich S.D., Emerson P.T.,
RA Entian K.-D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Chim S.-Y., Glaeser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guisepi G., Guy B.V., Haga K., Haiech J., Harwood C.R., Henaux A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.-F., Itaya M.,
RA Jones L.-M., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M.,
RA Klein C., Kobayashi Y., Koetter P., Koningsstein G., Krogh S.,
RA Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J.,
RA Lazarevic V., Lee S.-M., Levine A., Liu H., Masuda S., Manuel C.,
RA Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S.,
RA Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B.,
RA Park S.-H., Parro V., Pohl T.M., Portetelle D., Portwilk S.,

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RA Prescott A.M., Prescan E., Pujic P., Purnelle B., Rapoport G.,
RA Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B.,
RA Rose M., Sadie Y., Sato T., Scanlan E., Schleich S., Schroeter R.,
RA Scoffone F., Sekiguchi U., Sekowska A., Serron S.J., Serron P.,
RA Shin B.-S., Soldo B., Sorokin A., Taccani E., Takagi T., Takahashi H.,
RA Takemaru K., Takeuchi M., Takakoshi A., Tanaka T., Terpetra P.,
RA Toynoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F.,
RA Vaasartoci A., Viari A., Wambuit R., Wedler E., Wedler H.,
RA Weitznegger T., Winters P., Wipat A., Yamamoto H., Yamane K.,
RA Yasumoto K., Yata K., Yoshida K., Yoshikawa H.-F., Zumbstein E.,
RA Yoshikawa H., Zanchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis."
RL Nature 390:249-256(1997).
RN [4]
RP FUNCTION.
RX MEDLINE=96083053; PubMed=9422590;
RA Chung Y.S., Dubnau D.A.;
RT "All seven comg open reading frames are required for DNA binding
RT during transformation of competent Bacillus subtilis."
RL J. Bacteriol. 180:41-45(1998).
RN [5]
RP SUBCELLULAR LOCATION, AND PROBABLE DISULFIDE BOND.
RX MEDLINE=96389321; PubMed=9723928;
RA Chung Y.S., Breidt F., Dubnau D.A.;
RT "Cell surface localization and processing of the ComG proteins,"
RT required for DNA binding during transformation of Bacillus subtilis."
RL Mol. Microbiol. 29:905-913(1998).
CC CC -1- FUNCTION: Required for transformation and DNA binding.
CC CC -1- SUBUNIT: Homodimer; disulfide-linked. A minor fraction of comG is
CC CC found as a disulfide-bonded homodimer.
CC CC -1- SUBCELLULAR LOCATION: About half of pre-comG is present as a
CC CC peripheral membrane protein and the other half as an integral
CC CC protein. Upon (partial) processing comG is translocated to a
CC CC position outside the membrane.
CC CC -1- PTM: Partial processing of comG in competent cells requires comC.
CC CC
CC CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC CC the European Bioinformatics Institute. There are no restrictions on its
CC CC use as long as its content is in no way modified and this statement is not
CC CC removed.
CC CC -----
CC CC EMBL; M29691; AAA83373.1; -; Genomic DNA.
CC CC EMBL; D84432; BAA12538.1; -; Genomic DNA.
CC CC EMBL; Z99116; CAB14398.1; -; Genomic DNA.
CC CC PIR; H30338; H30338.
CC CC DR Subtilist; BG10489; comG.
CC CC KW Competence; Complete proteome; Signal; Transport.
CC CC FT SIGNAL 1
CC CC FT CHAIN 29 124 Comg operon protein 7.
CC CC FT DISULFID 34 34 Interchain (Probable).
CC CC SQ SEQUENCE 124 AA; 14540 MW; B3968089A6049421 CRC64;

Query Match 100.0%; Score 30; DB 1; Length 124;
Best Local Similarity 100.0%; Pred. NO. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
Db 80 SYTH 84

RESULT 10
VAL2 TYLCS
ID VAL2 TYLCS STANDARD; PRT; 135 AA.
AC P27263;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE AL2 protein (C2 protein).
GN Name=C2;
OS Tomato yellow leaf curl Sardinia virus.

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OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=123735;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=92107660; PubMed=1840676;
RA Khayat-Pour A., Bendahmane M., Matzeit V., Accotto G.P., Crespi S.,
  Gronenborn B.;
RT "Tomato yellow leaf curl virus from Sardinia is a whitefly-transmitted
  monopartite geminivirus.";
RL Nucleic Acids Res. 19:6763-6769 (1991).
CC -1- SIMILARITY: Belongs to the geminiviruses AL2 protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
  between the Swiss Institute of Bioinformatics and the EMBL outstation -
  the European Bioinformatics Institute. There are no restrictions on its
  use as long as its content is in no way modified and this statement is not
  removed.
CC -----
DR EMBL; X61153; CA943464.1; -; Genomic_DNA.
DR PIR; S22591; S22591.
DR InterPro; IPR000942; Gemini_AL2.
DR Pfam; PF01440; Gemini_AL2; 1.
DR PRINTS; PR00230; GEMCOATAL2.
DR PRODOM; PD001117; Gemini_AL2; 1.
SQ SEQUENCE 135 AA; 15719 MW; 3DE9A8DC8918A485 CRC64;

Query Match 100.0%; Score 30; DB 1; Length 135;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
Db 40 SYTH 44

RESULT 11
VAL2 TYLCU STANDARD; PRT; 135 AA.
ID VAL2 TYLCU
AC P38610;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE AL2 protein (C2 protein).
GN Name=C2;
OS Tomato yellow leaf curl virus (strain Murcia) (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=37139;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=94256836; PubMed=8198442;
RA Norris E., Hidalgo E., Accotto G., Moriones E.;
RT "High similarity among the tomato yellow leaf curl virus isolates from
  the west Mediterranean basin: the nucleotide sequence of an infectious
  clone from Spain.";
RL Arch. Virol. 135:165-170 (1994).
CC -1- SIMILARITY: Belongs to the geminiviruses AL2 protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
  between the Swiss Institute of Bioinformatics and the EMBL outstation -
  the European Bioinformatics Institute. There are no restrictions on its
  use as long as its content is in no way modified and this statement is not
  removed.
CC -----
DR EMBL; Z25751; CA81027.1; -; Genomic_DNA.
DR PIR; S39212; S39212.
DR InterPro; IPR000942; Gemini_AL2.
DR Pfam; PF01440; Gemini_AL2; 1.
DR PRINTS; PR00230; GEMCOATAL2.
DR PRODOM; PD001117; Gemini_AL2; 1.
SQ SEQUENCE 135 AA; 15687 MW; 90A70611624EC9AA CRC64;

Query Match 100.0%; Score 30; DB 1; Length 135;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
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- Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
Db 40 SYTH 44

RESULT 12
091596.9GEMI
ID 091596.9GEMI PRELIMINARY; PRT; 135 AA.
AC 091596;
DT 01-NOV-1998 (TRENBLrel. 08, Created)
DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE AC2 protein.
GN Name=AC2;
OS Mungbean yellow mosaic virus-Thailand.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=223294;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Kang H., Ikegami M.;
RL Submitted (Aug-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB017341; BAA33161.1; -; Genomic_DNA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000942; Gemini_AL2.
DR Pfam; PF01440; Gemini_AL2; 1.
DR PRINTS; PR00230; GEMCOATAL2.
DR PRODOM; PD001117; Gemini_AL2; 1.
SQ SEQUENCE 135 AA; 15269 MW; F0D277A5B37894BC CRC64;

Query Match 100.0%; Score 30; DB 2; Length 135;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 SYTH 5
Db 40 SYTH 44

RESULT 13
066UV8 TYLCS
ID 066UV8 TYLCS PRELIMINARY; PRT; 135 AA.
AC 066UV8;
DT 25-OCT-2004 (TRENBLrel. 28, Created)
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE Transcriptional activation protein.
OS Tomato yellow leaf curl Sardinia virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=123735;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Murcia;
RA El Mehrech K., Sedegui M., Arifi A., Hatimi A., Tahrouch S.,
  Czosnek H., Nakha M.K., Maxwell D.P.;
RT "Sequence of a full-length clone of Tomato yellow leaf curl Sardinia
  virus from Morocco.";
RL Submitted (Jul-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY02650; AAU08298.1; -; Genomic_DNA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000942; Gemini_AL2.
DR Pfam; PF01440; Gemini_AL2; 1.
DR PRINTS; PR00230; GEMCOATAL2.
DR PRODOM; PD001117; Gemini_AL2; 1.
SQ SEQUENCE 135 AA; 15656 MW; 95EA3AETB04EC9AA CRC64;

Query Match 100.0%; Score 30; DB 2; Length 135;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1 SYTH 5
|||||
Db 40 SYTH 44

RESULT 14

Q67619 TYLCS PRELIMINARY; PRT; 135 AA.
ID Q67619 TYLCS
AC Q67619
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE C2 protein.
OS Tomato yellow leaf curl Sardinia virus-[Spain2].
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_Taxid=221538;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Almeria;
RA Submitted (JMN-1994) to the EMBL/GenBank/DBJ databases.
RL EMBL; L27708; AAA47954.1; -, Genomic_DNA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR InterPro; IPR000942; Gemin AL2.
DR Pfam; PF01440; Gemin AL2; I.
DR PRINTS; PR00230; GEMCOATAL2.
DR ProDom; PD001117; Gemin AL2; 1.
SQ SEQUENCE 135 AA; 15690 MW; 95E21245624EC9AA CRC64;

Query Match 100.0%; Score 30; DB 2; Length 135;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYTH 5
|||||
Db 40 SYTH 44

RESULT 15

Q6WRU8_9GEMI PRELIMINARY; PRT; 135 AA.
ID Q6WRU8_9GEMI
AC Q6WRU8;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE AC2.
GN Name=AC2;
OS Mungbean yellow mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_Taxid=33726;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Tsai W.S.; Green S.K.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; AY21892; AAQ16298.1; -, Genomic_DNA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000942; Gemin AL2.
DR Pfam; PF01440; Gemin AL2; I.
DR PRINTS; PR00230; GEMCOATAL2.
DR ProDom; PD001117; Gemin AL2; 1.
SQ SEQUENCE 135 AA; 15255 MW; 310277A5B361BC1E CRC64;

Query Match 100.0%; Score 30; DB 2; Length 135;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYTH 5
|||||
Db 40 SYTH 44

RESULT 16
Q701P9_9GEMI PRELIMINARY; PRT; 135 AA.
ID Q701P9_9GEMI
AC Q701P9;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE AC2 protein.
GN Name=AC2;
OS Horsegram yellow mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_Taxid=263793;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Barnabas A.D.; Girish K.R.; Usha R.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; A627904; CAF29512.1; -, Genomic_DNA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR InterPro; IPR000942; Gemin AL2.
DR Pfam; PF01440; Gemin AL2; I.
DR PRINTS; PR00230; GEMCOATAL2.
DR ProDom; PD001117; Gemin AL2; 1.
SQ SEQUENCE 135 AA; 15409 MW; 48B33EDCD365929 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 135;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYTH 5
|||||
Db 40 SYTH 44

RESULT 17

Q7TLD7_9GEMI PRELIMINARY; PRT; 135 AA.
ID Q7TLD7_9GEMI
AC Q7TLD7;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE AC2.
GN Name=AC2;
OS Mungbean yellow mosaic virus - Soybean [Pakistan].
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_Taxid=269103;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Tsai W.S.; Green S.K.; Bashir M.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; AY269991; AAP34720.1; -, Genomic_DNA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000942; Gemin AL2.
DR Pfam; PF01440; Gemin AL2; I.
DR PRINTS; PR00230; GEMCOATAL2.
DR ProDom; PD001117; Gemin AL2; 1.
SQ SEQUENCE 135 AA; 15256 MW; 6824B706C371975 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 135;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYTH 5
|||||
Db 40 SYTH 44

RESULT 18

Q808T6_9GEMI PRELIMINARY; PRT; 135 AA.
ID Q808T6_9GEMI
AC Q808T6;
DT 01-JUN-2003 (TReMBLrel. 24, Created)

DT 01-JUN-2003 (TREMblrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
DE AC2.
GN Name=AC2;
OS Mungbean yellow mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=33726;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Tsai W.S., Green S.K.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY21896; AAP23257.1; -; Genomic_DNA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000942; Gemin AL2.
DR Pfam; PF01440; Gemin AL2; I.
DR PRINTS; PR00230; GEMCOATL2.
DR PRODOM; PD001117; Gemin AL2; 1.
SQ SEQUENCE 135 AA; 15321 MW; F84095235736DCB0 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 135;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYTH 5
Db 40 SYTH 44

RESULT 19
Q88950 TYLCS PRELIMINARY; PRT; 135 AA.
AC Q88950;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-FEB-2005 (TREMblrel. 29, Last annotation update)
DE C2 (Trap protein).
GN Name=C2;
OS Tomato yellow leaf curl Sardinia virus-[Sicily].
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=221539;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sicily;
RA Crespi S., Norris E., Valira A., Accotto G.;
RT "Improved detection and quantification of Tomato yellow leaf curl Sardinia virus using TaqMan real-time PCR."
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; Z28390; CAA82238.1; -; Genomic_DNA.
DR EMBL; AY326854; AAU84912.1; -; Genomic_DNA.
DR PIR; S39236; S39236.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000942; Gemin AL2.
DR Pfam; PF01440; Gemin AL2; I.
DR PRINTS; PR00230; GEMCOATL2.
DR PRODOM; PD001117; Gemin AL2; 1.
SQ SEQUENCE 135 AA; 15778 MW; 8A2BD8C641D6876A CRC64;

Query Match 100.0%; Score 30; DB 2; Length 135;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYTH 5
Db 40 SYTH 44

Db 40 SYTH 44

RESULT 20
Q8B6S6 TYLCS PRELIMINARY; PRT; 135 AA.
AC Q8B6S6;
DT 01-MAR-2003 (TREMblrel. 23, Created)
DT 01-MAR-2003 (TREMblrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
DE C2 protein.
OS Tomato yellow leaf curl Sardinia virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=123735;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Leaf;
RA Briddon R.W.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ519675; CAD58401.1; -; Genomic_DNA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000942; Gemin AL2.
DR Pfam; PF01440; Gemin AL2; I.
DR PRINTS; PR00230; GEMCOATL2.
DR PRODOM; PD001117; Gemin AL2; 1.
SQ SEQUENCE 135 AA; 15690 MW; 95E21245624EC9NA CRC64;

Query Match 100.0%; Score 30; DB 2; Length 135;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYTH 5
Db 40 SYTH 44

RESULT 21
Q8UYT7 GEMV PRELIMINARY; PRT; 135 AA.
AC Q8UYT7;
DT 01-MAR-2002 (TREMblrel. 20, Created)
DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)
DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
DE Transcription activation protein.
GN Name=AC2;
OS Mungbean yellow mosaic virus-Soybean[Madurai].
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=223293;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Madurai;
RA Gish K.R., Usha R.;
RT "Molecular characterization of two soybean-infecting begomoviruses from India: evidence for recombination among legume-infecting begomoviruses from South-East Asia."
RL Virus Res. 108:167-176(2005).
RL EMBL; AJ421642; CAD18842.1; -; Genomic_DNA.
DR EMBL; AJ421642; CAD18842.1; -; Genomic_DNA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000942; Gemin AL2.
DR Pfam; PF01440; Gemin AL2; I.
DR PRINTS; PR00230; GEMCOATL2.
DR PRODOM; PD001117; Gemin AL2; 1.
SQ SEQUENCE 135 AA; 15234 MW; 5548C0B487B084F CRC64;

Query Match 100.0%; Score 30; DB 2; Length 135;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYTH 5
Db 40 SYTH 44

```
RESULT 22
Q91M89_9GEMI PRELIMINARY; PRT; 135 AA.
AC Q91M89;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE C2.
OS Tobacco leaf curl Zimbabwe virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=223337;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21571657; PubMed=1171987;
RA Paximadis M., Rey M.E.;
RT "Genome organization of Tobacco leaf curl Zimbabwe virus, a new,
RT distinct monopartite begomovirus associated with subgenomic defective
RT DNA molecules.";
RL J. Gen. Virol. 82:3091-3097(2001).
DR EMBL; AF350330; AAK69689.1; -; Genomic_DNA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000942; Gemini AL2.
DR Pfam; PF01440; Gemini AL2; I.
DR PRINTS; PR00230; GEMCOATAL2.
DR ProDom; PD001117; Gemini AL2; 1.
SQ SEQUENCE 135 AA; 15362 MW; E93A6B1A53CEB55B CRC64;
```

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Query Match 100.0%; Score 30; DB 2; Length 135;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

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OY 1 SYTH 5
    ||||
Db 40 SYTH 44

RESULT 23
Q99DR8_9GEMI PRELIMINARY; PRT; 135 AA.
AC Q99DR8;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE C2 protein.
OS Mungbean yellow mosaic virus-Vigna[Maharashtra].
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=223299;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=soybean;
RA Teal W.S., Green S.K., Deshpande R.R.;
RL Submitted (OCF-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF14530; AAK06530.1; -; Genomic_DNA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000942; Gemini AL2.
DR Pfam; PF01440; Gemini AL2; 1.
DR PRINTS; PR00230; GEMCOATAL2.
DR ProDom; PD001117; Gemini AL2; 1.
SQ SEQUENCE 135 AA; 15270 MW; 47B26B3EC3051C1A CRC64;
```

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Query Match 100.0%; Score 30; DB 2; Length 135;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 24
Q9YPS3_9GEMI PRELIMINARY; PRT; 135 AA.
AC Q9YPS3;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE AC2 protein.
GN Name=AC2;
OS Mungbean yellow mosaic virus-Vigna.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=223295;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15290387; DOI=10.1007/s00705-004-0313-z;
RA Karthikeyan A.S., Vantharani R., Balaji V., Anuradha S., Balamani V.,
RA Thilachandrabaram P., Shivaprasad P.V., Parameswari C.,
RA Samanthan M., Veluthambi K.;
RT "Analysis of an isolate of Mungbean yellow mosaic virus (MYMV) with a
RT highly variable DNA B component.";
RL Arch. Virol. 149:1643-1652(2004).
DR EMBL; AJ132575; CA10706.1; -; Genomic_DNA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000942; Gemini AL2.
DR Pfam; PF01440; Gemini AL2; 1.
DR PRINTS; PR00230; GEMCOATAL2.
DR ProDom; PD001117; Gemini AL2; 1.
SQ SEQUENCE 135 AA; 15219 MW; 30D7E7A0493B1C1E CRC64;
```

```
Query Match 100.0%; Score 30; DB 2; Length 135;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

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OY 1 SYTH 5
    ||||
Db 40 SYTH 44

RESULT 25
Q534Y0_9GEMI PRELIMINARY; PRT; 135 AA.
AC Q534Y0;
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE Transactivator protein.
GN Name=AC2;
OS Mungbean yellow mosaic virus-Vigna.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=223295;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Chowda Reddy R.V., Colvin J., Muniyappa V., Seal S.;
RT "Molecular characterization of Mungbean yellow mosaic virus in cluster
RT bean at Ranipennur, Karnataka, India.";
RL Submitted (AUG-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY78104; AAM50915.1; -; Genomic_DNA.
SQ SEQUENCE 135 AA; 15232 MW; 310277A0493B1C1E CRC64;
```

```
Query Match 100.0%; Score 30; DB 2; Length 135;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 SYTH 5
    ||||
Db 40 SYTH 44

RESULT 26
Q8UKF4_9GEMI PRELIMINARY; PRT; 136 AA.
AC Q8UKF4;
```

DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Transcription activator protein AC2.
GN Name=AC2; yellow mosaic India virus-[Cowpea].
OS Mungbean yellow mosaic India virus-[Cowpea].
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=223289;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Surendranath B., Naghma A., Malathi V.G.;
RL Submitted (JUN-2002) to the EMBL/Genbank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Malathi V.G., Naghma A., Surendranath B.;
RL Submitted (JUN-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF481865; AAM48572.1; -; Genomic_DNA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000942; Gemin AL2.
DR Pfam; PF01440; Gemin AL2; I.
DR PRINTS; PR00230; GEMCOATL2.
DR ProDom; PD001117; Gemin AL2; 1.
SQ SEQUENCE 136 AA; 15336 MW; BBE841CF140FB81B CRC64;

Query Match 100.0%; Score 30; DB 2; Length 136;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
Db 40 SYTH 44

RESULT 27
Q913F0_9GEMI PRELIMINARY; PRT; 136 AA.
ID Q913F0_9GEMI PRELIMINARY; PRT; 136 AA.
AC Q913F0;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Transcription activator protein AC2.
GN Name=AC2;
OS Mungbean yellow mosaic India virus-[Soybean].
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=223291;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Usharani K.S., Malathi V.G.;
RL Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY049772; AAL00895.1; -; Genomic_DNA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000942; Gemin AL2.
DR Pfam; PF01440; Gemin AL2; 1.
DR PRINTS; PR00230; GEMCOATL2.
DR ProDom; PD001117; Gemin AL2; 1.
SQ SEQUENCE 136 AA; 15365 MW; B914B3C4776AF80F CRC64;

Query Match 100.0%; Score 30; DB 2; Length 136;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
Db 40 SYTH 44

RESULT 28
Q917N2_9GEMI PRELIMINARY; PRT; 136 AA.
ID Q917N2_9GEMI PRELIMINARY; PRT; 136 AA.
AC Q917N2;
DT 01-DEC-2001 (TREMBlrel. 19, Created)

DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Transcription activator protein.
GN Name=AC2; yellow mosaic India virus-[Mungbean].
OS Mungbean yellow mosaic India virus-[Mungbean].
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=223290;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Surendranath B., Biswas K., Varma A., Malathi V.G.;
RL Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF416742; AAL09039.1; -; Genomic_DNA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000942; Gemin AL2.
DR Pfam; PF01440; Gemin AL2; I.
DR PRINTS; PR00230; GEMCOATL2.
DR ProDom; PD001117; Gemin AL2; 1.
SQ SEQUENCE 136 AA; 15424 MW; 2969003D6DEC0E8F CRC64;

Query Match 100.0%; Score 30; DB 2; Length 136;
Best Local Similarity 100.0%; Pred. NO. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
Db 40 SYTH 44

RESULT 29
Q9WH23_9GEMI PRELIMINARY; PRT; 136 AA.
ID Q9WH23_9GEMI PRELIMINARY; PRT; 136 AA.
AC Q9WH23;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Transcription activator protein.
GN Name=AC2;
OS Mungbean yellow mosaic India virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=223287;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=bq3;
RX MEDLINE=21446688; PubMed=11562548;
RA Pant V., Gupta D., Choudhury N.R., Malathi V.G., Varma A.,
Mukherjee S.K.;
RT "Molecular characterization of the Rep protein of the blackgram
isolate of Indian mungbean yellow mosaic virus.";
RL J. Gen. Virol. 82:2559-2567(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=bq3;
RA Malathi V.G., Varma A.;
RL Submitted (FEB-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF126406; AAD20640.1; -; Genomic_DNA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000942; Gemin AL2.
DR Pfam; PF01440; Gemin AL2; 1.
DR PRINTS; PR00230; GEMCOATL2.
DR ProDom; PD001117; Gemin AL2; 1.
SQ SEQUENCE 136 AA; 15474 MW; CE657E9DF602B024 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 136;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
Db 40 SYTH 44

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RESULT 30
OS35C4_9GEMI PRELIMINARY; PRT; 136 AA.
ID OS35C4_9GEMI PRELIMINARY; PRT; 136 AA.
AC OS35C4_9GEMI PRELIMINARY; PRT; 136 AA.
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Transactivator protein.
GN Name=AC2;
OS Mungbean yellow mosaic India virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
NC NCB1_Taxid=223287;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Chowdhary R.V., Colvin J., Muniyappa V., Seal S.;
RT Molecular characterization of MYMIV in cowpea at Patna, India.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY738093; AAM50871.1 -; Genomic DNA.
SQ SEQUENCE 136 AA; 15552 MW; 9FFEAC670D514732 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 136;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
DB 40 SYTH 44

RESULT 31
OS6MX5_DICDI PRELIMINARY; PRT; 142 AA.
ID OS6MX5_DICDI PRELIMINARY; PRT; 142 AA.
AC OS6MX5_DICDI PRELIMINARY; PRT; 142 AA.
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Come (Fragment).
GN Name=come;
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
NC NCB1_Taxid=44689;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Kibler K., Nguyen T.-L., Svez J., Van Driessche N., Ibarra M.,
RT Thompson C., Shaw C., Shaulsky G.;
RT "A novel developmental mechanism in Dictyostelium revealed in a screen
for communication mutants.";
RL Dev. Biol. 01:0-0(2003).
DR EMBL: AY221642; AA034398.1 -; Genomic_DNA.
DR DictyBase: DDB0220032; come.
DR InterPro: IPR008615; FNIP.
DR Pfam: PF05725; FNIP; 2.
FT NON_TER 1
FT NON_TER 142
SQ SEQUENCE 142 AA; 15833 MW; 7ABBA782F4837A36 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 142;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
DB 11 SYTH 15

RESULT 32
OS1N71_9GEMI PRELIMINARY; PRT; 146 AA.
ID OS1N71_9GEMI PRELIMINARY; PRT; 146 AA.
AC OS1N71_9GEMI PRELIMINARY; PRT; 146 AA.
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE C2.
```

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OS Mungbean yellow mosaic India virus-[Bangladesh].
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
NC NCB1_Taxid=223288;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Tsai W.S., Nakha M.K., Green S.K., Rashid M.H., Maxwell D.P.;
RT Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF14145; AAK69591.1 -; Genomic_DNA.
DR GO: GO:0019028; C:Viral capsid; IEA.
DR GO: GO:0005198; F:Structural molecule activity; IEA.
DR InterPro: IPR000942; Gemin1_AL2.
DR Pfam: PF01440; Gemin1_AL2; 1.
DR PRINTS: PR00230; GEMCOATL2.
DR ProDom: PD001117; Gemin1_AL2; 1.
SQ SEQUENCE 146 AA; 16564 MW; 040F106CA23909C5 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
DB 50 SYTH 54

RESULT 33
OSYA42_9GEMI PRELIMINARY; PRT; 150 AA.
ID OSYA42_9GEMI PRELIMINARY; PRT; 150 AA.
AC OSYA42_9GEMI PRELIMINARY; PRT; 150 AA.
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Transcriptional activator protein.
GN Name=AC2;
OS Cowpea golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
NC NCB1_Taxid=69263;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Varanasi;
RA Chakraborty S., Singh S.K., Singh A.K., Pandey P.K.;
RT "Molecular characterization of begomoviruses causing yellow mosaic
disease on cowpea (Vigna unguiculata) and hyacinth bean (Lablab
purpureus).";
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY618902; AA097295.1 -; Genomic_DNA.
DR GO: GO:0019028; C:Viral capsid; IEA.
DR GO: GO:0005198; F:Structural molecule activity; IEA.
DR InterPro: IPR000942; Gemin1_AL2.
DR Pfam: PF01440; Gemin1_AL2; 1.
DR PRINTS: PR00230; GEMCOATL2.
DR ProDom: PD001117; Gemin1_AL2; 1.
SQ SEQUENCE 150 AA; 17194 MW; 321A265184694C9B CRC64;

Query Match 100.0%; Score 30; DB 2; Length 150;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
DB 54 SYTH 58

RESULT 34
OS7TUD3_9GEMI PRELIMINARY; PRT; 150 AA.
ID OS7TUD3_9GEMI PRELIMINARY; PRT; 150 AA.
AC OS7TUD3_9GEMI PRELIMINARY; PRT; 150 AA.
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE AC2.
GN Name=AC2;
OS Mungbean yellow mosaic India virus - [Mungbean Pakistan].
```

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OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=269102;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Tsai W.S., Green S.K., Bashir M.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY269992; AAP34726.1; -; Genomic_DNA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000942; Gemini_AL2.
DR Pfam; PF01440; Gemini_AL2; I.
DR PRINTS; PR00230; GEMCOATL2.
DR ProDom; PD001117; Gemini_AL2; 1.
SQ SEQUENCE 150 AA; 16390 MW; 10F7C24834C2B3276 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 150;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
Db 54 SYTH 58

RESULT 35
Q080U2_9GEMI PRELIMINARY; PRT; 150 AA.
ID Q080U2_9GEMI PRELIMINARY; PRT; 150 AA.
AC Q080U2;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE AC2.
GN Name=AC2;
OS Mungbean yellow mosaic India virus - [Nepal].
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=269101;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Tsai W.S., Green S.K.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY271895; AAP23251.1; -; Genomic_DNA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000942; Gemini_AL2.
DR Pfam; PF01440; Gemini_AL2; 1.
DR PRINTS; PR00230; GEMCOATL2.
DR ProDom; PD001117; Gemini_AL2; 1.
SQ SEQUENCE 150 AA; 16396 MW; 6D5204A3BCFB3272 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 150;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
Db 54 SYTH 58

RESULT 36
Q080V0_9GEMI PRELIMINARY; PRT; 150 AA.
ID Q080V0_9GEMI PRELIMINARY; PRT; 150 AA.
AC Q080V0;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE AC2.
GN Name=AC2;
OS Mungbean yellow mosaic India virus - [Akola].
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=269099;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Tsai W.S., Green S.K.;
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RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY271893; AAP23243.1; -; Genomic_DNA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000942; Gemini_AL2.
DR Pfam; PF01440; Gemini_AL2; 1.
DR PRINTS; PR00230; GEMCOATL2.
DR ProDom; PD001117; Gemini_AL2; 1.
SQ SEQUENCE 150 AA; 17028 MW; 574472005EC82B4D CRC64;

Query Match 100.0%; Score 30; DB 2; Length 150;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
Db 54 SYTH 58

RESULT 37
Q080P53_9GEMI PRELIMINARY; PRT; 150 AA.
ID Q080P53_9GEMI PRELIMINARY; PRT; 150 AA.
AC Q080P53;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Putative transcriptional activator protein.
GN Name=AC2;
OS Legume yellow mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=211101;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15045567; DOI=10.1007/s00705-003-0256-9;
RA Hameed S., Robinson D.U.;
RL "Begomoviruses from mungbeans in Pakistan: epitope profiles, DNA A
sequences and phylogenetic relationships.";
RL Arch. Virol. 149:809-819(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Hameed S.;
RL "Molecular diversity of begomoviruses of legumes and cucurbits in
Pakistan.";
RL Thesis (1999), Department of Biological Sciences, University of
Dundee, Dundee, United Kingdom.
DR EMBL; AJ512497; CAD54717.1; -; Genomic_DNA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000942; Gemini_AL2.
DR Pfam; PF01440; Gemini_AL2; 1.
DR PRINTS; PR00230; GEMCOATL2.
DR ProDom; PD001117; Gemini_AL2; 1.
SQ SEQUENCE 150 AA; 16390 MW; 6FA0E2F9F0B3272 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 150;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
Db 54 SYTH 58

RESULT 38
Q080P59_9GEMI PRELIMINARY; PRT; 150 AA.
ID Q080P59_9GEMI PRELIMINARY; PRT; 150 AA.
AC Q080P59;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Putative transcriptional activator protein.
GN Name=AC2;
OS Legume yellow mosaic virus.
```

```
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=211101;
RN
  [1]
  NUCLEOTIDE SEQUENCE.
RX PubMed=15045567; DOI=10.1007/s00705-003-0256-9;
RA Hameed S., Robinson D.J.;
RT "Begomoviruses from mungbeans in Pakistan: epitope profiles, DNA A
  RT sequences and phylogenetic relationships.";
  RL Arch. Virol. 149:809-819(2004).
  [2]
  NUCLEOTIDE SEQUENCE.
RA Hameed S.;
RT "Molecular diversity of begomoviruses of legumes and cucurbits in
  RT Pakistan.";
  RL Thesis (1999), Department of Biological Sciences, University of
  RL Dundee, Dundee, United Kingdom.
  EMBL; AJ512496; CAD54711.1; -; Genomic_DNA.
  DR GO; GO:0019028; C:viral capsid; IEA.
  DR GO; GO:0005198; F:structural molecule activity; IEA.
  DR InterPro; IPR000942; Gemini_AL2.
  DR Pfam; PF01440; Gemini_AL2; I.
  DR PRINTS; PR00230; GEMCOATAL2.
  DR ProDom; PD001117; Gemini_AL2; 1.
  SQ SEQUENCE 150 AA; 17066 MW; 7FE0F2F8E0962E1E CRC64;

Query Match 100.0%; Score 30; DB 2; Length 150;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 SYTTH 5
   |||||
Db 54 SYTTH 58

RESULT 39
O80P64.9GEMI PRELIMINARY; PRT; 150 AA.
ID O80P64.1
AC O80P64.1
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative transcriptional activator protein.
GN Name=AC2;
OS Legume yellow mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=211101;
RN
  [1]
  NUCLEOTIDE SEQUENCE.
RX PubMed=15045567; DOI=10.1007/s00705-003-0256-9;
RA Hameed S., Robinson D.J.;
RT "Begomoviruses from mungbeans in Pakistan: epitope profiles, DNA A
  RT sequences and phylogenetic relationships.";
  RL Arch. Virol. 149:809-819(2004).
  [2]
  NUCLEOTIDE SEQUENCE.
RA Hameed S.;
RT "Molecular diversity of begomoviruses of legumes and cucurbits in
  RT Pakistan.";
  RL Thesis (1999), Department of Biological Sciences, University of
  RL Dundee, Dundee, United Kingdom.
  EMBL; AJ512495; CAD54705.1; -; Genomic_DNA.
  DR GO; GO:0019028; C:viral capsid; IEA.
  DR GO; GO:0005198; F:structural molecule activity; IEA.
  DR InterPro; IPR000942; Gemini_AL2.
  DR Pfam; PF01440; Gemini_AL2; 1.
  DR PRINTS; PR00230; GEMCOATAL2.
  DR ProDom; PD001117; Gemini_AL2; 1.
  SQ SEQUENCE 150 AA; 16956 MW; 35AA48F9FD9B3F1F CRC64;

Query Match 100.0%; Score 30; DB 2; Length 150;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Oy 1 SYTTH 5
   |||||
Db 54 SYTTH 58

RESULT 40
O910Y8.9GEMI PRELIMINARY; PRT; 150 AA.
ID O910Y8.1
AC O910Y8.1
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE AC2 protein.
GN Name=AC2;
OS Mungbean yellow mosaic India virus-(SoybeanTN).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=223292;
RN
  [1]
  NUCLEOTIDE SEQUENCE.
RA Gish K.R., Usha R.;
RT "Molecular characterization of two soybean-infecting begomoviruses
  RT from India and evidence for recombination among legume-infecting
  RT begomoviruses from South-East Asia.";
  RL Virus Res. 108:167-176(2005).
  EMBL; AJ16349; CAC94876.1; -; Genomic_DNA.
  DR GO; GO:0019028; C:viral capsid; IEA.
  DR GO; GO:0005198; F:structural molecule activity; IEA.
  DR InterPro; IPR000942; Gemini_AL2.
  DR Pfam; PF01440; Gemini_AL2; 1.
  DR PRINTS; PR00230; GEMCOATAL2.
  DR ProDom; PD001117; Gemini_AL2; 1.
  SQ SEQUENCE 150 AA; 17168 MW; C4529E3BE55D1ED5 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 150;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 SYTTH 5
   |||||
Db 54 SYTTH 58

RESULT 41
O52U04.9GEMI PRELIMINARY; PRT; 150 AA.
ID O52U04.1
AC O52U04.1
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE AC2.
GN Name=AC2;
OS Mungbean yellow mosaic India virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=223287;
RN
  [1]
  NUCLEOTIDE SEQUENCE.
RA Priya J., Sivalingam P.N., Naveen K., Mishra A., Ahlawat Y.S.,
  RA Malathi V.G.;
RT "Nucleotide sequence of DNA A of Mungbean yellow mosaic India virus
  RT from Anand, Gujarat.";
  RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
  EMBL; AY937195; AAX84783.1; -; Genomic_DNA.
  DR EMBL; AY937195; AAX84783.1; -; Genomic_DNA.
  SQ SEQUENCE 150 AA; 17211 MW; AFS6A1676B0F558A CRC64;

Query Match 100.0%; Score 30; DB 2; Length 150;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 42
060A7_9GEMI PRELIMINARY; PRT; 150 AA.
ID O60A7_9GEMI PRELIMINARY; PRT; 150 AA.
AC O60A7_9GEMI PRELIMINARY; PRT; 150 AA.
DT 05-JUN-2004 (TREMBLrel. 27, Created)
DT 05-JUN-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUN-2004 (TREMBLrel. 27, Last annotation update)
DE Transcriptional activator protein.
GN Name=AC2;
OS Dolichos yellow mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OC NCBI_TaxID=235162;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Varanasi;
RA Singh S.K., Chakraborty S., Singh A.K., Pandey P.K.;
RT "Molecular characterization of begomoviruses causing yellow mosaic
RT disease on cowpea (Vigna unguiculata) and hyacinth bean (lablab
RT purpureus).";
RL Submitted (FEB-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL: AY547317; AAS55089.1; -; Genomic_DNA.
DR GO: GO:0019028; C:Structural molecule activity; IEA.
DR GO: GO:0005198; F:Structural molecule activity; IEA.
DR InterPro: IPR000942; Gemini AL2.
DR Pfam: PF01440; Gemini AL2.1.
DR PRINTS: PR00230; GEMCOATAL2.
DR Prodom: PD001117; Gemini AL2.1.
SQ SEQUENCE 150 AA; 17067 MW; 6D52086370FB3272 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 150;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYTH 5
Db 54 SYTH 58

RESULT 43
095978_HUMAN PRELIMINARY; PRT; 157 AA.
ID 095978_HUMAN PRELIMINARY; PRT; 157 AA.
AC 095978_HUMAN PRELIMINARY; PRT; 157 AA.
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 25, Last annotation update)
DE VHL protein precursor (Fragment).
GN Name=VHL;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OC NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Peripheral blood;
RA Jox A., Zander T., Kuipers R., Irsch J., Kanzler H., Kornacker M.,
RA Bohlen H., Diehl V., Wolf J., Kolf J.,
RT "Absence of immunoglobulin in Hodgkin-Reed Sternberg cells of a
RT patient with mixed cellularly Hodgkin's disease is associated with
RT somatic mutations within the untranslated regions of rearranged and
RT class switch recombined Ig genes.";
RL Submitted (APR-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL: AJ005570; CA06599.1; -; Genomic_DNA.
DR HSP: P01857; IGH.
DR Ensembl: ENSG00000130076; Homo sapiens.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR SMART: SMO0406; IGV: 1.
DR PROSITE: PSS0835; IG_LIKE; 1.
KW Signal.
FT SIGNAL 1 21 Potential.
FT NON_TER 157 157
SQ SEQUENCE 157 AA; 17304 MW; 86986EDDA84D88B5 CRC64;

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Query Match 100.0%; Score 30; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYTH 5
Db 50 SYTH 54

RESULT 44
09CUG6_MOUSE PRELIMINARY; PRT; 195 AA.
ID 09CUG6_MOUSE PRELIMINARY; PRT; 195 AA.
AC 09CUG6_MOUSE PRELIMINARY; PRT; 195 AA.
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Mus musculus adult male testis cDNA, RIKEN full-length enriched
DE library, clone:4930563023 product:hypothetical protein, full insert
DE sequence. (Fragment).
GN Name=4930563023Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RC MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RX Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RX Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arai T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bond H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batelov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi G., King B., Kochwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirli L.M., Straubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Kono H., Baldarelli R., Baren G.,
RA Blake J., Botfield D., Bojunga N., Cardini P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Guetlich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombauts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilting L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohzuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RC The FANTOM Consortium;
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RC MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RX Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";

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RL  Genome Res. 10:1617-1630 (2000).
RN
RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=C57BL/6J; TISSUE=Testis;
RA  MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA  Shihara K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA  Kono H., Akiyama J., Nishi K., Kltunai T., Tashiro H., Itoh M.,
RA  Suni N., Ishii Y., Nakamura S., Hazama N., Nishine T., Harada A.,
RA  Yamamoto R., Matsunami H., Sakaguchi S., Ikegami T., Kaishiji K.,
RA  Fujiwaki S., Inoue K., Ozawa Y., Izawa M., Ohara E., Watanabe K.,
RA  Yoneda Y., Ishikawa T., Oizawa K., Tanaka T., Matsura S., Kawai J.,
RA  Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT  "RIKEN integrated sequence analysis (RISA) system-384-format
RT  sequencing pipeline with 384 multicapillary sequencer.";
RL  Genome Res. 10:1757-1771 (2000).
RN
RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=C57BL/6J; TISSUE=Testis;
RA  Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA  Atakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furino M.,
RA  Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA  Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA  Kawai J., Kojima Y., Kono H., Kouda M., Koya S., Kurihara C.,
RA  Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA  Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai T.,
RA  Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA  Sogabe Y., Suzuki H., Tagami M., Tagawa M., Tanahashi F., Tanaka T.,
RA  Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA  Muramatsu M., Hayashizaki Y.;
RL  Submitted (JUL-2000) to the EMBL/Genbank/DBJ databases.
DR  EMBL; AK016199; BAB30145.1; -; mRNA.
DR  Ensembl; ENSMUSG0000051728; Mus musculus.
DR  MGI; MGI:1922578; 4930563D3R1K.
KW  Hypothetical protein.
FT  NON TER 195
SQ  SEQUENCE 195 AA; 22511 MW; EBF4D9962147DE39 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 195;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 SYTH 5
    |||||
Db 64 SYTH 68

RESULT 45
O5ONV4_ENTHI PRELIMINARY; PRT; 214 AA.
AC O5ONV4
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=414.t00001;
OS Entamoeba histolytica HM-1:IMSS.
OC Eukaryota; Entamoebidae; Entamoeba.
ON NCBI_TaxID=294381;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HM-1:IMSS;
RA PubMed=15729342; DOI=10.1038/nature03291;
RA Loftus B., Anderson I., Davies R., Alsmark U.C., Samuelson J.,
RA Amedeo P., Koncaglia P., Bertrian M., Hirt R.P., Mann B.O., Nozaki T.,
RA Suh B., Pop M., Duchene M., Ackers J., Tannich E., Leipe M.,
RA Hofer M., Bruchhaus I., Willhoft U., Bhattacharya A.,
RA Chillingworth T., Churcher C., Hance Z., Harris B., Harris D.,
RA Jagers K., Moule S., Mungall K., Ormond D., Squares R., Whitehead S.,
RA Quail M.A., Rabinowitsch E., Norberczak H., Price C., Wang Z.,
RA Guillen N., Glickert C., Strop S.E., Bhattacharya S., Lohia A.,
RA Foster P.G., Slichter C., Strop S.E., Bhattacharya S., Lohia A.,
RA El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M., Barrell B.,
RA Fraser C.M., Hall N.;

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RT  "The genome of the protist parasite Entamoeba histolytica.";
RL  Nature 433:865-868(2005).
CC  -1- CAUTION: The sequence shown here is derived from an
CC  EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
CC  preliminary data.
DR  EMBL; AAFB01001035; EAL43266.1; -; Genomic_DNA.
KW  Hypothetical protein.
SQ  SEQUENCE 214 AA; 25610 MW; 61C0CFDC8C8A7 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 214;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 SYTH 5
    |||||
Db 63 SYTH 67

RESULT 46
O7VTZ4_BORPE PRELIMINARY; PRT; 223 AA.
ID O7VTZ4_BORPE
AC O7VTZ4
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=BP3352;
OS Bordetella pertussis.
OC Bordetella pertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
ON NCBI_TaxID=520;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Tohama I / ATCC BAA-569 / NCTC 13251;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J., Sebatina M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltham S., Goble A., Hamlin N., Hauser H., Holtz S., Jogle K.,
RA Leathes S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
DR EMBL; BX640421; CAE43617.1; -; Genomic_DNA.
DR InterPro; IPR003738; DUF159.
DR Pfam; PF02586; DUF159.1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 223 AA; 24997 MW; 2D795C010C41F97D CRC64;

Query Match 100.0%; Score 30; DB 2; Length 223;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 SYTH 5
    |||||
Db 118 SYTH 122

RESULT 47
O8RE63_FUSNN PRELIMINARY; PRT; 233 AA.
ID O8RE63_FUSNN
AC O8RE63
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Two-component response regulator.
GN OrderedLocustNames=FNI261;
OS Fusobacterium nucleatum (subsp. nucleatum).

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OC Bacteria; Fusobacteria; Fusobacteriales; Fusobacteriaceae;
 OC Fusobacterium.
 OX NCBI_TaxID=76856;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=ATCC 25586;
 RX MEDLINE=21886394; PubMed=11889109;
 RX DOI=10.1128/0916.184.7.2005-2018.2002;
 RA Kapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
 RA Bhattacharya A., Barton A., Gardner W., Grecklin G., Zhu L.,
 RA Vasileva O., Chu L., Kogan Y., Chaga O., Gotsman E., Bernal A.,
 RA Larsen N., D'Souza M., Malunas T., Pusch G., Haselkorn R.,
 RA Forstner N., Kyrides N.C., Overbeek R.,
 RA "Genome sequence and analysis of the oral bacterium Fusobacterium
 RT necatum strain ATCC 25586."
 RL J. Bacteriol. 184:2005-2018(2002).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 DR EMBL; AE009551; AL95457.1; -; Genomic_DNA.
 DR HSSP; Q9WYN0; IKGS.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0000156; F:two-component response regulator activity; IEA.
 DR GO; GO:0007600; P:sensory perception; IEA.
 DR GO; GO:0006350; P:transcription; IEA.
 DR GO; GO:0000160; P:two-component signal transduction system (p. . .); IEA.
 DR InterPro; IPR001867; Response_reg.
 DR InterPro; IPR001867; Trans_reg_C.
 DR Pfam; PF00072; Response_reg; 1.
 DR Pfam; PF00486; Trans_reg_C; 1.
 DR ProDom; PD000039; Response_reg; 1.
 DR ProDom; PD000329; Trans_reg_C; 1.
 DR SMART; SM00448; REC; 1.
 DR PROSITE; PS01010; RESPONSE_REGULATORY; 1.
 KW Complete proteome; DNA-binding; Sensory transduction; Transcription;
 KW Transcription; regulation; Two-component regulatory system.
 SQ SEQUENCE 233 AA; 27321 MW; 3C3DE03679B8E4E5 CRC64;
 Query Match 100.0%; Score 30; DB 2; Length 233;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SYTH 5
 Db 215 SYTH 219
 RESULT 48
 Q8CD57 MOUSE
 ID Q8CD57 MOUSE PRELIMINARY; PRT; 251 AA.
 AC Q8CD57;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Mus musculus adult male testis cDNA, RIKEN full-length enriched
 DE library, clone:4930429C3 product:hypothetical protein, full insert
 DE sequence.
 GN Name=4930563D23Rik;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.,
 RT "High-efficiency full-length cDNA cloning."
 RL Mech. Enzymol. 303:19-44(1999).
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Konno S., Yamana K.,
 RA Saito T., Okazaki Y., Gotohori T., Bond H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido H., Pesole G., Quackenbush J.,
 RA Schmitt L.M., Staebli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guetincich S., Hill D., Hofmann M., Hume D.A., Kanuya M., Lee N.H.,
 RA Lyons P., Matchom L., Mashima J., Mazzarelli U., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilding L.,
 RA Wyshew-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RA The PANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes."
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagata S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
 RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Matsumi M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsumura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.,
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer."
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RA Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,
 RA Fukuda S., Furuno M., Hanagaki T., Hiraoka T., Hirozane T.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Karoh H., Kawai J., Kojima Y., Konno S., Konno H., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ono M., Ohata N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai K., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akaihi S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK029653; BAC26550.1; -; mRNA.
 DR Ensembl; ENSMUSG0000051728; Mus musculus.
 DR MGI; MGI:1922578; 4930563D23Rik.
 SQ SEQUENCE 251 AA; 29348 MW; 795B98CE5804A6C1 CRC64;
 Query Match 100.0%; Score 30; DB 2; Length 251;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SYTH 5
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 Db 64 SYTH 68

RESULT 49

Q4MGN2_BACCE
 ID Q4MGN2_BACCE PRELIMINARY; PRT; 253 AA.
 AC Q4MGN2_13-SEP-2005 (TREMBlrel. 31, Created)
 DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
 DE Methytransferase.
 GN ORFNames=BCE_G9241.0272;
 OS Bacillus cereus G9241.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
 OC Bacillus cereus group.
 OX NCBI_TaxID=269801;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=G9241;
 RX PubMed=15155910; DOI=10.1073/pnas.0402414101;
 RA Hofmeister A.R., Ravel J., Raeko D.A., Chapman G.D., Chute M.D.,
 RA Marston C.J., De B.K., Sacchi C.T., Fitzgerald C., Mayer L.W.,
 RA Maiden M.C.J., Priest F.G., Barker M., Jiang L., Cer R.Z.,
 RA Ristone J., Peterson S.N., Weyant R.S., Galloway D.R., Read T.D.,
 RA Popovic T., Frazer C.M.;
 RT "Identification of anthrax toxin genes in a Bacillus cereus associated
 with an illness resembling inhalation anthrax.";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:8449-8454(2004).
 CC -! CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC EMBL; AAK0100091; EAL1329.1; -; Genomic_DNA.
 KW Methytransferase; Transferase.
 SQ SEQUENCE 253 AA; 29976 MW; DQFA93867EC6D2D CRC64;

Query Match 100.0%; Score 30; DB 2; Length 253;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
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 Db 72 SYTH 76

RESULT 50

O45342_CAEEL
 ID O45342_CAEEL PRELIMINARY; PRT; 284 AA.
 AC O45342_01-JUN-1998 (TREMBlrel. 06, Created)
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Hypothetical protein F10A3.11.
 GN ORFNames=F10A3.11;
 OS Caenorhabditis elegans.
 CC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 CC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Bristol N2;
 RG MEDLINE=99068613; PubMed=9851916;
 RT "The C. elegans sequencing consortium;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology.";
 RL Science 282:2012-2018(1998).
 DR EMBL; Z92829; CAB07347.1; -; Genomic_DNA.
 DR PIR; T20684; T20684.
 DR Ensembl; F10A3.11; Caenorhabditis elegans.
 DR WormBase; WBGene00008636; F10A3.11.

DR WormPep; F10A3.11; CE15776.
 DR InterPro; IPR006583; CW.
 DR SMART; SM00605; CW; 1.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 284 AA; 32075 MW; F92C5A8514FD3BAC CRC64;

Query Match 100.0%; Score 30; DB 2; Length 284;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
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 Db 58 SYTH 62

Search completed: May 4, 2006, 13:10:22
 Job time : 84.8254 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 4, 2006, 13:09:53 ; Search time 11.2698 Seconds
(without alignments)
36.680 Million cell updates/sec

Title: US-10-700-632-1
Perfect score: 30
Sequence: 1 SYTH 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents_AA:*

1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCtus_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	100.0	5	1	US-08-137-117D-143
2	30	100.0	5	1	US-08-436-717-143
3	30	100.0	116	1	US-08-561-521-41
4	30	100.0	116	4	PCT-US95-01219-41
5	30	100.0	135	1	US-08-137-117D-27
6	30	100.0	135	1	US-08-137-117D-100
7	30	100.0	135	1	US-08-137-117D-102
8	30	100.0	135	1	US-08-137-117D-112
9	30	100.0	135	1	US-08-436-717-100
10	30	100.0	135	1	US-08-436-717-102
11	30	100.0	135	1	US-08-436-717-112
12	30	100.0	135	1	US-08-436-717-112
13	30	93.3	62	2	US-09-248-796A-24535
14	28	93.3	160	2	US-09-270-767-40412
15	28	93.3	160	2	US-09-270-767-55628
16	28	93.3	226	2	US-09-107-532A-3715
17	28	93.3	354	2	US-09-248-796A-18926
18	28	93.3	501	2	US-09-540-236-2017
19	28	93.3	659	2	US-09-189-462-4
20	28	93.3	659	2	US-09-189-462-4
21	28	93.3	659	2	US-09-189-462-4
22	28	93.3	1179	2	US-09-107-532A-6126
23	28	93.3	1213	1	US-08-937-102-2
24	28	93.3	1213	1	US-08-876-991-2
25	28	93.3	3898	1	US-09-059-853-2
26	28	93.3	3898	1	US-08-750-717-2
27	27	90.0	9	2	US-09-534-717-327

28	27	90.0	35	1	US-08-765-179B-5	Sequence 5, Appli
29	27	90.0	72	2	US-09-248-796A-26979	Sequence 26979, A
30	27	90.0	73	2	US-09-248-796A-22743	Sequence 22743, A
31	27	90.0	81	2	US-09-248-796A-23947	Sequence 23947, A
32	27	90.0	97	1	US-08-290-592E-16	Sequence 16, Appl
33	27	90.0	97	4	PCT-US95-10053-13	Sequence 13, Appl
34	27	90.0	97	4	PCT-US96-09448-16	Sequence 16, Appl
35	27	90.0	98	2	US-10-194-975-7	Sequence 7, Appli
36	27	90.0	117	2	US-08-545-809A-128	Sequence 128, App
37	27	90.0	117	2	US-09-157-370-2	Sequence 2, Appli
38	27	90.0	117	2	US-09-025-769B-22	Sequence 22, Appl
39	27	90.0	117	2	US-09-450-070A-22	Sequence 22, Appl
40	27	90.0	117	2	US-09-450-153-22	Sequence 22, Appl
41	27	90.0	117	2	US-09-450-324-22	Sequence 22, Appl
42	27	90.0	117	2	US-09-515-697-128	Sequence 128, App
43	27	90.0	120	2	US-09-025-769B-36	Sequence 36, Appl
44	27	90.0	120	2	US-09-025-769B-59	Sequence 59, Appl
45	27	90.0	120	2	US-09-450-070A-36	Sequence 36, Appl
46	27	90.0	120	2	US-09-450-070A-59	Sequence 59, Appl
47	27	90.0	120	2	US-09-450-153-36	Sequence 36, Appl
48	27	90.0	120	2	US-09-450-324-36	Sequence 36, Appl
49	27	90.0	120	2	US-09-450-324-59	Sequence 59, Appl
50	27	90.0	120	2	US-09-548-473B-12	Sequence 12, Appl
51	27	90.0	258	2	US-09-858-664A-14	Sequence 14, Appl
52	27	90.0	274	2	US-10-274-978-15	Sequence 15, Appl
53	27	90.0	274	2	US-10-274-978-15	Sequence 15, Appl
54	27	90.0	274	2	US-10-697-263-15	Sequence 15, Appl
55	27	90.0	325	2	US-09-270-767-59240	Sequence 59240, A
56	27	90.0	341	2	US-09-270-767-36602	Sequence 36602, A
57	27	90.0	341	2	US-09-270-767-51819	Sequence 51819, A
58	27	90.0	379	2	US-09-574-141A-64	Sequence 64, Appl
59	27	90.0	379	2	US-09-568-189A-64	Sequence 64, Appl
60	27	90.0	414	2	US-09-858-664A-13	Sequence 13, Appl
61	27	90.0	414	2	US-10-274-978-14	Sequence 14, Appl
62	27	90.0	414	2	US-10-697-263-14	Sequence 14, Appl
63	27	90.0	468	2	US-09-828-995B-5	Sequence 5, Appli
64	27	90.0	483	2	US-09-270-767-43858	Sequence 43858, A
65	27	90.0	753	2	US-09-248-796A-19291	Sequence 19291, A
66	27	90.0	782	2	US-09-585-858-29	Sequence 29, Appl
67	27	90.0	782	2	US-10-270-878-29	Sequence 29, Appl
68	27	90.0	797	2	US-09-585-858-30	Sequence 30, Appl
69	27	90.0	797	2	US-10-270-878-30	Sequence 30, Appl
70	27	90.0	2860	1	US-08-826-267-2	Sequence 2, Appli
71	27	90.0	3115	1	US-08-323-170B-2	Sequence 2, Appli
72	27	90.0	3135	2	US-08-954-441-2	Sequence 44, Appl
73	26	86.7	5	2	US-09-914-695-44	Sequence 44, Appl
74	26	86.7	6	2	US-09-724-409-8	Sequence 8, Appli
75	26	86.7	6	2	US-09-724-530-8	Sequence 8, Appli
76	26	86.7	6	2	US-09-328-396-8	Sequence 8, Appli
77	26	86.7	14	2	US-09-116-676-4	Sequence 4, Appli
78	26	86.7	44	2	US-09-627-118B-3	Sequence 3, Appli
79	26	86.7	57	2	US-09-270-767-40835	Sequence 40835, A
80	26	86.7	57	2	US-09-270-767-56051	Sequence 56051, A
81	26	86.7	62	2	US-09-107-532A-5115	Sequence 5115, Ap
82	26	86.7	65	2	US-09-248-796A-28159	Sequence 28159, A
83	26	86.7	67	2	US-09-673-395A-339	Sequence 339, App
84	26	86.7	68	2	US-09-489-039A-7375	Sequence 7375, Ap
85	26	86.7	75	2	US-09-270-767-39983	Sequence 3983, A
86	26	86.7	75	2	US-09-270-767-55200	Sequence 55200, A
87	26	86.7	80	2	US-09-248-796A-15929	Sequence 15929, A
88	26	86.7	86	2	US-09-270-767-36170	Sequence 36170, A
89	26	86.7	86	2	US-09-270-767-51387	Sequence 51387, A
90	26	86.7	91	2	US-09-248-796A-21393	Sequence 21393, A
91	26	86.7	98	2	US-09-270-767-40986	Sequence 40986, A
92	26	86.7	98	2	US-09-270-767-56202	Sequence 56202, A
93	26	86.7	99	2	US-09-513-999C-4125	Sequence 4125, Ap
94	26	86.7	103	2	US-09-270-767-539785	Sequence 39785, A
95	26	86.7	103	2	US-09-270-767-55002	Sequence 55002, A
96	26	86.7	107	2	US-09-270-767-60472	Sequence 60472, A
97	26	86.7	114	2	US-09-724-409-7	Sequence 7, Appli
98	26	86.7	114	2	US-09-724-530-7	Sequence 7, Appli
99	26	86.7	114	2	US-09-328-296-7	Sequence 7, Appli
100	26	86.7	121	2	US-09-698-705-8	Sequence 8, Appli

101	26	86.7	122	2	US-09-914-695-42	Sequence 42, Appl	174	26	86.7	896	2	US-08-780-562-3	Sequence 3, Appl1
102	26	86.7	130	2	US-09-621-976-4013	Sequence 4013, Ap	175	26	86.7	896	2	US-10-095-929-13	Sequence 10, Appl
103	26	86.7	136	2	US-09-564-329A-11	Sequence 11, Appl	176	26	86.7	896	2	US-10-014-156-13	Sequence 13, Appl
104	26	86.7	136	2	US-09-963-620-11	Sequence 11, Appl	177	26	86.7	898	1	US-08-693-697-36	Sequence 36, Appl
105	26	86.7	136	2	US-09-855-632-11	Sequence 11, Appl	178	26	86.7	898	2	US-08-588-189-3	Sequence 3, Appl1
106	26	86.7	136	2	US-09-934-773-11	Sequence 11, Appl	179	26	86.7	898	2	US-10-245-616-3	Sequence 3, Appl1
107	26	86.7	136	2	US-09-855-153-11	Sequence 11, Appl	180	26	86.7	906	1	US-08-640-389A-9	Sequence 9, Appl1
108	26	86.7	136	2	US-10-224-720-11	Sequence 18, Appl	181	26	86.7	906	2	US-08-618-957A-9	Sequence 9, Appl1
109	26	86.7	145	2	US-09-466-632C-18	Sequence 18, Appl	182	26	86.7	906	2	US-09-357-914-32	Sequence 32, Appl
110	26	86.7	161	2	US-09-134-001C-4805	Sequence 4805, Ap	183	26	86.7	906	2	US-10-095-929-9	Sequence 9, Appl1
111	26	86.7	162	2	US-09-270-767-40554	Sequence 40554, A	184	26	86.7	908	1	US-08-693-697-33	Sequence 3, Appl1
112	26	86.7	162	2	US-09-270-767-55770	Sequence 55770, A	185	26	86.7	908	1	US-08-588-526-3	Sequence 3, Appl1
113	26	86.7	163	2	US-09-270-767-35493	Sequence 35493, A	186	26	86.7	914	2	US-10-104-047-2923	Sequence 2923, Ap
114	26	86.7	175	2	US-09-270-767-50710	Sequence 50710, A	187	26	86.7	915	1	US-08-818-070-3	Sequence 2, Appl1
115	26	86.7	175	2	US-09-107-532A-4645	Sequence 4645, Ap	188	26	86.7	915	1	US-08-723-585-2	Sequence 2, Appl1
116	26	86.7	213	2	US-09-328-352-6121	Sequence 6121, Ap	189	26	86.7	921	2	US-09-206-800-9	Sequence 9, Appl1
117	26	86.7	221	2	US-09-248-796A-14337	Sequence 14327, A	190	26	86.7	921	2	US-09-206-800-10	Sequence 10, Appl
118	26	86.7	222	2	US-09-698-705-13	Sequence 13, Appl	191	26	86.7	921	2	US-09-206-800-11	Sequence 11, Appl
119	26	86.7	223	2	US-09-270-767-43439	Sequence 43439, A	192	26	86.7	923	2	US-08-780-562-4	Sequence 4, Appl1
120	26	86.7	234	2	US-09-902-540-16250	Sequence 16250, A	193	26	86.7	958	1	US-08-640-389A-8	Sequence 8, Appl1
121	26	86.7	267	2	US-09-134-000C-6273	Sequence 6273, Ap	194	26	86.7	958	2	US-08-618-957A-8	Sequence 8, Appl1
122	26	86.7	286	2	US-09-583-110-5254	Sequence 5254, Ap	195	26	86.7	958	2	US-10-095-929-8	Sequence 8, Appl1
123	26	86.7	291	2	US-09-107-433-3229	Sequence 3229, Ap	196	26	86.7	960	1	US-08-355-888A-8	Sequence 8, Appl1
124	26	86.7	299	2	US-09-270-767-38066	Sequence 38066, A	197	26	86.7	960	1	US-08-588-190-3	Sequence 3, Appl1
125	26	86.7	299	2	US-09-270-767-53283	Sequence 53283, A	198	26	86.7	960	1	US-08-693-697-8	Sequence 8, Appl1
126	26	86.7	301	2	US-09-270-767-42218	Sequence 42218, A	199	26	86.7	960	1	US-08-640-389A-3	Sequence 3, Appl1
127	26	86.7	309	2	US-09-134-000C-6599	Sequence 6599, Ap	200	26	86.7	960	2	US-08-693-696-8	Sequence 8, Appl1
128	26	86.7	314	2	US-09-134-001C-5405	Sequence 5405, Ap	201	26	86.7	960	2	US-08-618-957A-3	Sequence 3, Appl1
129	26	86.7	327	2	US-09-294-894-29	Sequence 29, Appl	202	26	86.7	960	2	US-09-357-914-8	Sequence 8, Appl1
130	26	86.7	328	2	US-09-734-237B-50	Sequence 50, Appl	203	26	86.7	960	2	US-10-095-929-3	Sequence 3, Appl1
131	26	86.7	328	2	US-09-734-237B-52	Sequence 52, Appl	204	26	86.7	1145	2	US-09-710-279-1432	Sequence 1432, Ap
132	26	86.7	333	2	US-09-828-313-33	Sequence 33, Appl	205	26	86.7	1150	1	US-08-589-756-3	Sequence 3, Appl1
133	26	86.7	372	1	US-09-489-039A-10607	Sequence 10607, A	206	26	86.7	1150	2	US-09-206-800-3	Sequence 3, Appl1
134	26	86.7	372	1	US-08-403-634-2	Sequence 30, Appl1	207	26	86.7	1150	2	US-09-206-888-3	Sequence 3, Appl1
135	26	86.7	372	1	US-08-403-634-30	Sequence 30, Appl	208	26	86.7	1150	2	US-09-870-122A-3	Sequence 3, Appl1
136	26	86.7	372	2	US-08-913-441B-2	Sequence 2, Appl1	209	26	86.7	1151	2	US-09-134-001C-3242	Sequence 3242, Ap
137	26	86.7	372	2	US-08-913-441B-30	Sequence 30, Appl1	210	26	86.7	1162	2	US-08-827-962-15	Sequence 15, Appl
138	26	86.7	372	2	US-09-571-985C-2	Sequence 2, Appl1	211	26	86.7	1162	2	US-08-827-962-20	Sequence 20, Appl
139	26	86.7	372	2	US-09-571-985C-30	Sequence 30, Appl	212	26	86.7	1162	2	US-08-803-346-1	Sequence 1, Appl1
140	26	86.7	372	2	US-09-771-161A-203	Sequence 203, App	213	26	86.7	1164	1	US-08-589-756-1	Sequence 1, Appl1
141	26	86.7	393	2	US-09-949-016-11708	Sequence 11708, A	214	26	86.7	1164	2	US-09-206-800-1	Sequence 1, Appl1
142	26	86.7	394	2	US-09-107-532A-3767	Sequence 3767, Ap	215	26	86.7	1164	2	US-09-206-898-1	Sequence 1, Appl1
143	26	86.7	397	1	US-08-415-823-2	Sequence 2, Appl1	216	26	86.7	1164	2	US-09-870-122A-1	Sequence 1, Appl1
144	26	86.7	397	1	US-09-086-662-2	Sequence 2, Appl1	217	26	86.7	1165	1	US-08-640-389A-11	Sequence 11, Appl
145	26	86.7	398	2	US-09-328-352-4507	Sequence 4507, Ap	218	26	86.7	1165	1	US-08-599-455B-4	Sequence 4, Appl1
146	26	86.7	409	2	US-09-270-767-43617	Sequence 43617, A	219	26	86.7	1165	2	US-09-093-814-1	Sequence 1, Appl1
147	26	86.7	450	2	US-10-199-024-61	Sequence 61, Appl	220	26	86.7	1165	2	US-09-069-781B-4	Sequence 4, Appl1
148	26	86.7	450	2	US-10-199-024-62	Sequence 62, Appl	221	26	86.7	1165	2	US-08-618-957A-11	Sequence 11, Appl
149	26	86.7	450	2	US-10-199-024-63	Sequence 63, Appl	222	26	86.7	1165	2	US-09-137-132-4	Sequence 4, Appl1
150	26	86.7	450	2	US-10-199-024-64	Sequence 64, Appl	223	26	86.7	1165	2	US-08-864-564A-4	Sequence 4, Appl1
151	26	86.7	496	2	US-09-902-540-12256	Sequence 12256, A	224	26	86.7	1165	2	US-09-094-410-4	Sequence 4, Appl1
152	26	86.7	502	1	US-08-484-840-3	Sequence 3, Appl1	225	26	86.7	1165	2	US-08-708-183A-4	Sequence 4, Appl1
153	26	86.7	502	1	US-08-483-094-3	Sequence 3, Appl1	226	26	86.7	1165	2	US-08-593-153A-4	Sequence 4, Appl1
154	26	86.7	509	2	US-09-134-001C-2996	Sequence 2996, Ap	227	26	86.7	1165	2	US-08-570-142D-4	Sequence 4, Appl1
155	26	86.7	532	2	US-09-270-767-44987	Sequence 44987, A	228	26	86.7	1165	2	US-08-780-562-2	Sequence 2, Appl1
156	26	86.7	532	2	US-09-540-236-3354	Sequence 3354, Ap	229	26	86.7	1165	2	US-08-618-524B-4	Sequence 4, Appl1
157	26	86.7	555	2	US-09-270-767-62436	Sequence 62436, A	230	26	86.7	1165	2	US-10-095-929-11	Sequence 11, Appl
158	26	86.7	568	2	US-09-710-279-2482	Sequence 2482, Ap	231	26	86.7	1167	1	US-08-589-756-2	Sequence 2, Appl1
159	26	86.7	585	2	US-09-370-807-4	Sequence 4, Appl1	232	26	86.7	1167	2	US-09-206-800-2	Sequence 2, Appl1
160	26	86.7	585	2	US-09-921-259-4	Sequence 2, Appl1	233	26	86.7	1167	2	US-09-206-898-2	Sequence 2, Appl1
161	26	86.7	611	2	US-09-370-807-2	Sequence 2, Appl1	234	26	86.7	1167	2	US-09-870-122A-2	Sequence 2, Appl1
162	26	86.7	611	2	US-09-921-259-2	Sequence 2, Appl1	235	26	86.7	1181	2	US-09-206-898-23	Sequence 23, Appl
163	26	86.7	636	2	US-09-543-681A-4558	Sequence 4558, Ap	236	26	86.7	1181	2	US-09-870-122A-23	Sequence 23, Appl
164	26	86.7	641	2	US-09-248-796A-17974	Sequence 17974, A	237	26	86.7	1221	2	US-08-982-430-2	Sequence 2, Appl1
165	26	86.7	655	2	US-09-712-363-207	Sequence 207, App	238	26	86.7	1416	1	US-08-061-465-4	Sequence 4, Appl1
166	26	86.7	804	2	US-09-116-676-10	Sequence 10, Appl	239	26	86.7	2616	6	5206163-3	Patent No. 5206163
167	26	86.7	883	2	US-08-982-430-1	Sequence 1, Appl1	240	25	83.3	10	1	US-08-237-418-42	Sequence 42, Appl
168	26	86.7	895	2	US-08-827-962-19	Sequence 19, Appl	241	25	83.3	10	2	US-08-468-337-42	Sequence 42, Appl
169	26	86.7	895	2	US-08-827-962-21	Sequence 21, Appl	242	25	83.3	10	2	US-09-758-318-42	Sequence 42, Appl
170	26	86.7	896	1	US-08-640-389A-10	Sequence 10, Appl	243	25	83.3	10	2	US-10-340-783-42	Sequence 42, Appl
171	26	86.7	896	1	US-08-618-957A-10	Sequence 10, Appl	244	25	83.3	20	1	US-08-237-418-44	Sequence 44, Appl
172	26	86.7	896	2	US-09-043-816E-13	Sequence 13, Appl	245	25	83.3	20	1	US-08-934-915-33	Sequence 33, Appl
173	26	86.7	896	2	US-09-357-914-33	Sequence 33, Appl	246	25	83.3	20	1	US-08-934-915-138	Sequence 138, App

247	25	83.3	20	2	US-08-468-337-44	Sequence 44, Appl	320	25	83.3	236	2	US-09-949-016-10071	Sequence 10071, A
248	25	83.3	20	2	US-09-758-318-44	Sequence 44, Appl	321	25	83.3	238	2	US-09-252-991A-29406	Sequence 29406, A
249	25	83.3	20	2	US-10-340-783-44	Sequence 44, Appl	322	25	83.3	240	2	US-09-270-767-48132	Sequence 48132, A
250	25	83.3	38	1	US-08-176-500-61	Sequence 61, Appl	323	25	83.3	253	2	US-08-985-326-27	Sequence 27, Appl
251	25	83.3	38	1	US-08-471-052A-61	Sequence 61, Appl	324	25	83.3	258	2	US-08-871-572B-5	Sequence 5, Appl
252	25	83.3	38	1	US-08-189-331-61	Sequence 61, Appl	325	25	83.3	265	2	US-09-248-796A-16392	Sequence 16392, A
253	25	83.3	38	1	US-08-471-939-61	Sequence 61, Appl	326	25	83.3	266	1	US-08-845-161A-6	Sequence 6, Appl
254	25	83.3	38	1	US-08-471-800-61	Sequence 61, Appl	327	25	83.3	266	1	US-09-270-751-6	Sequence 6, Appl
255	25	83.3	38	1	US-08-471-068-61	Sequence 61, Appl	328	25	83.3	266	2	US-09-168-218B-6	Sequence 6, Appl
256	25	83.3	54	1	US-08-936-165A-479	Sequence 479, App	329	25	83.3	288	2	US-09-270-767-45776	Sequence 45776, A
257	25	83.3	60	2	US-10-179-784-9	Sequence 9, Appl	330	25	83.3	304	2	US-09-270-767-41584	Sequence 41584, A
258	25	83.3	63	2	US-09-248-796A-25816	Sequence 25816, A	331	25	83.3	305	2	US-09-270-767-36889	Sequence 36889, A
259	25	83.3	65	2	US-09-270-767-51299	Sequence 61299, A	332	25	83.3	305	2	US-09-270-767-52106	Sequence 52106, A
260	25	83.3	69	2	US-09-270-767-34348	Sequence 34348, A	333	25	83.3	311	2	US-09-543-681A-5777	Sequence 5777, Ap
261	25	83.3	69	2	US-09-270-767-49565	Sequence 49565, A	334	25	83.3	322	2	US-09-252-991A-29347	Sequence 29347, A
262	25	83.3	71	2	US-09-248-796A-23003	Sequence 23003, A	335	25	83.3	337	2	US-09-044-004A-2	Sequence 2, Appl
263	25	83.3	75	2	US-09-270-767-38662	Sequence 38662, A	336	25	83.3	337	2	US-08-871-572B-1	Sequence 1, Appl
264	25	83.3	75	2	US-09-270-767-53879	Sequence 53879, A	337	25	83.3	337	2	US-08-871-572B-4	Sequence 4, Appl
265	25	83.3	78	2	US-09-471-276-852	Sequence 852, App	338	25	83.3	337	2	US-09-586-924-2	Sequence 2, Appl
266	25	83.3	84	2	US-09-248-796A-25627	Sequence 25627, A	339	25	83.3	337	2	US-09-265-540E-5	Sequence 5, Appl
267	25	83.3	85	1	US-08-928-383B-16	Sequence 16, Appl	340	25	83.3	337	2	US-09-949-002-383	Sequence 383, App
268	25	83.3	85	1	US-08-222-617A-10	Sequence 10, Appl	341	25	83.3	337	4	PCT-US94-14277-8	Sequence 8, Appl
269	25	83.3	89	2	US-09-328-352-6485	Sequence 6486, Ap	342	25	83.3	351	1	US-08-196-350-1	Sequence 1, Appl
270	25	83.3	92	2	US-09-270-767-34585	Sequence 34585, A	343	25	83.3	351	2	US-07-945-495-2	Sequence 2, Appl
271	25	83.3	92	2	US-09-270-767-34585	Sequence 34585, A	344	25	83.3	351	2	US-09-270-767-52106	Sequence 2, Appl
272	25	83.3	105	2	US-09-328-352-6477	Sequence 6477, Ap	345	25	83.3	351	4	PCT-US91-06418-1	Sequence 4, Appl
273	25	83.3	111	2	US-08-881-037-15	Sequence 15, Appl	346	25	83.3	355	2	US-09-248-796A-20592	Sequence 1, Appl
274	25	83.3	112	2	US-09-270-767-6637	Sequence 46637, A	347	25	83.3	355	1	US-08-472-666-4	Sequence 2, Appl
275	25	83.3	119	2	US-08-881-037-60	Sequence 60, Appl	348	25	83.3	355	2	US-09-362-012A-2	Sequence 2, Appl
276	25	83.3	119	2	US-09-107-532A-4767	Sequence 4767, Ap	349	25	83.3	355	2	US-09-362-012A-5	Sequence 5, Appl
277	25	83.3	120	2	US-09-513-999C-7802	Sequence 7802, Ap	350	25	83.3	355	4	PCT-US96-07615-4	Sequence 4, Appl
278	25	83.3	123	2	US-09-270-767-7953	Sequence 7953, A	351	25	83.3	371	2	US-10-176-884-11	Sequence 11, Appl
279	25	83.3	123	2	US-09-270-767-53170	Sequence 53170, A	352	25	83.3	373	2	US-09-248-796A-14832	Sequence 14832, A
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281	25	83.3	139	2	US-09-489-039A-11171	Sequence 11171, A	354	25	83.3	408	2	US-09-719-088B-2	Sequence 2, Appl
282	25	83.3	139	2	US-09-489-039A-11330	Sequence 11330, A	355	25	83.3	417	2	US-09-405-558-44	Sequence 44, Appl
283	25	83.3	140	2	US-09-634-238-339	Sequence 339, App	356	25	83.3	417	2	US-09-538-036-44	Sequence 44, Appl
284	25	83.3	142	2	US-09-543-681A-5092	Sequence 5092, Ap	357	25	83.3	420	2	US-09-255-368-6	Sequence 6, Appl
285	25	83.3	145	2	US-09-270-767-41006	Sequence 41006, A	358	25	83.3	420	2	US-09-405-558-6	Sequence 6, Appl
286	25	83.3	145	2	US-09-270-767-56222	Sequence 56222, A	359	25	83.3	420	2	US-09-538-036-6	Sequence 6, Appl
287	25	83.3	151	2	US-09-270-767-8976	Sequence 8976, A	360	25	83.3	426	2	US-08-737-248-4	Sequence 4, Appl
288	25	83.3	151	2	US-09-270-767-54193	Sequence 54193, A	361	25	83.3	428	2	US-09-198-452A-720	Sequence 720, App
289	25	83.3	154	2	US-09-471-276-893	Sequence 893, App	362	25	83.3	428	2	US-09-438-185A-682	Sequence 682, App
290	25	83.3	155	2	US-09-107-532A-5815	Sequence 5815, Ap	363	25	83.3	447	2	US-09-205-258-408	Sequence 408, App
291	25	83.3	155	2	US-09-605-703B-2484	Sequence 2484, Ap	364	25	83.3	447	2	US-10-004-860-408	Sequence 408, App
292	25	83.3	173	2	US-09-270-767-60146	Sequence 60146, A	365	25	83.3	461	2	US-09-991-181-301	Sequence 301, App
293	25	83.3	179	2	US-09-248-796A-22488	Sequence 22488, A	366	25	83.3	461	2	US-09-990-444-301	Sequence 301, App
294	25	83.3	182	2	US-09-270-767-33066	Sequence 33066, A	367	25	83.3	461	2	US-09-997-333-301	Sequence 301, App
295	25	83.3	182	2	US-09-270-767-48283	Sequence 48283, A	368	25	83.3	464	1	US-09-992-598-301	Sequence 301, App
296	25	83.3	197	2	US-08-737-248-15	Sequence 15, Appl	369	25	83.3	464	2	US-08-553-619B-9	Sequence 9, Appl
297	25	83.3	197	2	US-08-737-248-16	Sequence 16, Appl	370	25	83.3	466	2	US-09-949-016-10572	Sequence 10572, A
298	25	83.3	197	2	US-08-737-248-17	Sequence 17, Appl	371	25	83.3	474	1	US-08-459-100A-4	Sequence 4, Appl
299	25	83.3	197	2	US-09-248-796A-22226	Sequence 22226, A	372	25	83.3	492	1	US-10-390-579A-172	Sequence 172, App
300	25	83.3	198	2	US-08-737-248-6	Sequence 6, Appl	373	25	83.3	501	1	US-08-190-802A-28	Sequence 28, Appl
301	25	83.3	199	2	US-08-737-248-2	Sequence 2, Appl	374	25	83.3	501	1	US-08-705-660-10	Sequence 10, Appl
302	25	83.3	199	2	US-08-737-248-5	Sequence 5, Appl	375	25	83.3	501	2	US-08-989-045-10	Sequence 10, Appl
303	25	83.3	199	2	US-08-737-248-7	Sequence 7, Appl	376	25	83.3	501	2	US-08-477-346-28	Sequence 28, Appl
304	25	83.3	199	2	US-08-737-248-8	Sequence 8, Appl	377	25	83.3	501	2	US-08-473-089-28	Sequence 28, Appl
305	25	83.3	199	2	US-08-737-248-9	Sequence 9, Appl	378	25	83.3	501	2	US-08-487-072A-28	Sequence 28, Appl
306	25	83.3	199	2	US-08-737-248-10	Sequence 10, Appl	379	25	83.3	501	2	US-09-538-092-1311	Sequence 1311, Ap
307	25	83.3	199	2	US-08-737-248-11	Sequence 11, Appl	380	25	83.3	501	2	US-09-315-355A-48	Sequence 48, Appl
308	25	83.3	199	2	US-08-737-248-12	Sequence 12, Appl	381	25	83.3	501	2	US-09-315-355A-48	Sequence 48, Appl
309	25	83.3	199	2	US-08-737-248-13	Sequence 13, Appl	382	25	83.3	503	1	US-08-484-840-4	Sequence 4, Appl
310	25	83.3	199	2	US-08-737-248-14	Sequence 14, Appl	383	25	83.3	503	1	US-08-483-094-4	Sequence 4, Appl
311	25	83.3	212	1	US-08-737-129A-2	Sequence 2, Appl	384	25	83.3	503	2	US-09-248-796A-18992	Sequence 18992, A
312	25	83.3	217	2	US-09-252-991A-22224	Sequence 22224, A	385	25	83.3	510	2	US-08-508-761B-4	Sequence 4, Appl
313	25	83.3	220	2	US-09-270-767-38527	Sequence 38527, A	386	25	83.3	516	2	US-09-949-002-547	Sequence 547, App
314	25	83.3	220	2	US-09-270-767-45126	Sequence 45126, A	387	25	83.3	546	2	US-09-907-794A-250	Sequence 250, App
315	25	83.3	220	2	US-09-270-767-53744	Sequence 53744, A	388	25	83.3	546	2	US-09-905-125A-250	Sequence 250, App
316	25	83.3	228	1	US-09-065-330D-2	Sequence 2, Appl	389	25	83.3	546	2	US-09-902-775A-250	Sequence 250, App
317	25	83.3	229	1	US-08-028-463-2	Sequence 2, Appl	390	25	83.3	546	2	US-09-906-700-250	Sequence 250, App
318	25	83.3	229	1	US-08-461-836-2	Sequence 2, Appl	391	25	83.3	546	2	US-09-903-603A-250	Sequence 250, App
319	25	83.3	231	2	US-09-265-540B-4	Sequence 4, Appl	392	25	83.3	546	2	US-09-904-920A-250	Sequence 250, App

393	25	83.3	546	2	US-09-909-064-250	Sequence 250, App	466	24	80.0	60	2	US-09-248-796A-21803	Sequence 21803, A
394	25	83.3	546	2	US-09-905-381A-250	Sequence 250, App	467	24	80.0	63	2	US-09-543-681A-4176	Sequence 4176, Ap
395	25	83.3	546	2	US-09-906-618-250	Sequence 250, App	468	24	80.0	67	2	US-09-134-0D1C-5223	Sequence 5223, Ap
396	25	83.3	546	2	US-09-906-646-250	Sequence 250, App	469	24	80.0	67	2	US-09-248-796A-28120	Sequence 28120, A
397	25	83.3	546	2	US-09-904-462-250	Sequence 250, App	470	24	80.0	70	2	US-09-583-110-3746	Sequence 3746, Ap
398	25	83.3	546	2	US-09-902-736A-250	Sequence 250, App	471	24	80.0	71	2	US-09-107-433-4907	Sequence 4907, Ap
399	25	83.3	546	2	US-09-906-722A-250	Sequence 250, App	472	24	80.0	73	2	US-09-270-767-5976	Sequence 5976, A
400	25	83.3	565	2	US-09-716-964B-154	Sequence 154, App	473	24	80.0	81	2	US-09-634-238-340	Sequence 340, App
401	25	83.3	591	1	US-08-484-840-2	Sequence 2, Appl1	474	24	80.0	83	2	US-09-270-767-39816	Sequence 39816, A
402	25	83.3	591	1	US-08-483-094-2	Sequence 2, Appl1	475	24	80.0	83	2	US-09-270-767-55033	Sequence 55033, A
403	25	83.3	594	2	US-09-949-016-11089	Sequence 11089, A	476	24	80.0	85	2	US-09-270-767-39373	Sequence 39373, A
404	25	83.3	608	2	US-09-134-000C-4810	Sequence 4810, Ap	477	24	80.0	85	2	US-09-270-767-54590	Sequence 54590, A
405	25	83.3	609	2	US-09-248-796A-19292	Sequence 19292, A	478	24	80.0	87	2	US-09-270-767-62124	Sequence 62124, A
406	25	83.3	617	1	US-08-137-614A-25	Sequence 25, Appl	479	24	80.0	94	2	US-09-252-991A-31551	Sequence 31551, A
407	25	83.3	625	1	US-08-959-004-10	Sequence 10, Appl	480	24	80.0	94	2	US-09-543-681A-6309	Sequence 6309, Ap
408	25	83.3	634	1	US-07-779-049-3	Sequence 3, Appl1	481	24	80.0	97	2	US-09-270-767-60679	Sequence 60679, A
409	25	83.3	634	1	US-08-080-240-3	Sequence 36, Appl1	482	24	80.0	105	2	US-09-107-433-4405	Sequence 4405, Ap
410	25	83.3	661	2	US-09-198-452A-36	Sequence 42, Appl	483	24	80.0	110	2	US-09-248-796A-22030	Sequence 22030, A
411	25	83.3	676	2	US-09-518-550-42	Sequence 22, Appl	484	24	80.0	112	2	US-09-270-767-46531	Sequence 46531, A
412	25	83.3	705	2	US-09-438-185A-22	Sequence 16, Appl	485	24	80.0	123	2	US-09-248-796A-23294	Sequence 23294, A
413	25	83.3	706	1	US-08-484-105-16	Sequence 16, Appl	486	24	80.0	127	2	US-09-583-110-4717	Sequence 4717, Ap
414	25	83.3	706	1	US-08-484-106-16	Sequence 16, Appl	487	24	80.0	129	2	US-09-476-482-6	Sequence 6, Appl1
415	25	83.3	721	2	US-09-541-094-12	Sequence 12, Appl	488	24	80.0	131	2	US-09-270-767-40682	Sequence 40682, A
416	25	83.3	721	2	US-09-945-258-12	Sequence 29, Appl	489	24	80.0	131	2	US-09-270-767-55898	Sequence 55898, A
417	25	83.3	723	2	US-09-518-550-39	Sequence 29, Appl	490	24	80.0	132	1	US-08-463-911-5	Sequence 5, Appl1
418	25	83.3	737	2	US-09-949-016-9829	Sequence 9829, Ap	491	24	80.0	132	2	US-09-902-540-13906	Sequence 13906, A
419	25	83.3	824	2	US-09-949-002-448	Sequence 3018, App	492	24	80.0	133	2	US-09-634-238-372	Sequence 372, App
420	25	83.3	842	2	US-10-104-047-3018	Sequence 3018, App	493	24	80.0	144	2	US-09-134-000C-5590	Sequence 5590, Ap
421	25	83.3	946	2	US-09-538-092-1230	Sequence 1230, Ap	494	24	80.0	145	2	US-09-328-352-6032	Sequence 6092, Ap
422	25	83.3	946	2	US-09-949-016-6105	Sequence 6105, Ap	495	24	80.0	145	2	US-09-543-681A-5502	Sequence 5202, Ap
423	25	83.3	960	2	US-09-949-016-10492	Sequence 10492, A	496	24	80.0	147	2	US-09-270-767-38891	Sequence 38891, A
424	25	83.3	1025	1	US-08-304-309-2	Sequence 2, Appl1	497	24	80.0	147	2	US-09-270-767-41336	Sequence 41336, A
425	25	83.3	1025	1	US-08-304-309-4	Sequence 4, Appl1	498	24	80.0	148	2	US-09-270-767-41235	Sequence 41235, A
426	25	83.3	1025	2	US-08-991-942-2	Sequence 2, Appl1	499	24	80.0	150	2	US-09-270-767-56452	Sequence 56452, A
427	25	83.3	1025	2	US-08-991-942-4	Sequence 4, Appl1	500	24	80.0	150	2	US-09-134-001C-3502	Sequence 3502, Ap
428	25	83.3	1025	2	US-09-138-103-2	Sequence 2, Appl1	501	24	80.0	151	2	US-09-107-532A-6581	Sequence 6581, Ap
429	25	83.3	1025	2	US-09-854-886-2	Sequence 2, Appl1	502	24	80.0	152	2	US-09-415-551-4	Sequence 4, Appl1
430	25	83.3	1025	4	PCT-US95-04567-2	Sequence 2, Appl1	503	24	80.0	152	2	US-09-415-551-5	Sequence 5, Appl1
431	25	83.3	1025	4	PCT-US95-04567-4	Sequence 4, Appl1	504	24	80.0	152	2	US-09-975-607A-5	Sequence 5, Appl1
432	25	83.3	1204	4	US-09-583-110-4083	Sequence 4083, Ap	505	24	80.0	152	2	US-09-270-767-39294	Sequence 39294, A
433	25	83.3	1215	2	US-09-949-002-321	Sequence 321, App	506	24	80.0	153	2	US-09-270-767-39294	Sequence 39294, A
434	25	83.3	1220	1	US-08-158-232-43	Sequence 43, Appl	507	24	80.0	153	2	US-09-270-767-54511	Sequence 54511, A
435	25	83.3	1220	1	US-08-611-928-8	Sequence 43, Appl	508	24	80.0	155	2	US-09-270-767-62431	Sequence 62431, A
436	25	83.3	1245	1	US-09-173-891-43	Sequence 43, Appl	509	24	80.0	156	2	US-09-489-039A-13832	Sequence 13832, A
437	25	83.3	1245	1	US-08-158-232-8	Sequence 8, Appl1	510	24	80.0	156	2	US-09-134-000C-3896	Sequence 3896, Ap
438	25	83.3	1245	1	US-08-304-626-8	Sequence 8, Appl1	511	24	80.0	157	1	US-08-374-155A-6	Sequence 6, Appl1
439	25	83.3	1245	1	US-08-611-928-8	Sequence 8, Appl1	512	24	80.0	157	1	US-08-785-396-6	Sequence 6, Appl1
440	25	83.3	1245	1	US-09-173-891-8	Sequence 8, Appl1	513	24	80.0	157	2	US-10-061-269-6	Sequence 6, Appl1
441	25	83.3	1262	2	US-09-107-433-5067	Sequence 5067, Ap	514	24	80.0	159	2	US-09-583-110-4420	Sequence 4420, Ap
442	25	83.3	1529	2	US-09-252-991A-27005	Sequence 27005, A	515	24	80.0	159	2	US-09-270-767-44344	Sequence 44344, A
443	25	83.3	1529	2	US-09-215-694-1	Sequence 1, Appl1	516	24	80.0	161	2	US-09-415-551-3	Sequence 3, Appl1
444	25	83.3	1529	2	US-10-109-310-1	Sequence 1, Appl1	517	24	80.0	161	2	US-09-975-607A-3	Sequence 3, Appl1
445	25	83.3	1604	2	US-09-949-016-11186	Sequence 11186, A	518	24	80.0	165	2	US-09-270-767-48058	Sequence 48058, A
446	25	83.3	1912	2	US-08-913-832A-2	Sequence 2, Appl1	519	24	80.0	166	2	US-09-270-767-60166	Sequence 60166, A
447	25	83.3	1912	2	US-09-249-181A-2	Sequence 2, Appl1	520	24	80.0	167	2	US-09-107-433-3195	Sequence 4195, Ap
448	25	83.3	1912	2	US-09-158-707-2	Sequence 2, Appl1	521	24	80.0	167	2	US-09-902-540-11616	Sequence 11616, A
449	25	83.3	1935	2	US-09-949-016-10970	Sequence 10970, A	522	24	80.0	167	2	US-09-543-681A-5201	Sequence 5201, Ap
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451	25	83.3	2404	2	US-09-949-016-11691	Sequence 11691, A	524	24	80.0	176	2	US-09-270-767-53085	Sequence 53085, A
452	25	83.3	2547	2	US-09-058-489-35	Sequence 35, Appl	525	24	80.0	181	2	US-09-252-991A-26370	Sequence 26370, A
453	25	83.3	2547	2	US-09-538-092-1374	Sequence 1374, Ap	526	24	80.0	181	2	US-09-270-767-42331	Sequence 42331, A
454	25	83.3	2555	2	US-09-058-489-36	Sequence 36, Appl	527	24	80.0	188	2	US-09-107-532A-4007	Sequence 4007, Ap
455	25	83.3	2555	2	US-09-538-092-830	Sequence 820, App	528	24	80.0	194	2	US-09-248-786A-14889	Sequence 14889, A
456	25	83.3	3666	1	US-08-222-617A-12	Sequence 12, Appl	529	24	80.0	198	2	US-09-270-767-57480	Sequence 57480, A
457	25	83.3	3727	1	US-08-222-617A-27	Sequence 27, Appl1	530	24	80.0	203	2	US-09-328-352-42293	Sequence 4293, Ap
458	25	83.3	3778	1	US-09-440-781-90	Sequence 2, Appl1	531	24	80.0	204	2	US-09-134-001C-2975	Sequence 2975, Ap
459	24	80.0	3778	1	US-09-440-781-90	Sequence 90, Appl1	532	24	80.0	204	2	US-09-270-767-56032	Sequence 56032, A
460	24	80.0	38	2	US-09-270-767-60311	Sequence 60311, A	533	24	80.0	204	2	US-09-270-767-56032	Sequence 22772, A
461	24	80.0	38	2	US-09-270-767-36122	Sequence 36122, A	534	24	80.0	206	2	US-09-248-796A-12772	Sequence 12772, A
462	24	80.0	38	2	US-09-270-767-51339	Sequence 51339, A	535	24	80.0	211	2	US-09-605-703B-1252	Sequence 1252, Ap
463	24	80.0	52	2	US-09-270-767-35283	Sequence 35283, A	536	24	80.0	211	2	US-09-605-703B-1254	Sequence 1254, Ap
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465	24	80.0	60	2	US-09-270-767-44843	Sequence 44843, A	538	24	80.0	214	2	US-09-107-532A-6386	Sequence 6386, Ap

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540	24	80.0	224	2	US-09-902-540-11119	Sequence 11119, A	613	24	80.0	374	2	US-10-104-047-3578	Sequence 3578, Ap
541	24	80.0	226	2	US-09-198-452A-811	Sequence 811, App	614	24	80.0	379	2	US-09-252-91A-31570	Sequence 31570, A
542	24	80.0	226	2	US-09-328-352-7169	Sequence 7169, Ap	615	24	80.0	385	2	US-09-733-388-2	Sequence 2, Appli
543	24	80.0	226	2	US-09-438-185A-763	Sequence 763, App	616	24	80.0	385	2	US-10-446-175-2	Sequence 2, Appli
544	24	80.0	229	2	US-09-328-352-6458	Sequence 6458, App	617	24	80.0	388	2	US-09-949-016-7414	Sequence 7414, Ap
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546	24	80.0	240	2	US-09-248-796A-15041	Sequence 15041, A	619	24	80.0	392	1	US-09-080-538-1	Sequence 1, Appli
547	24	80.0	241	2	US-09-248-796A-27513	Sequence 27513, A	620	24	80.0	392	2	US-09-387-413-1	Sequence 1, Appli
548	24	80.0	244	2	US-09-328-352-6633	Sequence 6633, Ap	621	24	80.0	392	2	US-09-248-796A-26630	Sequence 26630, A
549	24	80.0	253	2	US-09-248-796A-15042	Sequence 15042, A	622	24	80.0	398	1	US-08-446-777-2	Sequence 2, Appli
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551	24	80.0	260	2	US-09-392-277-24	Sequence 24, Appli	624	24	80.0	400	2	US-09-134-000C-4389	Sequence 4389, Ap
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554	24	80.0	269	2	US-09-270-767-37552	Sequence 37552, A	627	24	80.0	409	2	US-09-270-767-40504	Sequence 40504, A
555	24	80.0	272	2	US-09-270-767-52769	Sequence 52769, A	628	24	80.0	409	2	US-09-270-767-55720	Sequence 55720, A
556	24	80.0	272	2	US-09-270-767-46810	Sequence 46810, A	629	24	80.0	410	2	US-09-540-336-5840	Sequence 3840, Ap
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558	24	80.0	275	1	US-08-645-193B-19	Sequence 19, Appli	631	24	80.0	420	2	US-09-248-796A-15323	Sequence 15323, A
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560	24	80.0	284	2	US-09-861-451A-20	Sequence 20, Appli	633	24	80.0	435	1	US-08-374-155A-5	Sequence 5, Appli
561	24	80.0	285	1	US-08-631-200-15	Sequence 15, Appli	634	24	80.0	435	1	US-08-785-396-5	Sequence 5, Appli
562	24	80.0	285	1	US-08-829-553-15	Sequence 15, Appli	635	24	80.0	435	2	US-10-061-669-5	Sequence 5, Appli
563	24	80.0	285	1	US-08-922-267A-15	Sequence 15, Appli	636	24	80.0	448	2	US-09-107-532A-4482	Sequence 4482, Ap
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565	24	80.0	285	1	US-08-936-706A-15	Sequence 15, Appli	638	24	80.0	453	2	US-09-538-092-472	Sequence 472, App
566	24	80.0	285	2	US-09-248-203-15	Sequence 15, Appli	639	24	80.0	453	2	US-09-107-433-3887	Sequence 3887, Ap
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569	24	80.0	285	2	US-08-697-766A-5	Sequence 5, Appli	642	24	80.0	469	2	US-09-270-767-49097	Sequence 49097, A
570	24	80.0	285	2	US-08-814-986-15	Sequence 15, Appli	643	24	80.0	472	2	US-09-486-192-3	Sequence 3, Appli
571	24	80.0	285	2	US-09-902-540-16089	Sequence 16089, A	644	24	80.0	472	2	US-10-328-459A-3	Sequence 3, Appli
572	24	80.0	293	2	US-09-270-767-44710	Sequence 44710, A	645	24	80.0	480	2	US-09-543-681A-7938	Sequence 7938, Ap
573	24	80.0	300	2	US-09-540-226-2089	Sequence 2089, Ap	646	24	80.0	507	2	US-08-860-635A-19	Sequence 19, Appli
574	24	80.0	301	2	US-09-902-540-15018	Sequence 15018, A	647	24	80.0	507	2	US-09-281-476-19	Sequence 19, Appli
575	24	80.0	302	2	US-09-270-767-45342	Sequence 45342, A	648	24	80.0	507	2	US-09-910-087-19	Sequence 19, Appli
576	24	80.0	306	2	US-09-634-238-367	Sequence 367, App	649	24	80.0	508	2	US-09-489-939A-7887	Sequence 7887, Ap
577	24	80.0	309	2	US-09-248-796A-17217	Sequence 17217, A	650	24	80.0	509	2	US-08-860-635A-21	Sequence 21, Appli
578	24	80.0	314	2	US-09-902-540-14628	Sequence 14628, A	651	24	80.0	509	2	US-09-281-476-21	Sequence 21, Appli
579	24	80.0	315	2	US-09-248-796A-14850	Sequence 14850, A	652	24	80.0	509	2	US-09-910-087-21	Sequence 21, Appli
580	24	80.0	316	2	US-08-961-083-156	Sequence 156, App	653	24	80.0	509	2	US-09-949-016-5930	Sequence 5930, Ap
581	24	80.0	316	2	US-09-536-784-156	Sequence 156, App	654	24	80.0	510	1	US-08-255-670A-2	Sequence 2, Appli
582	24	80.0	316	2	US-09-765-271-156	Sequence 156, App	655	24	80.0	510	2	US-09-252-991A-20463	Sequence 20463, A
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584	24	80.0	322	2	US-09-248-796A-17951	Sequence 17951, A	657	24	80.0	521	2	US-09-134-001C-4290	Sequence 4290, Ap
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588	24	80.0	324	1	US-08-868-577-13	Sequence 13, Appli	661	24	80.0	523	2	US-09-492-709A-354	Sequence 354, App
589	24	80.0	324	2	US-09-207-914-11	Sequence 11, Appli	662	24	80.0	535	2	US-09-137-077-2	Sequence 2, Appli
590	24	80.0	324	2	US-09-207-914-13	Sequence 13, Appli	663	24	80.0	536	2	US-09-583-110-4004	Sequence 4004, Ap
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592	24	80.0	331	2	US-08-810-712-24	Sequence 24, Appli	665	24	80.0	542	1	US-08-701-380-2	Sequence 2, Appli
593	24	80.0	338	2	US-09-330-611-6	Sequence 6, Appli	666	24	80.0	542	2	US-09-032-365A-13	Sequence 13, Appli
594	24	80.0	340	2	US-09-768-787-188	Sequence 188, App	667	24	80.0	544	2	US-09-107-532A-4136	Sequence 4136, Ap
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597	24	80.0	341	2	US-09-540-236-3002	Sequence 3002, App	670	24	80.0	555	1	US-08-039-177-3	Sequence 3, Appli
598	24	80.0	342	2	US-09-330-611-4	Sequence 4, Appli	671	24	80.0	555	1	US-08-611-361A-3	Sequence 3, Appli
599	24	80.0	344	2	US-09-543-681A-6393	Sequence 6393, Ap	672	24	80.0	556	2	US-09-107-433-3006	Sequence 3006, Ap
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602	24	80.0	349	2	US-08-955-918C-2	Sequence 2, Appli	675	24	80.0	557	2	US-09-285-957-33	Sequence 33, Appli
603	24	80.0	349	2	US-09-134-001C-4519	Sequence 4519, Ap	676	24	80.0	557	2	US-08-562-281-4	Sequence 4, Appli
604	24	80.0	349	2	US-08-697-766A-2	Sequence 2, Appli	677	24	80.0	560	2	US-09-634-338-242	Sequence 242, App
605	24	80.0	349	2	US-09-710-279-932	Sequence 932, App	678	24	80.0	568	2	US-09-911-909B-16	Sequence 16, Appli
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611	24	80.0	362	1	US-08-255-670A-4	Sequence 4, Appli	684	24	80.0	593	1	US-08-374-155A-14	Sequence 14, Appli

685	24	80.0	593	1	US-08-785-396-14	Sequence 14, Appl	758	24	80.0	1315	2	US-09-392-277-25	Sequence 25, Appl
686	24	80.0	593	2	US-10-061-259-14	Sequence 14, Appl	759	24	80.0	1315	2	US-09-258-0b0-2	Sequence 2, Appl
687	24	80.0	597	1	US-08-374-155A-12	Sequence 12, Appl	760	24	80.0	1315	2	US-09-258-0b0-25	Sequence 25, Appl
688	24	80.0	597	1	US-08-785-396-12	Sequence 12, Appl	761	24	80.0	1315	2	US-09-060-939A-10	Sequence 10, Appl
689	24	80.0	597	2	US-10-061-269-12	Sequence 12, Appl	762	24	80.0	1412	2	US-09-949-002-486	Sequence 486, App
690	24	80.0	600	1	US-08-374-155A-10	Sequence 10, Appl	763	24	80.0	1432	2	US-08-810-712-10	Sequence 10, Appl
691	24	80.0	600	1	US-08-785-396-10	Sequence 10, Appl	764	24	80.0	1431	2	US-09-538-092-1198	Sequence 1198, App
692	24	80.0	600	1	US-10-061-269-10	Sequence 10, Appl	765	24	80.0	1431	2	US-09-949-002-377	Sequence 377, App
693	24	80.0	603	1	US-08-190-802A-50	Sequence 50, Appl	766	24	80.0	1815	2	US-09-270-767-42654	Sequence 42654, A
694	24	80.0	603	2	US-08-477-346-50	Sequence 50, Appl	767	24	80.0	2119	2	US-09-583-110-4893	Sequence 4893, Ap
695	24	80.0	603	2	US-08-473-089-50	Sequence 50, Appl	768	24	80.0	2123	2	US-09-107-433-3728	Sequence 3728, Ap
696	24	80.0	603	2	US-08-487-072A-50	Sequence 50, Appl	769	24	80.0	3169	2	US-08-477-451-6	Sequence 6, Appl
697	24	80.0	610	2	US-09-270-767-42755	Sequence 42755, A	770	24	76.7	5	2	US-09-647-468-133	Sequence 133, App
698	24	80.0	622	2	US-09-949-016-9873	Sequence 9873, Ap	771	23	76.7	5	2	US-09-424-712-20	Sequence 20, Appl
699	24	80.0	629	1	US-08-374-155A-4	Sequence 4, Appl	772	23	76.7	5	2	US-09-339-596A-30	Sequence 30, Appl
700	24	80.0	629	1	US-08-785-396-4	Sequence 4, Appl	773	23	76.7	10	2	US-09-039-780A-101	Sequence 101, App
701	24	80.0	629	2	US-10-061-269-4	Sequence 4, Appl	774	23	76.7	10	2	US-09-802-083-7	Sequence 7, Appl
702	24	80.0	647	2	US-09-031-563-7	Sequence 7, Appl	775	23	76.7	16	2	US-09-039-780A-103	Sequence 103, App
703	24	80.0	647	2	US-09-392-277-7	Sequence 7, Appl	776	23	76.7	16	2	US-09-039-780A-105	Sequence 105, App
704	24	80.0	647	2	US-09-258-000-7	Sequence 7, Appl	777	23	76.7	17	1	US-08-097-938-20	Sequence 20, Appl
705	24	80.0	648	2	US-09-031-563-5	Sequence 5, Appl	778	23	76.7	17	1	US-08-476-000-20	Sequence 20, Appl
706	24	80.0	648	2	US-09-392-277-5	Sequence 5, Appl	779	23	76.7	17	1	US-08-476-876-20	Sequence 20, Appl
707	24	80.0	648	2	US-09-258-000-5	Sequence 5, Appl	780	23	76.7	17	1	US-08-476-976-20	Sequence 20, Appl
708	24	80.0	655	2	US-10-152-886-89	Sequence 89, Appl	781	23	76.7	17	2	US-08-474-410-20	Sequence 20, Appl
709	24	80.0	659	1	US-08-136-277-3	Sequence 3, Appl	782	23	76.7	22	2	US-08-486-673B-20	Sequence 20, Appl
710	24	80.0	659	1	US-08-479-403-3	Sequence 3, Appl	783	23	76.7	22	2	US-09-039-780A-102	Sequence 102, App
711	24	80.0	659	2	US-08-835-734-3	Sequence 3, Appl	784	23	76.7	25	2	US-09-039-780A-96	Sequence 96, Appl
712	24	80.0	663	2	US-09-134-078-61	Sequence 61, Appl	785	23	76.7	30	2	US-09-039-780A-98	Sequence 98, Appl
713	24	80.0	680	2	US-09-134-078-25	Sequence 25, Appl	786	23	76.7	30	2	US-09-039-780A-100	Sequence 100, App
714	24	80.0	680	2	US-09-949-001-15	Sequence 15, Appl	787	23	76.7	30	2	US-09-039-780A-104	Sequence 104, App
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ALIGNMENTS

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RESULT 1
US-08-137-117D-143
; Sequence 143, Application US/08137117D
; Patent No. 5795365
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
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; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
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Query Match 100.0%; Score 30; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 SYTH 5
Db 1 SYTH 5
```

```
RESULT 2
US-08-436-717-143
; Sequence 143, Application US/08436717
; Patent No. 5817790
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,717
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,117
; FILING DATE: 20-DEC-1993
; APPLICATION NUMBER: WO PCT/JP92/00544
; FILING DATE: 24-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-32084
; FILING DATE: 19-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-95476
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/126/AAOK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 143:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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US-08-436-717-143

Query Match 100.0%; Score 30; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
1 SYTH 5

Db 1 SYTH 5

RESULT 3

US-08-561-521-41
Sequence 41, Application US/08561521
Patent No. 5840299

GENERAL INFORMATION:

APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.

APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran

TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
Adhesion Molecule VLA-4

NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESSES:

ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California

COUNTRY: USA
ZIP: 94105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561,521

FILING DATE:
CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/186,269A
FILING DATE: 25-JAN-1994

ATTORNEY/AGENT INFORMATION:

NAME: Smith, William L.
REGISTRATION NUMBER: 30,223

REFERENCE/DOCKET NUMBER: 15270-14
TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043

INFORMATION FOR SEQ ID NO: 41:

SEQUENCE CHARACTERISTICS:

LENGTH: 116 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-561-521-41
Query Match 100.0%; Score 30; DB 1; Length 116;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
1 SYTH 5

Db 1 SYTH 5

RESULT 4

PCT-US95-01219-41

Sequence 41, Application PC/TUS9501219

GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.

APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
Adhesion Molecule VLA-4

NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESSES:

ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California

COUNTRY: USA
ZIP: 94105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01219

FILING DATE: 25-JAN-1995
CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/186,269
FILING DATE: 25-JAN-1994

ATTORNEY/AGENT INFORMATION:

NAME: Smith, William L.
REGISTRATION NUMBER: 30,223

REFERENCE/DOCKET NUMBER: 15270-14
TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043

INFORMATION FOR SEQ ID NO: 41:

SEQUENCE CHARACTERISTICS:

LENGTH: 116 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US95-01219-41
Query Match 100.0%; Score 30; DB 4; Length 116;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
1 SYTH 5

Db 1 SYTH 5

RESULT 5

US-08-137-117D-27
Sequence 27, Application US/08137117D
Patent No. 5795965

GENERAL INFORMATION:

APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh

APPLICANT: BENDIG, Mary
APPLICANT: JONES, Steven

APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
INTERLEUKIN-6 RECEPTOR

NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESSES:

ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.

COUNTRY: USA
ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117D
FILING DATE: 20-DEC-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-137-117D-27

Query Match 100.0%; Score 30; DB 1; Length 135;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYTH 5
|||||
Db 50 SYTH 54

RESULT 6
US-08-137-117D-100
Sequence 100, Application US/08137117D
Patent No. 5795965
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: JONES, Steven
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117D
FILING DATE: 20-DEC-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084

FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-137-117D-100

Query Match 100.0%; Score 30; DB 1; Length 135;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYTH 5
|||||
Db 50 SYTH 54

RESULT 7
US-08-137-117D-102
Sequence 102, Application US/08137117D
Patent No. 5795965
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: JONES, Steven
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117D
FILING DATE: 20-DEC-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300

TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-137-117D-102

Query Match 100.0%; Score 30; DB 1; Length 135;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
|||||
Db 50 SYTH 54

RESULT 8

US-08-137-117D-112
Sequence 112, Application US/08137117D
Patent No. 5795965

GENERAL INFORMATION:

APPLICANT: TSUCHIYA, Masayuki

APPLICANT: SATO, Koh

APPLICANT: BENDIG, Mary

APPLICANT: JONES, Steven

APPLICANT: SALDANHA, Jose

TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN

NUMBER OF SEQUENCES: 158

CORRESPONDENCE ADDRESS:

ADDRESS: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/137,117D

FILING DATE: 20-DEC-1993

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/JP92/00544

FILING DATE: 24-APR-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 4-32084

FILING DATE: 19-FEB-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 3-95476

FILING DATE: 25-APR-1991

ATTORNEY/AGENT INFORMATION:

NAME: WEGNER, Harold C.

REGISTRATION NUMBER: 25,258

REFERENCE/DOCKET NUMBER: 53466/126/AAOK

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 672-5300

TELEFAX: (202) 672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 112:

SEQUENCE CHARACTERISTICS:

LENGTH: 135 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-137-117D-112

Query Match 100.0%; Score 30; DB 1; Length 135;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
|||||
Db 50 SYTH 54

RESULT 9

US-08-436-717-27

Sequence 27, Application US/08436717

Patent No. 5817790

GENERAL INFORMATION:

APPLICANT: TSUCHIYA, Masayuki

APPLICANT: SATO, Koh

APPLICANT: BENDIG, Mary

APPLICANT: JONES, Steven

APPLICANT: SALDANHA, Jose

TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN

NUMBER OF SEQUENCES: 158

CORRESPONDENCE ADDRESS:

ADDRESS: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/436,717

FILING DATE:

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/137,117

FILING DATE: 20-DEC-1993

APPLICATION NUMBER: WO PCT/JP92/00544

FILING DATE: 24-APR-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 4-32084

FILING DATE: 19-FEB-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 3-95476

FILING DATE: 25-APR-1991

ATTORNEY/AGENT INFORMATION:

NAME: WEGNER, Harold C.

REGISTRATION NUMBER: 25,258

REFERENCE/DOCKET NUMBER: 53466/126/AAOK

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 672-5300

TELEFAX: (202) 672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:

LENGTH: 135 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-436-717-27

Query Match 100.0%; Score 30; DB 1; Length 135;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
|||||
Db 50 SYTH 54

```
RESULT 10
US-08-436-717-100
; Sequence 100, Application US/08436717
; Patent No. 5817790
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,717
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,117
; FILING DATE: 20-DEC-1993
; APPLICATION NUMBER: WO PCT/JP92/00544
; FILING DATE: 24-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-32084
; FILING DATE: 19-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-95476
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/126/AAOK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-436-717-100

Query Match      100.0%; Score 30; DB 1; Length 135;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SYTH 5
        |||||
Db       50 SYTH 54

RESULT 11
US-08-436-717-102
; Sequence 102, Application US/08436717
; Patent No. 5817790
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
```

```
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,717
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,117
; FILING DATE: 20-DEC-1993
; APPLICATION NUMBER: WO PCT/JP92/00544
; FILING DATE: 24-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-32084
; FILING DATE: 19-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-95476
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/126/AAOK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 102:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-436-717-102

Query Match      100.0%; Score 30; DB 1; Length 135;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SYTH 5
        |||||
Db       50 SYTH 54

RESULT 12
US-08-436-717-112
; Sequence 112, Application US/08436717
; Patent No. 5817790
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
```

STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,717
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/ANOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-436-717-112

Query Match 100.0%; Score 30; DB 1; Length 135;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
DB 50 SYTH 54

RESULT 13
US-09-248-796A-24535
Sequence 24535, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Kelch Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
PRIOR FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 24535
LENGTH: 62
TYPE: PRT
ORGANISM: Candida albicans
US-09-248-796A-24535

Query Match 93.3%; Score 28; DB 2; Length 62;

Best Local Similarity 80.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
DB 12 SYTH 16

RESULT 14
US-09-270-767-40412
Sequence 40412, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 40412
LENGTH: 160
TYPE: PRT
ORGANISM: Drosophila melanogaster
FEATURE:
OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-40412

Query Match 93.3%; Score 28; DB 2; Length 160;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
DB 137 SYTH 141

RESULT 15
US-09-270-767-55628
Sequence 55628, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 55628
LENGTH: 160
TYPE: PRT
ORGANISM: Drosophila melanogaster
FEATURE:
OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-55628

Query Match 93.3%; Score 28; DB 2; Length 160;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
DB 137 SYTH 141

RESULT 16
US-09-107-532A-3715
Sequence 3715, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354

COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:
NAME: Arinello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 3715:
SEQUENCE CHARACTERISTICS:
LENGTH: 226 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium

FEATURE:
NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...226
SEQUENCE DESCRIPTION: SEQ ID NO: 3715:
US-09-107-532A-3715

Query Match 93.3%; Score 28; DB 2; Length 226;
Best Local Similarity 80.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
|||:
Db 29 SYTH 33

RESULT 17
US-09-248-796A-18926
Sequence 18926, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 18926
LENGTH: 354
TYPE: PRT
ORGANISM: Candida albicans

US-09-248-796A-18926

Query Match 93.3%; Score 28; DB 2; Length 354;
Best Local Similarity 80.0%; Pred. No. 5.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
|||:
Db 135 SYTH 139

RESULT 18
US-09-540-236-2017
Sequence 2017, Application US/09540236
Patent No. 6673910
GENERAL INFORMATION:
APPLICANT: Gary L. Bretton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARR
FILE REFERENCE: 2709,2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 2017
LENGTH: 501
TYPE: PRT
ORGANISM: M. catarrhalis

US-09-540-236-2017

Query Match 93.3%; Score 28; DB 2; Length 501;
Best Local Similarity 80.0%; Pred. No. 8.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
|||:
Db 210 SYTH 214

RESULT 19
US-09-189-462-4
Sequence 4, Application US/09189462
Patent No. 6303502
GENERAL INFORMATION:
APPLICANT: Rupp, Steffan
APPLICANT: Robertson, Laura
APPLICANT: Summers, Eric F.
APPLICANT: Hecht, Peter
APPLICANT: Roberts, Radclyffe
APPLICANT: Madhani, Hiran
APPLICANT: Styles, Cora Ann
APPLICANT: Lo, Hsiu-Jung
APPLICANT: Sherman, Amir
APPLICANT: Cail, Brian
APPLICANT: Fink, Gerald
TITLE OF INVENTION: REGULATION OF FUNGAL GENE EXPRESSION
FILE REFERENCE: 50078/003002
CURRENT APPLICATION NUMBER: US/09/189,462
CURRENT FILING DATE: 1998-11-10
EARLIER APPLICATION NUMBER: 60/066,129
EARLIER FILING DATE: 1997-11-19
EARLIER APPLICATION NUMBER: 60/066,308
EARLIER FILING DATE: 1997-11-21
EARLIER APPLICATION NUMBER: 60/066,462
EARLIER FILING DATE: 1997-11-24
EARLIER APPLICATION NUMBER: 60/078,610
EARLIER FILING DATE: 1998-03-19
EARLIER APPLICATION NUMBER: 60/094,523
EARLIER FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 67
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 659
TYPE: PRT

ORGANISM: Candida albicans
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(659)
OTHER INFORMATION: Xaa = Any Amino Acid
US-09-189-462-4

Query Match 93.3%; Score 28; DB 2; Length 659;
Best Local Similarity 80.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYTH 5
|||:
Db 134 SYTH 138

RESULT 20
US-09-196-270-5
Sequence 5, Application US/09196270
Patent No. 6500636
GENERAL INFORMATION:
APPLICANT: Hecht, Peter
APPLICANT: Madden, Kevin
TITLE OF INVENTION: CHIMERIC PRE-ACTIVATED TRANSCRIPTION
FILE REFERENCE: 50078/004002
CURRENT FILING DATE: 1998-11-19
EARLIER APPLICATION NUMBER: 60/066,129
EARLIER FILING DATE: 1997-11-19
EARLIER APPLICATION NUMBER: 60/066,308
EARLIER FILING DATE: 1997-11-21
EARLIER APPLICATION NUMBER: 60/066,462
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 5
LENGTH: 659
TYPE: PRT
ORGANISM: Candida albicans
US-09-196-270-5

Query Match 93.3%; Score 28; DB 2; Length 659;
Best Local Similarity 80.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYTH 5
|||:
Db 134 SYTH 138

RESULT 21
US-09-863-040-4
Sequence 4, Application US/09863040
Patent No. 6599705
GENERAL INFORMATION:
APPLICANT: Rupp, Steffen
APPLICANT: Robertson, Laura
APPLICANT: Summers, Eric F.
APPLICANT: Hecht, Peter
APPLICANT: Roberts, Radclyffe
APPLICANT: Madhani, Hiren
APPLICANT: Styles, Cora Ann
APPLICANT: Lo, Hsin-Jung
APPLICANT: Sherman, Amit
APPLICANT: Cali, Brian
APPLICANT: Fink, Gerald R.
TITLE OF INVENTION: Regulation of Fungal Gene Expression
FILE REFERENCE: 109272.152
CURRENT FILING DATE: 2001-05-22
CURRENT APPLICATION NUMBER: US/09/863,040
PRIOR APPLICATION NUMBER: US 60/066,129

PRIOR FILING DATE: 1997-11-19
PRIOR APPLICATION NUMBER: US 60/066,308
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 60/066,462
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: US 60/078,610
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: US 60/094,523
PRIOR FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 659
TYPE: PRT
ORGANISM: Candida RIM1
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (43)...(43)
OTHER INFORMATION: Amino acid 43 is "Xaa" wherein "Xaa" = any amino acid.
US-09-863-040-4

Query Match 93.3%; Score 28; DB 2; Length 659;
Best Local Similarity 80.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYTH 5
|||:
Db 134 SYTH 138

RESULT 22
US-09-107-532A-6126
Sequence 6126, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Arinello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 6126:
SEQUENCE CHARACTERISTICS:
LENGTH: 1179 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES

```

; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (B) LOCATION 1...1179
; SEQUENCE DESCRIPTION: SEQ ID NO: 6126:
US-09-107-532A-6126

Query Match      93.3%; Score 28; DB 2; Length 1179;
Best Local Similarity 80.0%; Pred. No. 1.9e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 SYTH 5
DB      1021 SYTH 1025

RESULT 23
US-08-937-102-2
; Sequence 2, Application US/08937102A
; Patent No. 5965134
; GENERAL INFORMATION:
; APPLICANT: Thiel, Heinz-Jurgen
; APPLICANT: Elpers, Knut
; APPLICANT: Pauly, Thomas
; TITLE OF INVENTION: T Cell Stimulating Protein of Pestivirus
; FILE REFERENCE: 1/94108
; CURRENT APPLICATION NUMBER: US/08/937,102A
; CURRENT FILING DATE: 1997-09-24
; EARLIER APPLICATION NUMBER: 08/693,247
; EARLIER FILING DATE: 1996-08-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1213
; TYPE: PRT
; ORGANISM: Classical Swine Fever Virus
US-08-937-102-2

Query Match      93.3%; Score 28; DB 1; Length 1213;
Best Local Similarity 80.0%; Pred. No. 1.9e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 SYTH 5
DB      260 SYTH 264

RESULT 24
US-08-876-991-2
; Sequence 2, Application US/08876991
; Patent No. 5925360
; GENERAL INFORMATION:
; APPLICANT: Gregor Meyers, Tillmann R menapf,
; APPLICANT: Heinz-J rgen Thiel
; TITLE OF INVENTION: Hog cholera virus vaccine and diagnostic
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Organon Teknika Corporation
; ADDRESSEE: Biotechnology Research Institute
; STREET: 1330-A Piccard Drive
; CITY: Rockville
; STATE: Maryland
; COUNTRY: U.S.A.
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/876,991
; FILING DATE: 16-JUN-1997
```

```

; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/747,577
; FILING DATE:
; APPLICATION NUMBER: US/08/650,584
; FILING DATE:
; APPLICATION NUMBER: US/08/469,702
; FILING DATE:
; APPLICATION NUMBER: US/08/123,596
; FILING DATE:
; APPLICATION NUMBER: 07/797,554
; FILING DATE: 22-NOV-1991
; APPLICATION NUMBER: US 07/494,991
; FILING DATE: 16-MAR-1990
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: William M. Blackstone
; REGISTRATION NUMBER: 29,772
; REFERENCE/DOCKET NUMBER:
; TELEPHONE: (301) 258-5200
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3898 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-876-991-2

Query Match      93.3%; Score 28; DB 1; Length 3898;
Best Local Similarity 80.0%; Pred. No. 5.8e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 SYTH 5
DB      1390 SYTH 1394

RESULT 25
US-09-059-853-2
; Sequence 2, Application US/09059853
; Patent No. 5935582
; GENERAL INFORMATION:
; APPLICANT: Gregor Meyers, Tillmann R menapf,
; APPLICANT: Heinz-J rgen Thiel
; TITLE OF INVENTION: Hog cholera virus vaccine and diagnostic
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Organon Teknika Corporation
; ADDRESSEE: Biotechnology Research Institute
; STREET: 1330-A Piccard Drive
; CITY: Rockville
; STATE: Maryland
; COUNTRY: U.S.A.
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/059,853
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/797,554
; FILING DATE: 22-NOV-1991
; APPLICATION NUMBER: US 07/494,991
; FILING DATE: 16-MAR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: William M. Blackstone
; REGISTRATION NUMBER: 29,772
; REFERENCE/DOCKET NUMBER:
```

TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 258-5200
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3898 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-059-853-2

Query Match 93.3%; Score 28; DB 1; Length 3898;
Best Local Similarity 80.0%; Pred. No. 5.8e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 SYTH 5
Db 1390 SYTH 1394

RESULT 26

US-08-750-717-2
Sequence 2, Application US/08750717
Patent No. 6180109

GENERAL INFORMATION:
APPLICANT: MOORMANN, Robertus J. M.
APPLICANT: VAN RIJN, Petrus A.
TITLE OF INVENTION: Nucleotide Sequences of Pestivirus
TITLE OF INVENTION: Strains, Polypeptides Encoded by These Sequences and Use
TITLE OF INVENTION: Thereof for Diagnosis and Prevention of Pestivirus
TITLE OF INVENTION: Infections
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSEE: YOUNG & THOMPSON
STREET: 745 South 23rd Street
CITY: Arlington
STATE: Virginia
COUNTRY: USA
ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,717
FILING DATE: 24-DEC-1996
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94201743.5
FILING DATE: 17-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/NL95/00214
FILING DATE: 16-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: PATCH, Andrew J.
REGISTRATION NUMBER: 32,925
REFERENCE/DOCKET NUMBER: BO 39123
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-521-2297
TELEFAX: 703-685-0573
TELEX: 248425 EMBON

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3898 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-750-717-2

Query Match 93.3%; Score 28; DB 2; Length 3898;
Best Local Similarity 80.0%; Pred. No. 5.8e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 SYTH 5
Db 1390 SYTH 1394

RESULT 27

US-09-534-717-327
Sequence 327, Application US/09534717
Patent No. 6914128

GENERAL INFORMATION:
APPLICANT: Jochen, Salfeld et al.
TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
FILE REFERENCE: BBI-093CP
CURRENT APPLICATION NUMBER: US/09/534,717
CURRENT FILING DATE: 2000-03-24
EARLIER APPLICATION NUMBER: 60/126,603
EARLIER FILING DATE: March 25, 1999
NUMBER OF SEQ ID NOS: 675
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 327
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-09-534-717-327

Query Match 90.0%; Score 27; DB 2; Length 9;
Best Local Similarity 80.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 SYTH 5
Db 5 SYTH 9

RESULT 28

US-08-765-179B-5
Sequence 5, Application US/08765179B
Patent No. 5854027

GENERAL INFORMATION:
APPLICANT: STEINBACHER, Stefan
TITLE OF INVENTION: PROCESS FOR MODIFYING THE STABILITY
TITLE OF INVENTION: OF ANTIBODIES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Nikaido, Marmelstein, Murtay & Oram LLP
STREET: 655 Fifteenth Street N.W. Suite 330
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-5701

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,179B
FILING DATE: 14-JAN-1997
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/02626
FILING DATE: 06-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 25 115.7
FILING DATE: 15-JUL-1994
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein

Query Match 93.3%; Score 28; DB 2; Length 3898;
Best Local Similarity 80.0%; Pred. No. 5.8e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

US-06-765-179B-5

Query Match 90.0%; Score 27; DB 1; Length 35;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
:||||
Db 31 SYTH 35

RESULT 29

US-09-248-796A-26979
; Sequence 26979, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 26979
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-26979

Query Match 90.0%; Score 27; DB 2; Length 72;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
:||||
Db 47 TYTH 51

RESULT 30

US-09-248-796A-22743
; Sequence 22743, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 22743
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-22743

Query Match 90.0%; Score 27; DB 2; Length 73;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
:||||
Db 48 TYTH 52

RESULT 31

US-09-248-796A-23947
; Sequence 23947, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 23947
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-23947

Query Match 90.0%; Score 27; DB 2; Length 81;
Best Local Similarity 80.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
:||||
Db 56 TYTH 60

RESULT 32

US-08-290-592E-16
; Sequence 16, Application US/08290592E
; Patent No. 5824507
; GENERAL INFORMATION:
; APPLICANT: JOHNSON, L.
; TITLE OF INVENTION: Human Murine Chimeric Antibodies Against
; TITLE OF INVENTION: Respiratory Syncytical Virus
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI, STEWART &
; ADDRESSEE: OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSERLAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/290,592E
; FILING DATE: August 15, 1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/813,372
; FILING DATE: December 23, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliot M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 469201-257
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 97 AMINO ACIDS
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN

US-08-290-592E-16

Query Match 90.0%; Score 27; DB 1; Length 97;

Best Local Similarity 80.0%; Pred. No. 2.7e+02; Indels 0; Gaps 0;

Matches 4; Conservative 1; Mismatches 0;

QY 1 SYTH 5

Db 31 SYTH 35

RESULT 33

PCT-US95-10053-13

Sequence 13, Application PC/TUS9510053

GENERAL INFORMATION:

APPLICANT: JOHNSON, L.

TITLE OF INVENTION: Human Murine Chimeric Antibodies Against Respiratory Syncytia

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,

ADDRESS: CECCHI, STEWART & OLSTEIN

STREET: 6 BECKER FARM ROAD

CITY: ROSELAND

STATE: NEW JERSEY

COUNTRY: USA

ZIP: 07068

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 INCH DISKETTE

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS

SOFTWARE: WORD PERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/10053

FILING DATE: Concurrently

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/290,592

FILING DATE: August 15, 1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/813,372

FILING DATE: December 23, 1991

ATTORNEY/AGENT INFORMATION:

NAME: FERRARO, GREGORY D.

REGISTRATION NUMBER: 36,134

REFERENCE/DOCKET NUMBER: 469201-274

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-994-1700

TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 97 AMINO ACIDS

TYPE: AMINO ACID

STRANDEDNESS:

TOPOLOGY: LINEAR

MOLECULE TYPE: PROTEIN

PCT-US95-10053-13

Query Match 90.0%; Score 27; DB 4; Length 97;

Best Local Similarity 80.0%; Pred. No. 2.7e+02; Indels 0; Gaps 0;

Matches 4; Conservative 1; Mismatches 0;

QY 1 SYTH 5

Db 31 SYTH 35

RESULT 34

PCT-US96-09448-16

Sequence 16, Application PC/TUS9609448

GENERAL INFORMATION:

APPLICANT: JOHNSON, L.

TITLE OF INVENTION: Human Murine Chimeric Antibodies Against Respiratory Syncytia

NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:

ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,

ADDRESS: CECCHI, STEWART & OLSTEIN

STREET: 6 BECKER FARM ROAD

CITY: ROSELAND

STATE: NEW JERSEY

COUNTRY: USA

ZIP: 07068

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 INCH DISKETTE

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS

SOFTWARE: WORD PERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/09448

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/290,592

FILING DATE: August 15, 1994

APPLICATION NUMBER: 07/813,372

FILING DATE: December 23, 1991

ATTORNEY/AGENT INFORMATION:

NAME: HERRON, CHARLES J.

REGISTRATION NUMBER: 28,019

REFERENCE/DOCKET NUMBER: 469201-257

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-994-1700

TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 97 AMINO ACIDS

TYPE: AMINO ACID

STRANDEDNESS:

TOPOLOGY: LINEAR

MOLECULE TYPE: PROTEIN

PCT-US96-09448-16

Query Match 90.0%; Score 27; DB 4; Length 97;

Best Local Similarity 80.0%; Pred. No. 2.7e+02; Indels 0; Gaps 0;

Matches 4; Conservative 1; Mismatches 0;

QY 1 SYTH 5

Db 31 SYTH 35

RESULT 35

US-10-194-975-7

Sequence 7, Application US/10194975

Patent No. 6881557

GENERAL INFORMATION:

APPLICANT: Foote, Jefferson

TITLE OF INVENTION: Super Humanized Antibodies

FILE REFERENCE: 501231.01

CURRENT APPLICATION NUMBER: US/10/194,975

CURRENT FILING DATE: 2002-10-10

PRIOR APPLICATION NUMBER: US 60/305,111

PRIOR FILING DATE: 2001-07-12

NUMBER OF SEQ ID NOS: 122

SOFTWARE: PatentIn version 3.1

SEQ ID NO 7

LENGTH: 98

TYPE: PRT

ORGANISM: Homo sapiens

US-10-194-975-7

Query Match 90.0%; Score 27; DB 2; Length 98;

Best Local Similarity 80.0%; Pred. No. 2.7e+02; Indels 0; Gaps 0;

Matches 4; Conservative 1; Mismatches 0;

QY 1 SYTH 5

Db 31 SYTH 35

RESULT 36

PCT-US96-09448-16

Sequence 16, Application PC/TUS9609448

GENERAL INFORMATION:

APPLICANT: JOHNSON, L.

TITLE OF INVENTION: Human Murine Chimeric Antibodies Against Respiratory Syncytia

NUMBER OF SEQUENCES: 42

Db 31 SYNM 35

RESULT 36

US-08-545-809A-128
Sequence 128, Application US/08545809A

Patent No. 6096878

GENERAL INFORMATION:

APPLICANT: Honjo, Tasuku

APPLICANT: Matsuda, Rumiiko

TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE

TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME

NUMBER OF SEQUENCES: 145

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson, P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: US

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

OPERATING SYSTEM: Windows95

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/545,809A

FILING DATE: 27-MAR-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/JP93/00603

FILING DATE: 10-MAY-1993

ATTORNEY/AGENT INFORMATION:

NAME: Freeman, John W.

REGISTRATION NUMBER: 29,066

REFERENCE/DOCKET NUMBER: 06501/004001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-542-5070

TELEFAX: 617-542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 128:

SEQUENCE CHARACTERISTICS:

LENGTH: 117 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-545-809A-128

Query Match 90.0%; Score 27; DB 2; Length 117;

Best Local Similarity 80.0%; Pred. No. 3.2e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYNM 5

Db 50 SYNM 54

RESULT 37

US-09-157-370-2

Sequence 2, Application US/09157370A

Patent No. 6262238

GENERAL INFORMATION:

APPLICANT: STEIPE, Boris

APPLICANT: STEINBACHER, Stefan

TITLE OF INVENTION: PROCESS FOR MODIFYING THE STABILITY OF ANTIBODIES

FILE REFERENCE: P8341-8072

CURRENT APPLICATION NUMBER: US/09/157,370A

EARLIER FILING DATE: 1998-09-21

EARLIER FILING DATE: 1997-01-14

EARLIER FILING DATE: 1995-07-06

EARLIER FILING DATE: 1994-07-15

EARLIER FILING DATE: 1994-07-15

NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 117
TYPE: PRT
ORGANISM: Mus sp.
US-09-157-370-2

Query Match 90.0%; Score 27; DB 2; Length 117;

Best Local Similarity 80.0%; Pred. No. 3.2e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYNM 5

Db 31 SYNM 35

RESULT 38

US-09-025-769B-22

Sequence 22, Application US/09025769B

Patent No. 6300064

GENERAL INFORMATION:

APPLICANT: Knappik, Achim

APPLICANT: Pack, Peter

APPLICANT: Ilag, Vic

APPLICANT: Ge, Liming

APPLICANT: Moroney, Simon

APPLICANT: Plueckhuhn, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769B

FILING DATE: 18-FEB-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 596-9000

TELEFAX: (212) 596-9090

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 117 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-025-769B-22

Query Match 90.0%; Score 27; DB 2; Length 117;

Best Local Similarity 80.0%; Pred. No. 3.2e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYNM 5

Db 31 SYNM 35

RESULT 39
US-09-490-070A-22
Sequence 22, Application US/09490070A
Patent No. 6696248
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
STREET: 1666 K Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-490-070A-22
Query Match 90.0%; Score 27; DB 2; Length 117;
Best Local Similarity 80.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 SYTH 5
Db 31 SYTH 35
RESULT 40
US-09-490-153-22
Sequence 22, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave

STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-490-153-22
Query Match 90.0%; Score 27; DB 2; Length 117;
Best Local Similarity 80.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 SYTH 5
Db 31 SYTH 35
RESULT 41
US-09-490-324-22
Sequence 22, Application US/09490324
Patent No. 6828422
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
STRANDEDNESS: <unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-490-324-22

Query Match 90.0%; Score 27; DB 2; Length 117;
Best Local Similarity 80.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYTH 5
Db 31 SYTH 35

RESULT 42
US-09-515-697-128
Sequence 128, Application US/09515697
Patent No. 6936705
GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
Matsuda, Fumihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/515,697
FILING DATE: 29-Feb-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/545,809
FILING DATE: 27-MAR-1995
APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 06501/004001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 128:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 128:
US-09-515-697-128

Query Match 90.0%; Score 27; DB 2; Length 117;
Best Local Similarity 80.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYTH 5
Db 50 SYTH 54

RESULT 43
US-09-025-769B-36
Sequence 36, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Motoney, Simon
APPLICANT: Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-36

Query Match 90.0%; Score 27; DB 2; Length 120;
Best Local Similarity 80.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYTH 5
Db 31 SYTH 35

RESULT 44
US-09-025-769B-59
Sequence 59, Application US/09025769B
Patent No. 6300064

GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-59
Query Match 90.0%; Score 27; DB 2; Length 120;
Best Local Similarity 80.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Cy 1 SYTH 5
|||:
Db 31 SYTH 35
RESULT 45
US-09-490-070A-36
Sequence 36, Application US/09490070A
Patent No. 6696248
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
White & McAuliffe
STREET: 1666 K Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS: <unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-09-490-070A-36
Query Match 90.0%; Score 27; DB 2; Length 120;
Best Local Similarity 80.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Cy 1 SYTH 5
|||:
Db 31 SYTH 35
RESULT 46
US-09-490-070A-59
Sequence 59, Application US/09490070A
Patent No. 6696248
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
White & McAuliffe
STREET: 1666 K Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 59:
US-09-490-070A-59

Query Match 90.0%; Score 27; DB 2; Length 120;
Best Local Similarity 80.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYTH 5
|||:
31 SYTH 35

Db 31 SYTH 35

RESULT 47
US-09-490-153-36
Sequence 36, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESSES:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9090
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
STRANDEDNESS: <Unknown>
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-09-490-153-36

Query Match 90.0%; Score 27; DB 2; Length 120;
Best Local Similarity 80.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYTH 5
|||:
31 SYTH 35

Db 31 SYTH 35

RESULT 48
US-09-490-153-59
Sequence 59, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESSES:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9090
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 59:
US-09-490-153-59

Query Match 90.0%; Score 27; DB 2; Length 120;
Best Local Similarity 80.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYTH 5
|||:
31 SYTH 35

Db 31 SYTH 35

RESULT 49
US-09-490-324-36
Sequence 36, Application US/09490324
Patent No. 6828422
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming

Mooney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Proteiin/(poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESSES:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-09-490-324-36
Query Match 90.0%; Score 27; DB 2; Length 120;
Best Local Similarity 80.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 SYTH 5
Db 31 SYTH 35
RESULT 50
US-09-490-324-59
Sequence 59, Application US/09490324
Patent No. 6828422
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESSES:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
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SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 59:
US-09-490-324-59
Query Match 90.0%; Score 27; DB 2; Length 120;
Best Local Similarity 80.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Job time : 20.2698 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

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Title: US-10-700-632-1
Perfect score: 30
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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110	28	93.3	153	4	US-10-767-701-50714	Sequence 50714, A	183	27	90.0	107	4	US-10-425-115-267373	Sequence 267373,
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149	27	90.0	40	4	US-10-424-599-167452	Sequence 167452,	222	27	90.0	248	4	US-10-293-418-1178	Sequence 1178, Ap
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152	27	90.0	52	4	US-10-425-115-219605	Sequence 219605,	225	27	90.0	249	4	US-10-293-418-1290	Sequence 1290, Ap
153	27	90.0	54	4	US-10-425-115-263005	Sequence 263005,	226	27	90.0	249	4	US-10-293-418-1290	Sequence 1290, Ap
154	27	90.0	55	4	US-10-767-701-46606	Sequence 46606, A	227	27	90.0	249	4	US-10-688-925-14	Sequence 14, Appl
155	27	90.0	55	4	US-10-424-599-202971	Sequence 202971,	228	27	90.0	250	3	US-10-688-925-26	Sequence 26, Appl
156	27	90.0	64	4	US-10-424-598-198613	Sequence 198613,	229	27	90.0	250	3	US-09-880-748-2093	Sequence 2093, Ap
157	27	90.0	66	4	US-10-424-599-151718	Sequence 175178,	230	27	90.0	250	4	US-09-880-748-2097	Sequence 2097, Ap
158	27	90.0	67	4	US-10-424-599-151718	Sequence 191474,	231	27	90.0	250	4	US-10-293-418-2093	Sequence 2093, Ap
159	27	90.0	71	4	US-10-425-115-282362	Sequence 282362,	232	27	90.0	250	4	US-10-293-418-2097	Sequence 2097, Ap
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161	27	90.0	83	4	US-10-083-357-681	Sequence 681, App	234	27	90.0	251	3	US-10-293-418-2001	Sequence 2001, Ap
162	27	90.0	84	4	US-10-425-115-317645	Sequence 317645,	235	27	90.0	252	3	US-09-880-748-1366	Sequence 1366, Ap
163	27	90.0	84	4	US-10-425-115-281759	Sequence 281759,	236	27	90.0	252	4	US-10-293-418-1366	Sequence 1366, Ap
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166	27	90.0	97	3	US-10-425-115-230814	Sequence 7, Appl	239	27	90.0	253	3	US-09-880-748-1936	Sequence 1936, Ap
167	27	90.0	97	4	US-10-194-975-7	Sequence 47, Appl	240	27	90.0	253	3	US-09-880-748-1951	Sequence 1951, Ap
168	27	90.0	98	4	US-10-308-817-47	Sequence 47, Appl	241	27	90.0	253	3	US-09-880-748-2101	Sequence 2101, Ap
169	27	90.0	98	4	US-10-032-037B-48	Sequence 48, Appl	242	27	90.0	253	4	US-10-293-418-1895	Sequence 1895, Ap
170	27	90.0	98	4	US-10-032-037B-49	Sequence 48, Appl	243	27	90.0	253	4	US-10-293-418-1936	Sequence 1936, Ap
171	27	90.0	98	4	US-10-029-988B-48	Sequence 48, Appl	244	27	90.0	253	4	US-10-293-418-1951	Sequence 1951, Ap
172	27	90.0	98	4	US-10-029-988B-48	Sequence 48, Appl	245	27	90.0	253	4	US-10-293-418-2098	Sequence 2098, Ap
173	27	90.0	98	4	US-10-029-988B-49	Sequence 49, Appl	246	27	90.0	253	4	US-10-293-418-2101	Sequence 2101, Ap

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248	27	90.0	254	3	US-09-880-748-1983	Sequence 1983, Ap	321	26	86.7	5	4	US-10-762-059-44	Sequence 44, App1
249	27	90.0	254	4	US-10-293-418-1961	Sequence 1961, Ap	322	26	86.7	5	5	US-10-949-115-20	Sequence 20, App1
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251	27	90.0	255	3	US-09-880-748-857	Sequence 857, App	324	26	86.7	6	5	US-10-846-941-8	Sequence 8, App1
252	27	90.0	255	3	US-09-880-748-1156	Sequence 1156, Ap	325	26	86.7	6	5	US-10-919-923-8	Sequence 8, App1
253	27	90.0	255	4	US-10-293-418-857	Sequence 857, App	326	26	86.7	10	5	US-10-769-308-28	Sequence 28, App1
254	27	90.0	255	4	US-10-293-418-1156	Sequence 1156, Ap	327	26	86.7	10	5	US-10-726-332-57	Sequence 57, App1
255	27	90.0	259	3	US-09-880-748-1567	Sequence 1567, Ap	328	26	86.7	10	5	US-10-769-074-18	Sequence 28, App1
256	27	90.0	259	4	US-10-293-418-1567	Sequence 1567, Ap	329	26	86.7	10	5	US-10-996-316-114	Sequence 114, App
257	27	90.0	260	5	US-10-935-290-116	Sequence 116, App	330	26	86.7	10	5	US-10-996-316-145	Sequence 145, App
258	27	90.0	274	3	US-09-858-664A-14	Sequence 14, App1	331	26	86.7	10	5	US-10-996-316-146	Sequence 146, App
259	27	90.0	274	3	US-10-274-978-15	Sequence 15, App1	332	26	86.7	10	6	US-11-009-443-7	Sequence 7, App1
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261	27	90.0	274	5	US-10-921-168-15	Sequence 15, App1	334	26	86.7	14	3	US-09-116-676-4	Sequence 4, App1
262	27	90.0	292	4	US-10-042-194-2	Sequence 2, App1	335	26	86.7	18	3	US-09-880-748-2964	Sequence 2964, Ap
263	27	90.0	336	4	US-10-664-421-117	Sequence 117, App	336	26	86.7	18	4	US-10-293-418-2964	Sequence 2964, Ap
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266	27	90.0	338	4	US-10-292-798-1704	Sequence 1704, Ap	339	26	86.7	31	4	US-10-424-599-214272	Sequence 214272, A
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273	27	90.0	414	4	US-10-697-263-14	Sequence 14, App1	346	26	86.7	44	4	US-10-355-780-3	Sequence 3, App1
274	27	90.0	414	5	US-10-921-168-14	Sequence 14, App1	347	26	86.7	44	4	US-10-425-115-326219	Sequence 326219, A
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287	27	90.0	713	4	US-10-437-963-136049	Sequence 7649, Ap	360	26	86.7	53	4	US-10-424-599-262095	Sequence 262095, A
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292	27	90.0	782	4	US-10-270-878-29	Sequence 29, App1	365	26	86.7	56	4	US-10-424-599-270098	Sequence 270098, A
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419	26	86.7	100	3	US-09-925-301-1664	Sequence 1664, Ap	492	26	86.7	143	4	US-10-424-599-173744	Sequence 173744,
420	26	86.7	102	3	US-09-796-692-1627	Sequence 1627, Ap	493	26	86.7	144	4	US-10-424-599-229715	Sequence 229715,
421	26	86.7	102	4	US-10-040-862-1627	Sequence 1627, Ap	494	26	86.7	144	4	US-10-425-115-237519	Sequence 237519,
422	26	86.7	102	4	US-10-057-475B-1627	Sequence 1627, Ap	495	26	86.7	149	4	US-10-767-701-31650	Sequence 31650, A
423	26	86.7	102	4	US-10-154-884B-1627	Sequence 1627, Ap	496	26	86.7	155	4	US-10-425-115-237530	Sequence 237530,
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425	26	86.7	102	4	US-10-425-114-58139	Sequence 58139, A	498	26	86.7	158	4	US-10-767-701-55218	Sequence 55218, A
426	26	86.7	102	4	US-10-764-324-1627	Sequence 1627, Ap	499	26	86.7	156	4	US-10-425-115-317838	Sequence 317838,
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428	26	86.7	103	4	US-10-437-963-192456	Sequence 192456,	501	26	86.7	156	5	US-10-450-763-312156	Sequence 44771, A
429	26	86.7	103	4	US-10-425-115-238620	Sequence 238620,	502	26	86.7	157	4	US-10-425-115-312156	Sequence 312156,
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431	26	86.7	105	4	US-10-437-963-16624	Sequence 166244,	504	26	86.7	161	4	US-10-425-115-322753	Sequence 322753,
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589	26	86.7	249	4	US-10-293-418-1730	Sequence 1730, Ap	662	26	86.7	321	4	US-10-072-012-367	Sequence 367, App
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594	26	86.7	251	6	US-11-017-030-19	Sequence 19, Appl1	667	26	86.7	325	4	US-10-302-267-62	Sequence 62, Appl1
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596	26	86.7	253	3	US-09-880-748-1007	Sequence 1007, Ap	669	26	86.7	325	4	US-10-412-699B-554	Sequence 554, App
597	26	86.7	253	3	US-09-880-748-1526	Sequence 1526, Ap	670	26	86.7	325	5	US-10-225-068-246	Sequence 246, App
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689	26	86.7	372	3	US-09-771-161A-203	Sequence 203, Appl	762	26	86.7	590	4	US-10-437-963-143500	Sequence 143500, A
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691	26	86.7	372	4	US-10-394-322A-14	Sequence 14, Appl	764	26	86.7	616	4	US-10-437-963-182828	Sequence 182828, A
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696	26	86.7	385	4	US-10-195-517-5	Sequence 5, Appli	769	26	86.7	631	5	US-10-741-600-1278	Sequence 1278, Ap
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706	26	86.7	421	4	US-10-437-963-202796	Sequence 202796, A	779	26	86.7	667	4	US-10-282-122A-46652	Sequence 46652, A
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710	26	86.7	434	4	US-10-425-114-69145	Sequence 69145, A	783	26	86.7	686	6	US-10-437-963-142183	Sequence 142183, A
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ALIGNMENTS

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; Publication No. US20040213795A1
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary et al.
; TITLE OF INVENTION: ANTIBODIES AGAINST PD-1 AND USES THEREFOR
; FILE REFERENCE: 08702.0098-00000
; CURRENT APPLICATION NUMBER: US/10/741,481
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.1
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US-10-741-481-29

Query Match          100.0%; Score 30; DB 4; Length 5;
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RESULT 2
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; Sequence 1, Application US/10700632
; Publication No. US20050118183A1
; GENERAL INFORMATION:
; APPLICANT: Immunogen, Inc.
; TITLE OF INVENTION: ANTI-CD3 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID
; FILE REFERENCE: A8427
; CURRENT APPLICATION NUMBER: US/10/700,632
; CURRENT FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: US 60/424,332
; PRIOR FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 5
```

```
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-700-632-1
```

```
Query Match          100.0%; Score 30; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 1,7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 SYTH 5
      |||||
Db      1 SYTH 5
```

```
RESULT 3
US-10-700-632-58
; Sequence 58, Application US/10700632
; Publication No. US20050118183A1
; GENERAL INFORMATION:
; APPLICANT: Immunogen, Inc.
; TITLE OF INVENTION: ANTI-CD3 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID
; FILE REFERENCE: A8427
; CURRENT APPLICATION NUMBER: US/10/700,632
; CURRENT FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: US 60/424,332
; PRIOR FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-700-632-58
```

```
Query Match          100.0%; Score 30; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 SYTH 5
      |||||
Db      6 SYTH 10
```

```
RESULT 4
US-10-767-701-48523
; Sequence 48523, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 48523
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3481-039-Pl-KL-E9-pep
US-10-767-701-48523
```

```
Query Match          100.0%; Score 30; DB 4; Length 57;
Best Local Similarity 100.0%; Pred. No. 1,7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 SYTH 5
      |||||
Db      47 SYTH 51
```

```
RESULT 5
US-10-424-599-171709
; Sequence 171709, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 171709
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_126068C.1.pep
US-10-424-599-171709
```

```
Query Match          100.0%; Score 30; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 SYTH 5
        |||||
Db      26 SYTH 30
```

```
RESULT 6
US-10-425-115-282660
; Sequence 282660, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 282660
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_20884C.1.pep
US-10-425-115-282660
```

```
Query Match          100.0%; Score 30; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 SYTH 5
        |||||
Db      34 SYTH 38
```

```
RESULT 7
US-10-437-963-180531
; Sequence 180531, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
```

```
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 180531
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(72)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_77893C.1.pep
US-10-437-963-180531
```

```
Query Match          100.0%; Score 30; DB 4; Length 72;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 SYTH 5
        |||||
Db      51 SYTH 55
```

```
RESULT 8
US-10-437-963-169394
; Sequence 169394, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 169394
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(115)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_67819C.1.pep
US-10-437-963-169394
```

```
Query Match          100.0%; Score 30; DB 4; Length 115;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 SYTH 5
        |||||
Db      99 SYTH 103
```

```
RESULT 9
```

US-10-763-424-50
; Sequence 50, Application US/10763424
; Publication No. US20050069541A1
; GENERAL INFORMATION:
; APPLICANT: Karlik, Stephen J.
; APPLICANT: Pleiss, Michael A.
; APPLICANT: Konradi, Andrei W.
; APPLICANT: Grant, Francine S.
; APPLICANT: Semko, Christopher M.
; APPLICANT: Driesen, Darren B.
; APPLICANT: Messersmith, Elizabeth
; APPLICANT: Freedman, Stephen
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Composition for and Treatment of Demyelinating Diseases
; TITLE OF INVENTION: and Paralysis By Administration of Remyelinating Agents
; FILE REFERENCE: 034008-061
; CURRENT APPLICATION NUMBER: US/10/763,424
; CURRENT FILING DATE: 2004-01-26
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PasteSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-763-424-50

Query Match 100.0%; Score 30; DB 5; Length 116;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYTH 5
|||
Db 31 SYTH 35

RESULT 10
US-10-837-904-126
; Sequence 126, Application US/10837904
; Publication No. US20050142635A1
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; SATO, Koh
; BENDIG, Mary Margaret
; JONES, Steven Tarran
; SALDANHA, Jose William
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 134
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/837,904
; FILING DATE: 04-May-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/114,285
; FILING DATE: 13-Jul-1998
; APPLICATION NUMBER: US 08/436,717
; FILING DATE: 08-May-1995
; APPLICATION NUMBER: US 08/137,117
; FILING DATE: 20-Dec-1993
; APPLICATION NUMBER: WO PCT/JP92/00544
; FILING DATE: 24-Apr-1992

APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991

ATTORNEY/AGENT INFORMATION:
NAME: Wegner, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/234
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399

INFORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 126:
US-10-837-904-126

Query Match 100.0%; Score 30; DB 5; Length 116;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYTH 5
|||
Db 31 SYTH 35

RESULT 11
US-10-837-904-127
; Sequence 127, Application US/10837904
; Publication No. US20050142635A1
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; SATO, Koh
; BENDIG, Mary Margaret
; JONES, Steven Tarran
; SALDANHA, Jose William
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 134
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/837,904
; FILING DATE: 04-May-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/114,285
; FILING DATE: 13-Jul-1998
; APPLICATION NUMBER: US 08/436,717
; FILING DATE: 08-May-1995
; APPLICATION NUMBER: US 08/137,117
; FILING DATE: 20-Dec-1993
; APPLICATION NUMBER: WO PCT/JP92/00544
; FILING DATE: 24-Apr-1992
; APPLICATION NUMBER: JP 4-32084
; FILING DATE: 19-FEB-1992
; APPLICATION NUMBER: JP 3-95476
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:

NAME: Wegner, Harold C.
REGISTRATION NUMBER: 25, 258
REFERENCE/DOCKET NUMBER: 53466/234
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5399
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 127:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 127:
US-10-837-904-127

Query Match 100.0%; Score 30; DB 5; Length 116;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYTH 5
|||
Db 31 SYTH 35

RESULT 12
US-10-837-904-128
Sequence 128, Application US/10837904
Publication No. US20050142635A1
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
SATO, Koh
BENDIG, Mary Margaret
JONES, Steven Tarran
SALDANHA, Jose William
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 134
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/837,904
FILING DATE: 04-May-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/114,285
FILING DATE: 13-Jul-1998
APPLICATION NUMBER: US 08/436,717
FILING DATE: 08-May-1995
APPLICATION NUMBER: US 08/137,117
FILING DATE: 20-Dec-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-Apr-1992
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-Feb-1992
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-Apr-1991
ATTORNEY/AGENT INFORMATION:
NAME: Wegner, Harold C.
REGISTRATION NUMBER: 25, 258
REFERENCE/DOCKET NUMBER: 53466/234
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5399

TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 128:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 128:
US-10-837-904-128

Query Match 100.0%; Score 30; DB 5; Length 116;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYTH 5
|||
Db 31 SYTH 35

RESULT 13
US-10-837-904-129
Sequence 129, Application US/10837904
Publication No. US20050142635A1
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
SATO, Koh
BENDIG, Mary Margaret
JONES, Steven Tarran
SALDANHA, Jose William
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 134
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/837,904
FILING DATE: 04-May-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/114,285
FILING DATE: 13-Jul-1998
APPLICATION NUMBER: US 08/436,717
FILING DATE: 08-May-1995
APPLICATION NUMBER: US 08/137,117
FILING DATE: 20-Dec-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-Apr-1992
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-Feb-1992
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-Apr-1991
ATTORNEY/AGENT INFORMATION:
NAME: Wegner, Harold C.
REGISTRATION NUMBER: 25, 258
REFERENCE/DOCKET NUMBER: 53466/234
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5399
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 129:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 129:

US-10-837-904-129

Query Match 100.0%; Score 30; DB 5; Length 116;

Best Local Similarity 100.0%; Pred. No. 3.3e+02; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYIYH 5

Db 31 SYIYH 35

RESULT 14

US-10-837-904-131

Sequence 131, Application US/10837904

Publication No. US20050142635A1

GENERAL INFORMATION:

APPLICANT: TSUCHIYA, Masayuki

SATO, Koh

BENDIG, Mary Margaret

JONES, Steven Tarran

SALDANHA, Jose William

TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN

INTERLEUKIN-6 RECEPTOR

NUMBER OF SEQUENCES: 134

CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY & LARDNER

STREET: 3000 K Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/837,904

FILING DATE: 04-May-2004

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/114,285

FILING DATE: 13-Jul-1998

APPLICATION NUMBER: US 08/436,717

FILING DATE: 08-May-1995

APPLICATION NUMBER: US 08/137,117

FILING DATE: 20-DEC-1993

APPLICATION NUMBER: WO PCT/JP92/00544

FILING DATE: 24-APR-1992

APPLICATION NUMBER: JP 4-32084

FILING DATE: 19-FEB-1992

APPLICATION NUMBER: JP 3-95476

FILING DATE: 25-APR-1991

ATTORNEY/AGENT INFORMATION:

NAME: Wegner, Harold C.

REGISTRATION NUMBER: 25,258

REFERENCE/DOCKET NUMBER: 53466/234

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 672-5300

TELEFAX: (202) 672-5399

INFORMATION FOR SEQ ID NO: 131:

SEQUENCE CHARACTERISTICS:

LENGTH: 116 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 131:

US-10-837-904-131

Query Match 100.0%; Score 30; DB 5; Length 116;

Best Local Similarity 100.0%; Pred. No. 3.3e+02; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYIYH 5

Db 31 SYIYH 35

RESULT 15

US-10-837-904-132

Sequence 132, Application US/10837904

Publication No. US20050142635A1

GENERAL INFORMATION:

APPLICANT: TSUCHIYA, Masayuki

SATO, Koh

BENDIG, Mary Margaret

JONES, Steven Tarran

SALDANHA, Jose William

TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN

INTERLEUKIN-6 RECEPTOR

NUMBER OF SEQUENCES: 134

CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY & LARDNER

STREET: 3000 K Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/837,904

FILING DATE: 04-May-2004

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/114,285

FILING DATE: 13-Jul-1998

APPLICATION NUMBER: US 08/436,717

FILING DATE: 08-May-1995

APPLICATION NUMBER: US 08/137,117

FILING DATE: 20-DEC-1993

APPLICATION NUMBER: WO PCT/JP92/00544

FILING DATE: 24-APR-1992

APPLICATION NUMBER: JP 4-32084

FILING DATE: 19-FEB-1992

APPLICATION NUMBER: JP 3-95476

FILING DATE: 25-APR-1991

ATTORNEY/AGENT INFORMATION:

NAME: Wegner, Harold C.

REGISTRATION NUMBER: 25,258

REFERENCE/DOCKET NUMBER: 53466/234

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 672-5300

TELEFAX: (202) 672-5399

INFORMATION FOR SEQ ID NO: 132:

SEQUENCE CHARACTERISTICS:

LENGTH: 116 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 132:

US-10-837-904-132

Query Match 100.0%; Score 30; DB 5; Length 116;

Best Local Similarity 100.0%; Pred. No. 3.3e+02; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
|||
Db 31 SYTH 35

RESULT 16

US-10-837-904-133
; Sequence 133, Application US/10837904
; Publication No. US20050142635A1
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; SATO, Koh
; BENDIG, Mary Margaret
; JONES, Steven Tarran
; SALDANHA, Jose William
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 134
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/837,904
; FILING DATE: 04-May-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/114,285
; FILING DATE: 13-Jul-1998
; APPLICATION NUMBER: US 08/436,717
; FILING DATE: 08-May-1995
; APPLICATION NUMBER: US 08/137,117
; FILING DATE: 20-Dec-1993
; APPLICATION NUMBER: WO PCT/JP92/00544
; FILING DATE: 24-Apr-1992
; APPLICATION NUMBER: JP 4-32084
; FILING DATE: 19-Feb-1992
; APPLICATION NUMBER: JP 3-95476
; FILING DATE: 25-Apr-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Wegner, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/234
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 133:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; MOLECULE TYPE: linear
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 133:
US-10-837-904-133

Query Match 100.0%; Score 30; DB 5; Length 116;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
|||
Db 31 SYTH 35

RESULT 17
US-10-837-904-134
; Sequence 134, Application US/10837904
; Publication No. US20050142635A1
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; SATO, Koh
; BENDIG, Mary Margaret
; JONES, Steven Tarran
; SALDANHA, Jose William
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 134
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/837,904
; FILING DATE: 04-May-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/114,285
; FILING DATE: 13-Jul-1998
; APPLICATION NUMBER: US 08/436,717
; FILING DATE: 08-May-1995
; APPLICATION NUMBER: US 08/137,117
; FILING DATE: 20-Dec-1993
; APPLICATION NUMBER: WO PCT/JP92/00544
; FILING DATE: 24-Apr-1992
; APPLICATION NUMBER: JP 4-32084
; FILING DATE: 19-Feb-1992
; APPLICATION NUMBER: JP 3-95476
; FILING DATE: 25-Apr-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Wegner, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/234
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 134:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; MOLECULE TYPE: linear
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 134:
US-10-837-904-134

Query Match 100.0%; Score 30; DB 5; Length 116;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
|||
Db 31 SYTH 35

RESULT 18
US-10-763-539-50
; Sequence 50, Application US/10763539
; Publication No. US20050215565A1
; GENERAL INFORMATION:

```

; APPLICANT: Karlík, Stephen J.
; APPLICANT: Pleiss, Michael A.
; APPLICANT: Konradi, Andrei W.
; APPLICANT: Grant, Francine S.
; APPLICANT: Semko, Christopher M.
; APPLICANT: Dessen, Darren B.
; APPLICANT: Messersmith, Elizabeth
; APPLICANT: Freedman, Stephen
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Composition for and Treatment of Demyelinating Diseases
; TITLE OF INVENTION: and Paralysis By Administration of Remyelinating Agents
; FILE REFERENCE: 002010-854
; CURRENT APPLICATION NUMBER: US/10/763,539
; CURRENT FILING DATE: 2004-01-26
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-763-539-50
```

```
Query Match          100.0%; Score 30; DB 5; Length 116;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 SYTH 5
      |||||
Db      31 SYTH 35
```

```

RESULT 19
US-10-700-632-73
; Sequence 73, Application US/10700632
; Publication No. US20050118183A1
; GENERAL INFORMATION:
; APPLICANT: Immunogen, Inc.
; TITLE OF INVENTION: ANTI-CD3 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID
; TITLE OF INVENTION: LEUKEMIA USING THE SAME
; FILE REFERENCE: A8427
; CURRENT APPLICATION NUMBER: US/10/700,632
; CURRENT FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: US 60/424,332
; PRIOR FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 73
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-700-632-73
```

```
Query Match          100.0%; Score 30; DB 5; Length 117;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 SYTH 5
      |||||
Db      31 SYTH 35
```

```

RESULT 20
US-10-700-632-7
; Sequence 7, Application US/10700632
; Publication No. US20050118183A1
; GENERAL INFORMATION:
; APPLICANT: Immunogen, Inc.
; TITLE OF INVENTION: ANTI-CD3 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID
; TITLE OF INVENTION: LEUKEMIA USING THE SAME
; FILE REFERENCE: A8427
; CURRENT APPLICATION NUMBER: US/10/700,632
; CURRENT FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: US 60/424,332
```

```

; PRIOR FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-700-632-7
```

```
Query Match          100.0%; Score 30; DB 5; Length 118;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 SYTH 5
      |||||
Db      31 SYTH 35
```

```

RESULT 21
US-10-700-632-9
; Sequence 9, Application US/10700632
; Publication No. US20050118183A1
; GENERAL INFORMATION:
; APPLICANT: Immunogen, Inc.
; TITLE OF INVENTION: ANTI-CD3 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID
; TITLE OF INVENTION: LEUKEMIA USING THE SAME
; FILE REFERENCE: A8427
; CURRENT APPLICATION NUMBER: US/10/700,632
; CURRENT FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: US 60/424,332
; PRIOR FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized My9-6 antibody heavy chain variable region
US-10-700-632-9
```

```
Query Match          100.0%; Score 30; DB 5; Length 118;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 SYTH 5
      |||||
Db      31 SYTH 35
```

```

RESULT 22
US-10-741-481-10
; Sequence 10, Application US/10741481
; Publication No. US20040213795A1
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary et al.
; TITLE OF INVENTION: ANTIBODIES AGAINST PD-1 AND USES THEREFOR
; FILE REFERENCE: 08702,0098-00000
; CURRENT APPLICATION NUMBER: US/10/741,481
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-481-10
```

```
Query Match          100.0%; Score 30; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 SYTH 5
```

Db 31 SYTH 35

RESULT 23
US-10-310-674A-38
; Sequence 38, Application US/10310674A
; Publication No. US20030166860A1
; GENERAL INFORMATION:
; APPLICANT: Tegenero GmbH
; TITLE OF INVENTION: Peptide Or Protein Containing A C'-D Loop Of The CD28 Receptor
; TITLE OF INVENTION: Family
; FILE REFERENCE: 00140/004001
; CURRENT APPLICATION NUMBER: US/10/310,674A
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: No. US20030166860A1 Sequence
US-10-310-674A-38

Query Match 100.0%; Score 30; DB 4; Length 120;
Best Local Similarity 100.0%; Pred. No. 3,4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
Db 31 SYTH 35

RESULT 24
US-10-389-679-14
; Sequence 14, Application US/10389679
; Publication No. US20040092718A1
; GENERAL INFORMATION:
; APPLICANT: Tegenero GmbH
; APPLICANT: Hunig, Thomas
; TITLE OF INVENTION: Use of a CD28 Binding Substance for Making a Pharmaceutical
; FILE REFERENCE: 00140/009001, TEG/US/0302
; CURRENT APPLICATION NUMBER: US/10/389,679
; CURRENT FILING DATE: 2003-03-13
; PRIOR FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 120
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(120)
; OTHER INFORMATION: mab
US-10-389-679-14

Query Match 100.0%; Score 30; DB 4; Length 120;
Best Local Similarity 100.0%; Pred. No. 3,4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
Db 31 SYTH 35

RESULT 25
US-10-389-679-19
; Sequence 19, Application US/10389679

; Publication No. US20040092718A1
; GENERAL INFORMATION:
; APPLICANT: Tegenero GmbH
; APPLICANT: Hunig, Thomas
; TITLE OF INVENTION: Use of a CD28 Binding Substance for Making a Pharmaceutical
; FILE REFERENCE: 00140/009001, TEG/US/0302
; CURRENT APPLICATION NUMBER: US/10/389,679
; CURRENT FILING DATE: 2003-03-13
; PRIOR FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 120
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(120)
; OTHER INFORMATION: mab
US-10-389-679-19

Query Match 100.0%; Score 30; DB 4; Length 120;
Best Local Similarity 100.0%; Pred. No. 3,4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
Db 31 SYTH 35

RESULT 26
US-10-371-942-46
; Sequence 46, Application US/10371942
; Publication No. US20030223994A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Henricus Renerus Jacobus Mattheus
; APPLICANT: Reiter, Yoram
; TITLE OF INVENTION: MHC-PEPTIDE COMPLEX BINDING LIGANDS
; FILE REFERENCE: 10280-034001
; CURRENT APPLICATION NUMBER: US/10/371,942
; CURRENT FILING DATE: 2003-02-20
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-371-942-46

Query Match 100.0%; Score 30; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 3,6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
Db 31 SYTH 35

RESULT 27
US-10-837-904-27
; Sequence 27, Application US/10837904
; Publication No. US20050142635A1
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary Margaret
; APPLICANT: JONES, Steven Tarran
; APPLICANT: SALDANHA, Jose William

TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 134
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/837,904
FILING DATE: 04-May-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/114,285
FILING DATE: 13-Jul-1998
APPLICATION NUMBER: US 08/436,717
FILING DATE: 08-MAY-1995
APPLICATION NUMBER: US 08/137,117
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Wegner, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/234
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-10-837-904-27
Query Match 100.0%; Score 30; DB 5; Length 135;
Best Local Similarity 100.0%; Pred. No. 3,7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SYTH 5
|||
Db 50 SYTH 54
RESULT 28
US-10-837-904-97
; Sequence 97, Application US/10837904
; Publication No. US20050142635A1
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; SATO, Koh
; BENDIG, Mary Margaret
; JONES, Steven Tarran
; SALDANHA, Jose William
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 134
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; MEDIUM TYPE: floppy disk

CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/837,904
FILING DATE: 04-May-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/114,285
FILING DATE: 13-Jul-1998
APPLICATION NUMBER: US 08/436,717
FILING DATE: 08-MAY-1995
APPLICATION NUMBER: US 08/137,117
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Wegner, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/234
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 97:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 97:
US-10-837-904-97
Query Match 100.0%; Score 30; DB 5; Length 135;
Best Local Similarity 100.0%; Pred. No. 3,7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SYTH 5
|||
Db 50 SYTH 54
RESULT 29
US-10-837-904-99
; Sequence 99, Application US/10837904
; Publication No. US20050142635A1
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; SATO, Koh
; BENDIG, Mary Margaret
; JONES, Steven Tarran
; SALDANHA, Jose William
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 134
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/837,904
FILING DATE: 04-May-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/114,285
FILING DATE: 13-Jul-1998
APPLICATION NUMBER: US 08/436,717
FILING DATE: 08-May-1995
APPLICATION NUMBER: US 08/137,117
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Wegner, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/234
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 99:
US-10-837-904-99

Query Match 100.0%; Score 30; DB 5; Length 135;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
Db 50 SYTH 54

RESULT 30
US-10-837-904-109
Sequence 109, Application US/10837904
Publication No. US20050142635A1
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
SATO, Koh
BENDIG, Mary Margaret
JONES, Steven Tarran
SALDANHA, Jose William
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 134
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/837,904
FILING DATE: 04-May-2004

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/114,285
FILING DATE: 13-Jul-1998
APPLICATION NUMBER: US 08/436,717
FILING DATE: 08-May-1995
APPLICATION NUMBER: US 08/137,117
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Wegner, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/234
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 109:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 109:
US-10-837-904-109

Query Match 100.0%; Score 30; DB 5; Length 135;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
Db 50 SYTH 54

RESULT 31
US-10-425-115-241095
Sequence 241095, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 241095
LENGTH: 150
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
NAME/KEY: unsure
LOCATION: (1)-(150)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_151457C.1.pep
US-10-425-115-241095

Query Match 100.0%; Score 30; DB 4; Length 150;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
Db 123 SYTH 127

```
RESULT 32
US-10-425-115-221622
; Sequence 221622, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 221622
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(220)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_133710C.1.pep
US-10-425-115-221622
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```
Query Match          100.0%; Score 30; DB 4; Length 220;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 SYTH 5
        |||||
Db      128 SYTH 132
```

```
RESULT 33
US-10-935-290-72
; Sequence 72, Application US/10935290
; Publication No. US2005069542A1
; GENERAL INFORMATION:
; APPLICANT: Baker et al.
; TITLE OF INVENTION: Antibodies that Specifically Bind to GMAD
; FILE REFERENCE: PFS84P1
; CURRENT APPLICATION NUMBER: US/10/935,290
; CURRENT FILING DATE: 2004-09-08
; PRIOR APPLICATION NUMBER: PCT/US03/09625
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 60/368,813
; PRIOR FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 234
; SEQ ID NO 72
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: scFv protein GMEC646
US-10-935-290-72
```

```
Query Match          100.0%; Score 30; DB 5; Length 241;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 SYTH 5
        |||||
Db      31 SYTH 35
```

```
RESULT 34
US-09-880-748-2089
; Sequence 2089, Application US/09880748
```

```
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patentia Ver. 2.0
; SEQ ID NO 2089
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2089
```

```
Query Match          100.0%; Score 30; DB 3; Length 245;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 SYTH 5
        |||||
Db      31 SYTH 35
```

```
RESULT 35
US-10-293-418-2089
; Sequence 2089, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2089
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-2089
```

```
Query Match          100.0%; Score 30; DB 4; Length 245;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 SYTH 5
        |||||
```

Db 31 SYT1H 35

```
RESULT 36
US-10-981-692-31
; Sequence 31, Application US/10981692
; Publication No. US2005016377A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B
; FILE REFERENCE: PFS90P1
; CURRENT APPLICATION NUMBER: US/10/981,692
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: PCT/US03/16802
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: 60/383,802
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: NO24D08 scFv
US-10-981-692-31
```

Query Match 100.0%; Score 30; DB 5; Length 245;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 SYT1H 5
|||
Db 31 SYT1H 35

```
RESULT 37
US-09-880-748-2090
; Sequence 2090, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2090
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2090
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Query Match 100.0%; Score 30; DB 3; Length 258;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 SYT1H 5
|||
Db 31 SYT1H 35

RESULT 38

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US-10-293-418-2090
; Sequence 2090, Application US/10293418
; Publication No. US2003022396A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2090
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-2090
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Query Match 100.0%; Score 30; DB 4; Length 258;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 SYT1H 5
|||
Db 31 SYT1H 35

```
RESULT 39
US-10-425-115-189637
; Sequence 189637, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 189637
; LENGTH: 48
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_104532C.1.pep
US-10-425-115-189637
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Query Match 96.7%; Score 29; DB 4; Length 48;
Best Local Similarity 80.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 SYT1H 5
|||
Db 28 SYT1H 32

```
RESULT 40
US-10-425-115-295110
; Sequence 295110, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 295110
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_32220C.1.pep
US-10-425-115-295110
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```
Query Match          96.7%; Score 29; DB 4; Length 59;
Best Local Similarity 80.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 SYTH 5
        |||:|
Db       39 SYTH 43
```

```
RESULT 41
US-10-424-599-282127
; Sequence 282127, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 282127
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_96782C.1.pep
US-10-424-599-282127
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```
Query Match          96.7%; Score 29; DB 4; Length 98;
Best Local Similarity 80.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
OY      1 SYTH 5
        |||:|
Db       32 SYTH 36
```

```
RESULT 42
US-10-425-115-198368
; Sequence 198368, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
```

```
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 198368
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_11248C.1.pep
US-10-425-115-198368
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Query Match          96.7%; Score 29; DB 4; Length 140;
Best Local Similarity 80.0%; Pred. No. 6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 SYTH 5
        |||:|
Db       128 SYTH 132
```

```
RESULT 43
US-09-764-868-981
; Sequence 981, Application US/09764868
; Patent No. US20020168711A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT232
; CURRENT APPLICATION NUMBER: US/09/764,868
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 981
; LENGTH: 207
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (177)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-868-981
```

```
Query Match          96.7%; Score 29; DB 3; Length 207;
Best Local Similarity 80.0%; Pred. No. 8.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 SYTH 5
        |||:|
Db       185 SYTH 189
```

```
RESULT 44
US-10-158-057-295
; Sequence 295, Application US/10158057
; Publication No. US20040014039A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P205C1
; CURRENT APPLICATION NUMBER: US/10/158,057
; CURRENT FILING DATE: 2002-06-12
; Prior application removed - See file Wrapper or Palm
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 295
; LENGTH: 207
; TYPE: PRT
; ORGANISM: Homo sapiens
```


FEATURE:
NAME/KEY: misc_feature
LOCATION: (177)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-158-057-295

Query Match
Best Local Similarity 96.7%; Score 29; DB 4; Length 207;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYVH 5
Db 185 SYVH 189

RESULT 45
US-09-801-944B-193
Sequence 193, Application US/09801944B
Publication No. US20040014169A1
GENERAL INFORMATION:
APPLICANT: Vogel, Linda S.
APPLICANT: Wood, Linda S.
TITLE OF INVENTION: No. US20040014169A1 G Protein-Coupled Receptors
FILE REFERENCE: 00100US1
CURRENT FILING DATE: 2003-08-01
PRIOR APPLICATION NUMBER: 60/187,828
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/187,715
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/187,929
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/187,930
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/187,825
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/187,833
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/187,830
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/187,829
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/187,582
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/187,581
PRIOR FILING DATE: 2000-03-08
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 273
SOFTWARE: PatentIn version 3.0
SEQ ID NO 193
LENGTH: 208
TYPE: PRT
ORGANISM: Homo sapiens
US-09-801-944B-193

Query Match
Best Local Similarity 96.7%; Score 29; DB 3; Length 208;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYVH 5
Db 157 SYVH 161

RESULT 46
US-09-880-748-1406
Sequence 1406, Application US/09880748
Publication No. US2003005937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PFS23
CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1406
LENGTH: 243
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-1406

Query Match
Best Local Similarity 96.7%; Score 29; DB 3; Length 243;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYVH 5
Db 31 SYVH 35

RESULT 47
US-10-293-418-1406
Sequence 1406, Application US/10293418
Publication No. US20030223996A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PFS23P2
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1406
LENGTH: 243
TYPE: PRT
ORGANISM: Homo sapiens
US-10-293-418-1406

Query Match
Best Local Similarity 96.7%; Score 29; DB 4; Length 243;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYVH 5
Db 31 SYVH 35

RESULT 48
US-09-880-748-1384
Sequence 1384, Application US/09880748

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; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1384
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1384
```

```
Query Match          96.7%; Score 29; DB 3; Length 247;
Best Local Similarity 80.0%; Pred. No. 1e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 SYVVH 5
      |||:|
Db      31 SYVVH 35
```

```
RESULT 49
US-10-293-418-1384
; Sequence 1384, Application US/10293418
; Publication No. US2003023996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1384
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1384
```

```
Query Match          96.7%; Score 29; DB 4; Length 247;
Best Local Similarity 80.0%; Pred. No. 1e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 SYVVH 5
      |||:|
```

```
Db      31 SYVVH 35
```

```
RESULT 50
US-10-425-115-207239
; Sequence 207239, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; PRIOR FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 207239
; LENGTH: 433
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_12058C.1.pep
US-10-425-115-207239
```

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Query Match          96.7%; Score 29; DB 4; Length 433;
Best Local Similarity 80.0%; Pred. No. 1.7e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 SYVVH 5
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Db      79 SYVVH 83
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Job time : 50.4365 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 4, 2006, 13:46:13 ; Search time 5.79365 Seconds
(without alignments)
39.944 Million cell updates/sec

Title: US-10-700-632-1
Perfect score: 30
Sequence: 1 SYRHH 5

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 235405 seqs, 46284737 residues

Total number of hits satisfying chosen parameters: 235405

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 1000 summaries

Database :

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2: /SID55/ptodata/2/pubpaa/US06_NEW_PUB.pep1.*
3: /SID55/ptodata/2/pubpaa/US07_NEW_PUB.pep1.*
4: /SID55/ptodata/2/pubpaa/US08_NEW_PUB.pep1.*
5: /SID55/ptodata/2/pubpaa/FCI_NEW_PUB.pep1.*
6: /SID55/ptodata/2/pubpaa/US09_NEW_PUB.pep1.*
7: /SID55/ptodata/2/pubpaa/US09_NEW_PUB.pep1.*
8: /SID55/ptodata/2/pubpaa/US10_NEW_PUB.pep1.*
9: /SID55/ptodata/2/pubpaa/US10_NEW_PUB.pep1.*
10: /SID55/ptodata/2/pubpaa/US11_NEW_PUB.pep1.*
11: /SID55/ptodata/2/pubpaa/US11_NEW_PUB.pep1.*
12: /SID55/ptodata/2/pubpaa/US60_NEW_PUB.pep1.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	116	11 US-11-096-074-50	Sequence 50, Appl
2	30	100.0	116	11 US-11-095-822-50	Sequence 50, Appl
3	30	100.0	118	9 US-10-507-662-10	Sequence 30, Appl
4	30	100.0	118	9 US-10-507-662-11	Sequence 31, Appl
5	30	100.0	118	9 US-10-507-662-14	Sequence 35, Appl
6	30	100.0	118	9 US-10-507-662-35	Sequence 36, Appl
7	30	100.0	118	9 US-10-507-662-36	Sequence 36, Appl
8	30	100.0	120	9 US-10-946-836A-14	Sequence 14, Appl
9	30	100.0	120	9 US-10-946-836A-19	Sequence 19, Appl
10	30	100.0	120	9 US-10-988-207-14	Sequence 14, Appl
11	30	100.0	120	9 US-10-988-207-19	Sequence 19, Appl
12	30	100.0	120	9 US-10-988-207-26	Sequence 26, Appl
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14	30	100.0	245	11 US-11-266-444-2089	Sequence 2089, Ap
15	30	100.0	258	11 US-11-054-515-2090	Sequence 2090, Ap
16	30	100.0	258	11 US-11-266-444-2090	Sequence 2090, Ap
17	30	100.0	774	11 US-11-188-298-3002	Sequence 3002, Ap
18	29	96.7	61	9 US-10-895-054-1817	Sequence 1817, Ap
19	29	96.7	61	11 US-11-129-741-1817	Sequence 1817, Ap
20	29	96.7	243	11 US-11-054-515-1406	Sequence 1406, Ap
21	29	96.7	243	11 US-11-266-444-1406	Sequence 1406, Ap

22	29	96.7	244	11 US-11-079-463-7470	Sequence 7470, Ap
23	29	96.7	247	11 US-11-054-515-1384	Sequence 1384, Ap
24	29	96.7	247	11 US-11-266-444-1384	Sequence 1384, Ap
25	29	96.7	1210	9 US-10-624-932-26	Sequence 26, Appl
26	29	96.7	1213	11 US-11-039-398-14	Sequence 14, Appl
27	29	96.7	1216	11 US-11-039-398-12	Sequence 12, Appl
28	29	96.7	1219	11 US-11-039-398-10	Sequence 10, Appl
29	29	96.7	1222	11 US-11-039-398-8	Sequence 8, Appl
30	29	96.7	1232	11 US-11-039-398-18	Sequence 18, Appl
31	29	96.7	1235	11 US-11-039-398-16	Sequence 16, Appl
32	29	96.7	1249	11 US-11-039-398-22	Sequence 22, Appl
33	29	96.7	1252	11 US-11-039-398-20	Sequence 20, Appl
34	29	96.7	62	11 US-11-096-568A-4404	Sequence 4404, Ap
35	28	93.3	74	11 US-11-096-568A-4402	Sequence 4402, Ap
36	28	93.3	118	9 US-10-507-662-33	Sequence 33, Appl
37	28	93.3	256	11 US-11-054-515-1967	Sequence 1967, Ap
38	28	93.3	256	11 US-11-266-444-1967	Sequence 1967, Ap
39	28	93.3	288	9 US-10-467-657-8598	Sequence 8598, Ap
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41	27	90.0	5	11 US-11-125-837-10	Sequence 10, Appl
42	27	90.0	5	11 US-11-201-825-34	Sequence 34, Appl
43	27	90.0	10	11 US-11-194-989-3	Sequence 3, Appl
44	27	90.0	10	11 US-11-195-207-3	Sequence 3, Appl
45	27	90.0	31	11 US-11-004-399-2005	Sequence 2005, Ap
46	27	90.0	98	11 US-11-221-902-58	Sequence 58, Appl
47	27	90.0	98	11 US-11-054-669-7	Sequence 7, Appl
48	27	90.0	98	11 US-11-084-554-20	Sequence 20, Appl
49	27	90.0	98	11 US-11-004-590-7	Sequence 7, Appl
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52	27	90.0	116	11 US-11-195-207-1	Sequence 1, Appl
53	27	90.0	117	9 US-10-834-397-22	Sequence 22, Appl
54	27	90.0	117	11 US-11-201-825-13	Sequence 13, Appl
55	27	90.0	117	11 US-11-201-825-28	Sequence 28, Appl
56	27	90.0	118	11 US-11-112-240-10	Sequence 10, Appl
57	27	90.0	118	11 US-11-112-240-10	Sequence 10, Appl
58	27	90.0	120	9 US-10-834-397-36	Sequence 36, Appl
59	27	90.0	120	9 US-10-834-397-59	Sequence 59, Appl
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62	27	90.0	138	11 US-11-125-837-22	Sequence 22, Appl
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68	27	90.0	245	11 US-11-054-515-1919	Sequence 1919, Ap
69	27	90.0	245	11 US-11-054-515-1950	Sequence 1950, Ap
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71	27	90.0	245	11 US-11-266-444-1902	Sequence 1902, Ap
72	27	90.0	245	11 US-11-266-444-1919	Sequence 1919, Ap
73	27	90.0	245	11 US-11-266-444-1950	Sequence 1950, Ap
74	27	90.0	247	11 US-11-054-515-1729	Sequence 1729, Ap
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76	27	90.0	248	11 US-11-054-515-1178	Sequence 1178, Ap
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91	27	90.0	252	11 US-11-266-444-1366	Sequence 1366, Ap
92	27	90.0	253	11 US-11-054-515-1895	Sequence 1895, Ap
93	27	90.0	253	11 US-11-054-515-1936	Sequence 1936, Ap
94	27	90.0	253	11 US-11-054-515-1951	Sequence 1951, Ap

95	27	90.0	253	11	US-11-054-515-2098	Sequence 2098, Ap	168	26	86.7	498	11	US-11-045-004-2061	Sequence 2061, Ap
96	27	90.0	253	11	US-11-054-515-2101	Sequence 2101, Ap	169	26	86.7	500	11	US-11-079-463-5773	Sequence 5773, Ap
97	27	90.0	253	11	US-11-266-444-1895	Sequence 1895, Ap	170	26	86.7	507	11	US-11-096-568A-33997	Sequence 33997, A
98	27	90.0	253	11	US-11-266-444-1936	Sequence 1936, Ap	171	26	86.7	508	9	US-10-793-626-2482	Sequence 2482, Ap
99	27	90.0	253	11	US-11-266-444-1951	Sequence 1951, Ap	172	26	86.7	632	11	US-11-096-568A-33996	Sequence 33996, A
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101	27	90.0	253	11	US-11-266-444-2101	Sequence 2101, Ap	174	26	86.7	695	11	US-11-079-463-5291	Sequence 5291, Ap
102	27	90.0	254	11	US-11-054-515-1961	Sequence 1961, Ap	175	26	86.7	707	11	US-11-079-463-9670	Sequence 9670, Ap
103	27	90.0	254	11	US-11-054-515-1983	Sequence 1983, Ap	176	26	86.7	737	9	US-10-501-035-254	Sequence 254, Ap
104	27	90.0	254	11	US-11-266-444-1961	Sequence 1961, Ap	177	26	86.7	806	11	US-11-192-219-3	Sequence 3, Ap
105	27	90.0	254	11	US-11-266-444-1983	Sequence 1983, Ap	178	26	86.7	898	11	US-11-166-730-3	Sequence 3, Ap
106	27	90.0	255	11	US-11-054-515-857	Sequence 857, Ap	179	26	86.7	914	11	US-11-072-512-2923	Sequence 2923, Ap
107	27	90.0	255	11	US-11-054-515-1156	Sequence 1156, Ap	180	26	86.7	923	11	US-11-192-219-4	Sequence 4, Ap
108	27	90.0	255	11	US-11-266-444-857	Sequence 857, Ap	181	26	86.7	1075	8	US-10-322-836-48	Sequence 48, Ap
109	27	90.0	255	11	US-11-266-444-1156	Sequence 1156, Ap	182	26	86.7	1145	9	US-10-793-626-1432	Sequence 1432, Ap
110	27	90.0	255	11	US-11-054-515-1567	Sequence 1567, Ap	183	26	86.7	1165	11	US-11-192-219-2	Sequence 2, Ap
111	27	90.0	259	11	US-11-266-444-1567	Sequence 1567, Ap	184	26	86.7	1185	11	US-11-202-330-4	Sequence 4, Ap
112	27	90.0	442	11	US-11-194-989-11	Sequence 11, Ap	185	25	83.3	9	11	US-11-136-079-298	Sequence 298, Ap
113	27	90.0	442	11	US-11-195-207-11	Sequence 11, Ap	186	25	83.3	13	9	US-10-895-064-2100	Sequence 2100, Ap
114	27	90.0	495	11	US-11-079-463-7682	Sequence 7682, Ap	187	25	83.3	13	11	US-11-129-741-2100	Sequence 2100, Ap
115	27	90.0	527	11	US-11-079-463-6635	Sequence 6635, Ap	188	25	83.3	20	11	US-11-054-515-2743	Sequence 2743, Ap
116	26	86.7	6	11	US-11-102-743-8	Sequence 8, Ap	189	25	83.3	20	11	US-11-266-444-2743	Sequence 2743, Ap
117	26	86.7	10	11	US-11-171-567-114	Sequence 11, Ap	190	25	83.3	73	11	US-11-096-568A-1334	Sequence 1334, Ap
118	26	86.7	10	11	US-11-171-567-145	Sequence 145, Ap	191	25	83.3	96	11	US-11-096-568A-1592	Sequence 1592, Ap
119	26	86.7	10	11	US-11-171-567-146	Sequence 146, Ap	192	25	83.3	101	11	US-11-096-568A-1333	Sequence 1333, Ap
120	26	86.7	18	11	US-11-054-515-2964	Sequence 2964, Ap	193	25	83.3	127	11	US-11-096-568A-1591	Sequence 1591, Ap
121	26	86.7	18	11	US-11-266-444-2964	Sequence 2964, Ap	194	25	83.3	127	11	US-11-240-769-95	Sequence 95, Ap
122	26	86.7	65	11	US-11-087-099-348	Sequence 348, Ap	195	25	83.3	127	11	US-11-045-004-1249	Sequence 1249, Ap
123	26	86.7	66	11	US-11-087-099-890	Sequence 890, Ap	196	25	83.3	127	11	US-10-735-594-1	Sequence 1, Ap
124	26	86.7	66	11	US-11-087-099-5553	Sequence 5553, Ap	197	25	83.3	127	11	US-10-735-594-4	Sequence 4, Ap
125	26	86.7	66	11	US-11-087-099-6088	Sequence 6088, Ap	198	25	83.3	208	11	US-11-045-004-1458	Sequence 1458, Ap
126	26	86.7	82	11	US-11-087-099-7060	Sequence 7060, Ap	199	25	83.3	227	9	US-10-735-594-3	Sequence 3, Ap
127	26	86.7	82	11	US-11-087-099-11699	Sequence 11699, A	200	25	83.3	227	9	US-10-821-234-1633	Sequence 1633, Ap
128	26	86.7	86	11	US-11-087-099-3891	Sequence 3891, Ap	201	25	83.3	227	11	US-11-087-099-3192	Sequence 3192, Ap
129	26	86.7	114	11	US-11-102-743-7	Sequence 7, Ap	202	25	83.3	227	11	US-11-096-568A-184	Sequence 184, Ap
130	26	86.7	116	11	US-11-097-812-31	Sequence 31, Ap	203	25	83.3	224	11	US-11-096-568A-185	Sequence 185, Ap
131	26	86.7	117	9	US-10-932-334-76	Sequence 76, Ap	204	25	83.3	245	11	US-11-054-515-1864	Sequence 1864, Ap
132	26	86.7	120	11	US-11-097-812-153	Sequence 153, Ap	205	25	83.3	251	11	US-11-266-444-1864	Sequence 871, Ap
133	26	86.7	122	11	US-11-171-567-202	Sequence 202, Ap	206	25	83.3	251	11	US-11-054-515-882	Sequence 882, Ap
134	26	86.7	123	11	US-11-087-099-2025	Sequence 2025, Ap	207	25	83.3	251	11	US-11-266-444-871	Sequence 871, Ap
135	26	86.7	216	7	US-09-978-360A-671	Sequence 671, Ap	208	25	83.3	251	11	US-11-266-444-882	Sequence 882, Ap
136	26	86.7	228	11	US-11-188-298-1950	Sequence 1950, Ap	209	25	83.3	251	11	US-11-054-515-1394	Sequence 1394, Ap
137	26	86.7	233	11	US-11-087-099-949	Sequence 949, Ap	210	25	83.3	252	11	US-11-266-444-1846	Sequence 1846, Ap
138	26	86.7	235	11	US-11-087-099-949	Sequence 1303, Ap	211	25	83.3	254	11	US-11-054-515-2082	Sequence 2082, Ap
139	26	86.7	241	11	US-11-054-515-1303	Sequence 1948, Ap	212	25	83.3	254	11	US-11-054-515-1846	Sequence 1846, Ap
140	26	86.7	241	11	US-11-054-515-1948	Sequence 1303, Ap	213	25	83.3	254	11	US-11-054-515-2082	Sequence 2082, Ap
141	26	86.7	241	11	US-11-266-444-1303	Sequence 1948, Ap	214	25	83.3	254	11	US-11-266-444-1846	Sequence 1846, Ap
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143	26	86.7	248	11	US-11-054-515-967	Sequence 967, Ap	216	25	83.3	255	11	US-11-054-515-1849	Sequence 1849, Ap
144	26	86.7	248	11	US-11-266-444-967	Sequence 967, Ap	217	25	83.3	255	11	US-11-266-444-1849	Sequence 1849, Ap
145	26	86.7	249	11	US-11-054-515-1730	Sequence 1730, Ap	218	25	83.3	255	11	US-11-266-444-1849	Sequence 1849, Ap
146	26	86.7	249	11	US-11-266-444-1730	Sequence 1730, Ap	219	25	83.3	277	9	US-10-506-454-1158	Sequence 1158, Ap
147	26	86.7	253	11	US-11-054-515-1003	Sequence 1003, Ap	220	25	83.3	292	11	US-11-096-568A-20448	Sequence 20448, A
148	26	86.7	253	11	US-11-054-515-1003	Sequence 1003, Ap	221	25	83.3	292	11	US-11-096-568A-22742	Sequence 22742, A
149	26	86.7	253	11	US-11-054-515-1526	Sequence 1526, Ap	222	25	83.3	297	11	US-11-096-568A-17221	Sequence 17221, A
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151	26	86.7	253	11	US-11-266-444-1007	Sequence 1007, Ap	224	25	83.3	303	11	US-11-096-568A-17220	Sequence 17220, A
152	26	86.7	253	11	US-11-266-444-1526	Sequence 1526, Ap	225	25	83.3	303	11	US-11-096-568A-23326	Sequence 23326, A
153	26	86.7	255	11	US-11-096-568A-32032	Sequence 32032, A	226	25	83.3	322	11	US-11-087-099-6568	Sequence 6568, Ap
154	26	86.7	255	11	US-11-096-568A-32031	Sequence 32031, A	227	25	83.3	324	11	US-11-096-568A-22741	Sequence 22741, A
155	26	86.7	284	11	US-11-045-004-2755	Sequence 2755, A	228	25	83.3	332	11	US-11-087-099-6145	Sequence 6145, Ap
156	26	86.7	298	8	US-10-322-836-50	Sequence 50, Ap	229	25	83.3	332	11	US-11-087-099-11650	Sequence 11650, A
157	26	86.7	312	11	US-11-087-099-1653	Sequence 1653, Ap	230	25	83.3	332	11	US-11-096-568A-17219	Sequence 17219, A
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159	26	86.7	315	11	US-11-087-099-11558	Sequence 11558, A	232	25	83.3	333	11	US-11-087-099-1308	Sequence 1308, Ap
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161	26	86.7	325	11	US-11-096-568A-32030	Sequence 32030, A	234	25	83.3	333	11	US-11-087-099-8052	Sequence 8052, Ap
162	26	86.7	327	11	US-11-045-004-2127	Sequence 2127, Ap	235	25	83.3	333	11	US-11-087-099-10608	Sequence 10608, A
163	26	86.7	359	11	US-11-079-463-9005	Sequence 9005, Ap	236	25	83.3	333	11	US-11-087-099-11467	Sequence 11467, A
164	26	86.7	433	11	US-11-045-004-2606	Sequence 2606, Ap	237	25	83.3	333	11	US-11-087-099-11467	Sequence 11467, A
165	26	86.7	455	11	US-11-096-568A-10949	Sequence 10949, A	238	25	83.3	333	11	US-11-087-099-12348	Sequence 12348, A
166	26	86.7	480	11	US-11-096-568A-33998	Sequence 33998, A	239	25	83.3	335	11	US-11-087-099-423	Sequence 423, Ap
167	26	86.7	491	11	US-11-045-004-1074	Sequence 1074, Ap	240	25	83.3	335	11	US-11-087-099-5152	Sequence 5152, Ap

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243	25	83.3	337	11	US-11-096-568A-20446	Sequence 20446, A	316	24	80.0	134	9	US-11-096-568A-22697	Sequence 22697, A
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245	25	83.3	344	11	US-11-087-099-4327	Sequence 4327, Ap	318	24	80.0	142	11	US-11-158-505-36	Sequence 36, Appl
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252	25	83.3	397	11	US-11-096-568A-13387	Sequence 13387, A	325	24	80.0	213	11	US-11-072-512-2722	Sequence 2722, Ap
253	25	83.3	411	11	US-11-079-463-8798	Sequence 8798, Ap	326	24	80.0	213	11	US-11-096-568A-4374	Sequence 4374, Ap
254	25	83.3	417	11	US-10-992-577-44	Sequence 44, Appl	327	24	80.0	214	11	US-11-096-568A-4373	Sequence 4373, Ap
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256	25	83.3	420	9	US-10-992-577-6	Sequence 6, Appl1	329	24	80.0	231	11	US-11-018-868-93	Sequence 93, Appl
257	25	83.3	420	11	US-11-096-568A-10495	Sequence 10495, A	330	24	80.0	234	11	US-11-045-004-194	Sequence 194, Ap
258	25	83.3	426	9	US-10-517-959-240	Sequence 240, Ap	331	24	80.0	237	11	US-11-096-568A-33414	Sequence 33414, A
259	25	83.3	426	11	US-11-188-298-7212	Sequence 7212, Ap	332	24	80.0	237	11	US-11-242-650-32	Sequence 32, Appl
260	25	83.3	426	11	US-11-188-298-21748	Sequence 21748, A	333	24	80.0	246	11	US-11-054-515-1996	Sequence 1996, Ap
261	25	83.3	441	11	US-11-024-959-410	Sequence 410, Ap	334	24	80.0	246	11	US-11-266-444-1996	Sequence 1996, Ap
262	25	83.3	447	11	US-11-024-959-286	Sequence 286, Ap	335	24	80.0	246	11	US-11-045-004-2271	Sequence 2271, Ap
263	25	83.3	452	11	US-11-079-463-9287	Sequence 9287, Ap	336	24	80.0	247	11	US-11-054-515-2076	Sequence 2076, Ap
264	25	83.3	461	9	US-10-131-826A-454	Sequence 454, Ap	337	24	80.0	247	11	US-11-266-444-2076	Sequence 2076, Ap
265	25	83.3	461	9	US-10-973-115B-454	Sequence 454, Ap	338	24	80.0	248	11	US-11-054-515-1386	Sequence 1386, Ap
266	25	83.3	461	9	US-10-137-873A-454	Sequence 454, Ap	339	24	80.0	248	11	US-11-054-515-1388	Sequence 1388, Ap
267	25	83.3	461	9	US-10-152-370-454	Sequence 454, Ap	340	24	80.0	248	11	US-11-054-515-2094	Sequence 2094, Ap
268	25	83.3	461	11	US-11-280-153-454	Sequence 454, Ap	341	24	80.0	248	11	US-11-266-444-1386	Sequence 1386, Ap
269	25	83.3	465	11	US-11-096-568A-23324	Sequence 23324, A	342	24	80.0	248	11	US-11-266-444-1384	Sequence 1384, Ap
270	25	83.3	473	11	US-11-087-099-12288	Sequence 12288, A	343	24	80.0	248	11	US-11-266-444-1388	Sequence 1388, Ap
271	25	83.3	474	11	US-11-037-829A-13	Sequence 13, Appl	344	24	80.0	249	11	US-11-266-444-2094	Sequence 2094, Ap
272	25	83.3	474	11	US-11-188-298-15570	Sequence 15570, A	345	24	80.0	249	11	US-11-054-515-963	Sequence 963, Ap
273	25	83.3	510	11	US-11-024-959-409	Sequence 409, Ap	346	24	80.0	251	11	US-11-266-444-963	Sequence 963, Ap
274	25	83.3	522	9	US-10-510-018-2	Sequence 2, Appl1	347	24	80.0	251	11	US-11-054-515-176	Sequence 176, Ap
275	25	83.3	542	11	US-11-188-298-10073	Sequence 10073, A	348	24	80.0	251	11	US-11-054-515-1459	Sequence 1459, Ap
276	25	83.3	546	9	US-10-194-487-412	Sequence 412, Ap	349	24	80.0	251	11	US-11-266-444-176	Sequence 176, Ap
277	25	83.3	546	9	US-10-195-883-412	Sequence 412, Ap	350	24	80.0	251	11	US-11-266-444-1459	Sequence 1459, Ap
278	25	83.3	546	9	US-10-195-888-412	Sequence 412, Ap	351	24	80.0	251	11	US-11-266-444-1358	Sequence 1358, Ap
279	25	83.3	546	9	US-10-195-889-412	Sequence 412, Ap	352	24	80.0	253	11	US-11-054-515-1358	Sequence 1358, Ap
280	25	83.3	546	9	US-10-218-784-124	Sequence 124, Ap	353	24	80.0	253	11	US-11-266-444-1358	Sequence 1358, Ap
281	25	83.3	546	9	US-10-219-061-124	Sequence 124, Ap	354	24	80.0	254	11	US-11-054-515-1893	Sequence 1893, Ap
282	25	83.3	546	9	US-10-219-062-124	Sequence 124, Ap	355	24	80.0	254	11	US-11-266-444-1893	Sequence 1893, Ap
283	25	83.3	546	9	US-10-219-064-124	Sequence 124, Ap	356	24	80.0	255	11	US-11-054-515-1407	Sequence 1407, Ap
284	25	83.3	546	9	US-10-233-134-124	Sequence 134, Ap	357	24	80.0	255	11	US-11-266-444-1407	Sequence 1407, Ap
285	25	83.3	571	11	US-10-506-454-152	Sequence 152, Ap	358	24	80.0	256	11	US-11-054-515-1301	Sequence 1301, Ap
286	25	83.3	611	11	US-11-188-298-5827	Sequence 5827, Ap	359	24	80.0	256	11	US-11-266-444-1301	Sequence 1301, Ap
287	25	83.3	694	11	US-11-079-463-6032	Sequence 6032, Ap	360	24	80.0	261	11	US-11-096-568A-17990	Sequence 17990, A
288	25	83.3	697	11	US-11-103-957-39	Sequence 39, Appl	361	24	80.0	273	11	US-11-178-230-8	Sequence 8, Appl1
289	25	83.3	784	11	US-11-188-298-2774	Sequence 2774, Ap	362	24	80.0	273	11	US-11-178-230-9	Sequence 9, Appl1
290	25	83.3	842	11	US-11-072-512-3018	Sequence 3018, Ap	363	24	80.0	283	11	US-11-096-568A-28896	Sequence 28896, A
291	25	83.3	865	11	US-11-079-463-9886	Sequence 9886, Ap	364	24	80.0	303	11	US-11-087-099-11407	Sequence 11407, A
292	25	83.3	946	9	US-10-501-035-278	Sequence 278, Ap	365	24	80.0	316	11	US-11-096-568A-24774	Sequence 24774, A
293	25	83.3	967	11	US-11-171-701-4	Sequence 4, Appl1	366	24	80.0	316	11	US-11-188-298-6715	Sequence 6715, Ap
294	25	83.3	1025	8	US-10-505-928-505	Sequence 505, Ap	367	24	80.0	316	11	US-11-188-298-15032	Sequence 15032, A
295	25	83.3	1025	11	US-11-169-041-164	Sequence 164, Ap	368	24	80.0	318	11	US-11-096-568A-5601	Sequence 5601, Ap
296	25	83.3	1215	8	US-10-505-928-75	Sequence 75, Appl	369	24	80.0	319	11	US-11-087-099-2526	Sequence 2526, Ap
297	25	83.3	1912	8	US-10-511-937-2561	Sequence 2561, Ap	370	24	80.0	319	11	US-11-188-298-13357	Sequence 13357, A
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299	25	83.3	4961	9	US-10-453-372-1132	Sequence 1132, Ap	372	24	80.0	324	11	US-11-087-099-4871	Sequence 4871, Ap
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301	24	80.0	9	11	US-11-136-079-307	Sequence 307, Ap	374	24	80.0	330	10	US-11-125-402-32	Sequence 32, Appl
302	24	80.0	9	11	US-11-136-079-308	Sequence 308, Ap	375	24	80.0	333	11	US-11-079-463-6233	Sequence 6233, Ap
303	24	80.0	9	11	US-11-136-079-309	Sequence 309, Ap	376	24	80.0	334	11	US-11-079-463-10143	Sequence 10143, A
304	24	80.0	9	11	US-11-136-079-310	Sequence 310, Ap	377	24	80.0	335	11	US-11-087-099-2180	Sequence 2180, Ap
305	24	80.0	10	11	US-11-171-567-115	Sequence 115, Ap	378	24	80.0	336	11	US-11-087-099-3799	Sequence 3799, Ap
306	24	80.0	16	11	US-11-054-515-2295	Sequence 2295, Ap	379	24	80.0	337	11	US-11-087-099-3345	Sequence 3345, Ap
307	24	80.0	16	11	US-11-266-444-2295	Sequence 2295, Ap	380	24	80.0	340	9	US-10-873-528-188	Sequence 188, Ap
308	24	80.0	17	11	US-11-054-515-2960	Sequence 2960, Ap	381	24	80.0	340	9	US-11-087-099-1599	Sequence 1599, Ap
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311	24	80.0	110	11	US-11-097-812-3	Sequence 3, Appl1	384	24	80.0	348	11	US-11-098-686-8740	Sequence 8740, Ap
312	24	80.0	110	11	US-11-097-812-4	Sequence 4, Appl1	385	24	80.0	348	11	US-11-098-686-11203	Sequence 11203, A
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388	24	80.0	354	11	US-11-087-099-12334	Sequence 12334, A	461	23	76.7	10	11	US-11-171-567-137	Sequence 137, App
389	24	80.0	355	11	US-11-241-056-10	Sequence 10, Appl	462	23	76.7	16	11	US-11-152-974A-219	Sequence 219, App
390	24	80.0	355	11	US-11-108-088-55	Sequence 55, Appl	463	23	76.7	16	11	US-11-153-144A-219	Sequence 219, App
391	24	80.0	361	11	US-11-096-568A-4590	Sequence 4590, Ap	464	23	76.7	23	11	US-11-225-709-37	Sequence 37, Appl
392	24	80.0	371	11	US-11-045-004-2702	Sequence 2702, Ap	465	23	76.7	24	11	US-11-225-709-39	Sequence 39, Appl
393	24	80.0	373	11	US-11-087-099-2679	Sequence 2679, Ap	466	23	76.7	34	9	US-10-895-064-2346	Sequence 2346, Ap
394	24	80.0	374	9	US-10-537-094-6	Sequence 6, Appl	467	23	76.7	34	11	US-11-129-741-2346	Sequence 2346, Ap
395	24	80.0	374	9	US-10-537-094-8	Sequence 8, Appl	468	23	76.7	62	11	US-11-079-466-9356	Sequence 9356, Ap
396	24	80.0	374	11	US-11-072-512-3578	Sequence 3578, Ap	469	23	76.7	62	11	US-11-079-466-9394	Sequence 9394, Ap
397	24	80.0	374	11	US-11-188-298-18689	Sequence 18689, A	470	23	76.7	66	9	US-10-992-577-4	Sequence 4, Appl
398	24	80.0	382	11	US-11-087-099-3195	Sequence 3195, Ap	471	23	76.7	98	10	US-11-221-902-52	Sequence 52, Appl
399	24	80.0	384	11	US-11-096-568A-4589	Sequence 4589, Ap	472	23	76.7	98	10	US-11-221-902-62	Sequence 62, Appl
400	24	80.0	399	11	US-11-178-230-3	Sequence 3, Appl	473	23	76.7	98	10	US-11-221-902-64	Sequence 64, Appl
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402	24	80.0	400	11	US-11-051-724-34	Sequence 34, Appl	475	23	76.7	98	11	US-11-054-669-11	Sequence 11, Appl
403	24	80.0	402	11	US-11-178-230-5	Sequence 5, Appl	476	23	76.7	98	11	US-11-084-554-16	Sequence 16, Appl
404	24	80.0	403	11	US-11-178-230-5	Sequence 5, Appl	477	23	76.7	98	11	US-11-004-590-10	Sequence 10, Appl
405	24	80.0	411	11	US-11-098-686-10968	Sequence 10968, A	478	23	76.7	98	11	US-11-136-250-16	Sequence 16, Appl
406	24	80.0	411	9	US-10-485-517-419	Sequence 1755, Ap	479	23	76.7	114	11	US-11-037-199-15	Sequence 15, Appl
407	24	80.0	419	11	US-11-079-663-6424	Sequence 6424, Ap	480	23	76.7	114	11	US-11-165-023-16	Sequence 16, Appl
408	24	80.0	440	11	US-11-096-568A-31181	Sequence 31181, A	481	23	76.7	115	11	US-11-165-023-31	Sequence 31, Appl
409	24	80.0	444	11	US-11-096-568A-31180	Sequence 31180, A	482	23	76.7	115	11	US-11-165-023-31	Sequence 31, Appl
410	24	80.0	463	11	US-11-045-004-1168	Sequence 1168, Ap	483	23	76.7	115	11	US-11-165-023-32	Sequence 32, Appl
411	24	80.0	470	11	US-11-024-959-297	Sequence 297, App	484	23	76.7	116	11	US-11-179-820-2	Sequence 2, Appl
412	24	80.0	472	11	US-11-008-331-3	Sequence 3, Appl	485	23	76.7	117	11	US-11-004-590-121	Sequence 121, App
413	24	80.0	472	11	US-11-096-568A-31179	Sequence 31179, A	486	23	76.7	119	9	US-10-477-950-2	Sequence 2, Appl
414	24	80.0	474	11	US-11-086-860-6	Sequence 6, Appl	487	23	76.7	120	10	US-11-221-902-18	Sequence 18, Appl
415	24	80.0	477	11	US-11-087-099-7285	Sequence 7285, Ap	488	23	76.7	120	10	US-11-221-902-19	Sequence 19, Appl
416	24	80.0	482	11	US-11-045-004-2627	Sequence 2627, Ap	489	23	76.7	120	10	US-11-221-902-21	Sequence 21, Appl
417	24	80.0	490	11	US-11-051-724-32	Sequence 32, Appl	490	23	76.7	123	9	US-10-793-626-246	Sequence 246, App
418	24	80.0	497	11	US-11-079-663-6669	Sequence 6669, Ap	491	23	76.7	123	11	US-11-171-567-201	Sequence 201, App
419	24	80.0	508	11	US-11-096-568A-157	Sequence 157, App	492	23	76.7	124	11	US-11-040-159-8	Sequence 8, Appl
420	24	80.0	508	11	US-11-087-099-11410	Sequence 11410, A	493	23	76.7	137	11	US-11-083-327-6	Sequence 6, Appl
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422	24	80.0	548	11	US-11-045-004-2026	Sequence 2026, Ap	495	23	76.7	140	11	US-11-098-686-10643	Sequence 10643, A
423	24	80.0	553	11	US-11-045-004-2822	Sequence 2822, Ap	496	23	76.7	141	9	US-10-506-454-612	Sequence 612, App
424	24	80.0	554	11	US-11-074-176-320	Sequence 320, App	497	23	76.7	193	11	US-11-096-568A-12819	Sequence 12819, A
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426	24	80.0	576	11	US-11-188-298-21338	Sequence 21338, A	499	23	76.7	205	9	US-10-793-626-2184	Sequence 2184, Ap
427	24	80.0	578	11	US-11-096-568A-156	Sequence 156, App	500	23	76.7	218	9	US-10-793-626-562	Sequence 562, App
428	24	80.0	598	11	US-11-079-663-9329	Sequence 9329, Ap	501	23	76.7	221	11	US-11-096-568A-21901	Sequence 21901, A
429	24	80.0	611	11	US-11-079-663-10057	Sequence 10057, A	502	23	76.7	223	11	US-11-079-463-8375	Sequence 8375, Ap
430	24	80.0	634	11	US-11-096-568A-155	Sequence 155, App	503	23	76.7	223	11	US-11-172-740-319	Sequence 319, App
431	24	80.0	669	9	US-10-203-486-12	Sequence 12, Appl	504	23	76.7	235	11	US-11-172-740-317	Sequence 317, App
432	24	80.0	676	11	US-11-188-298-5921	Sequence 5921, Ap	505	23	76.7	238	11	US-11-172-740-318	Sequence 318, App
433	24	80.0	686	11	US-11-096-568A-30902	Sequence 30902, A	506	23	76.7	241	11	US-11-054-515-2008	Sequence 2008, Ap
434	24	80.0	703	11	US-11-096-568A-30901	Sequence 30901, A	507	23	76.7	241	11	US-11-054-515-2031	Sequence 2031, Ap
435	24	80.0	704	11	US-11-072-512-3501	Sequence 3501, Ap	508	23	76.7	241	11	US-11-054-515-2032	Sequence 2032, Ap
436	24	80.0	710	11	US-11-096-568A-158	Sequence 158, App	509	23	76.7	241	11	US-11-266-444-2008	Sequence 2008, Ap
437	24	80.0	712	11	US-11-037-243-69	Sequence 69, Appl	510	23	76.7	241	11	US-11-266-444-2031	Sequence 2031, Ap
438	24	80.0	734	11	US-11-096-568A-30900	Sequence 30900, A	511	23	76.7	242	11	US-11-266-444-2032	Sequence 2032, Ap
439	24	80.0	765	11	US-11-024-959-476	Sequence 476, App	512	23	76.7	242	11	US-11-054-515-2021	Sequence 2021, Ap
440	24	80.0	805	9	US-10-467-657-8246	Sequence 8246, Ap	513	23	76.7	242	11	US-11-054-515-2046	Sequence 2046, Ap
441	24	80.0	897	9	US-10-821-234-1523	Sequence 1523, Ap	514	23	76.7	242	11	US-11-054-515-2106	Sequence 2106, Ap
442	24	80.0	1240	11	US-11-096-568A-30789	Sequence 30789, A	515	23	76.7	242	11	US-11-266-444-2021	Sequence 2021, Ap
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444	24	80.0	1285	11	US-11-096-568A-30787	Sequence 30787, A	517	23	76.7	242	11	US-11-266-444-2106	Sequence 2106, Ap
445	24	80.0	1315	11	US-11-086-960-8	Sequence 8, Appl	518	23	76.7	243	9	US-10-016-686-1	Sequence 1, Appl
446	24	80.0	1326	11	US-11-079-463-5820	Sequence 5820, Ap	519	23	76.7	243	11	US-11-054-515-2009	Sequence 2009, Ap
447	24	80.0	1431	9	US-10-501-035-220	Sequence 220, App	520	23	76.7	243	11	US-11-054-515-2012	Sequence 2012, Ap
448	24	80.0	3748	11	US-11-132-686-8	Sequence 8, Appl	521	23	76.7	243	11	US-11-054-515-2014	Sequence 2014, Ap
449	24	80.0	3749	11	US-11-132-686-6	Sequence 6, Appl	522	23	76.7	243	11	US-11-054-515-2063	Sequence 2063, Ap
450	24	80.0	3749	11	US-11-132-686-12	Sequence 12, Appl	523	23	76.7	243	11	US-11-054-515-2107	Sequence 2107, Ap
451	24	80.0	3912	11	US-11-132-686-7	Sequence 7, Appl	524	23	76.7	243	11	US-11-054-515-2109	Sequence 2109, Ap
452	24	80.0	3913	11	US-11-132-686-5	Sequence 5, Appl	525	23	76.7	243	11	US-11-266-444-2009	Sequence 2009, Ap
453	24	80.0	3913	11	US-11-132-686-9	Sequence 9, Appl	526	23	76.7	243	11	US-11-266-444-2012	Sequence 2012, Ap
454	23	76.7	9	9	US-10-530-061-195	Sequence 195, App	527	23	76.7	243	11	US-11-266-444-2014	Sequence 2014, Ap
455	23	76.7	9	9	US-10-530-061-992	Sequence 922, App	528	23	76.7	243	11	US-11-266-444-2063	Sequence 2063, Ap
456	23	76.7	9	9	US-10-530-061-923	Sequence 923, App	529	23	76.7	243	11	US-11-266-444-2107	Sequence 2107, Ap
457	23	76.7	10	9	US-10-880-238-36	Sequence 36, Appl	530	23	76.7	243	11	US-11-266-444-2109	Sequence 2109, Ap
458	23	76.7	10	9	US-10-880-238-39	Sequence 39, Appl	531	23	76.7	244	11	US-11-054-515-1908	Sequence 1908, Ap
459	23	76.7	10	11	US-11-171-567-111	Sequence 111, App	532	23	76.7	244	11	US-11-054-515-2011	Sequence 2011, Ap

533	23	76.7	244	11	US-11-054-515-2026	Sequence 2026, Ap	606	23	76.7	432	9	US-10-992-577-2	Sequence 2, Appl1
534	23	76.7	244	11	US-11-054-515-2037	Sequence 2037, Ap	607	23	76.7	432	11	US-11-223-292-37	Sequence 37, Appl1
535	23	76.7	244	11	US-11-266-444-1908	Sequence 1908, Ap	608	23	76.7	447	10	US-11-221-902-4	Sequence 4, Appl1
536	23	76.7	244	11	US-11-266-444-2011	Sequence 2011, Ap	609	23	76.7	447	10	US-11-221-902-6	Sequence 6, Appl1
537	23	76.7	244	11	US-11-266-444-2026	Sequence 2026, Ap	610	23	76.7	447	10	US-11-221-902-8	Sequence 8, Appl1
538	23	76.7	244	11	US-11-266-444-2037	Sequence 2037, Ap	611	23	76.7	447	10	US-11-221-902-10	Sequence 10, Appl1
539	23	76.7	245	11	US-11-054-515-1946	Sequence 1946, Ap	612	23	76.7	447	10	US-11-221-902-12	Sequence 12, Appl1
540	23	76.7	245	11	US-11-054-515-2004	Sequence 2004, Ap	613	23	76.7	447	10	US-11-221-902-84	Sequence 84, Appl1
541	23	76.7	245	11	US-11-054-515-2042	Sequence 2042, Ap	614	23	76.7	450	10	US-11-221-902-2	Sequence 2, Appl1
542	23	76.7	245	11	US-11-054-515-2116	Sequence 2116, Ap	615	23	76.7	459	11	US-11-079-603-5558	Sequence 5558, Ap
543	23	76.7	245	11	US-11-266-444-1946	Sequence 1946, Ap	616	23	76.7	482	11	US-11-045-004-854	Sequence 854, Ap
544	23	76.7	245	11	US-11-266-444-2004	Sequence 2004, Ap	617	23	76.7	488	9	US-10-016-686-3	Sequence 3, Appl1
545	23	76.7	245	11	US-11-266-444-2042	Sequence 2042, Ap	618	23	76.7	549	11	US-11-188-298-3355	Sequence 3355, Ap
546	23	76.7	245	11	US-11-266-444-2116	Sequence 2116, Ap	619	23	76.7	577	9	US-10-527-771-14	Sequence 14, Appl1
547	23	76.7	246	11	US-11-054-515-1638	Sequence 1638, Ap	620	23	76.7	574	11	US-11-124-3688-232	Sequence 232, App
548	23	76.7	246	11	US-11-266-444-1638	Sequence 1638, Ap	621	23	76.7	592	9	US-10-016-686-4	Sequence 4, Appl1
549	23	76.7	247	11	US-11-054-515-1899	Sequence 1899, Ap	622	23	76.7	602	11	US-11-079-463-6002	Sequence 6002, Ap
550	23	76.7	247	11	US-11-266-444-1899	Sequence 1899, Ap	623	23	76.7	619	11	US-11-098-686-10201	Sequence 10201, A
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552	23	76.7	248	11	US-11-054-515-2091	Sequence 2091, Ap	625	23	76.7	644	11	US-11-045-004-125	Sequence 125, App
553	23	76.7	248	11	US-11-266-444-2091	Sequence 959, App	626	23	76.7	671	11	US-11-202-5078-8	Sequence 8, Appl1
554	23	76.7	249	11	US-11-266-444-2091	Sequence 2091, Ap	627	23	76.7	671	11	US-11-202-5078-14	Sequence 14, Appl1
555	23	76.7	249	11	US-11-054-515-1635	Sequence 1635, Ap	628	23	76.7	672	11	US-11-202-5078-6	Sequence 6, Appl1
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566	23	76.7	251	11	US-11-266-444-945	Sequence 945, App	639	23	76.7	800	11	US-11-188-298-2496	Sequence 2496, Ap
567	23	76.7	251	11	US-11-266-444-1688	Sequence 1688, App	640	23	76.7	806	11	US-11-188-298-11019	Sequence 11019, A
568	23	76.7	251	11	US-11-266-444-1806	Sequence 1806, Ap	641	23	76.7	806	11	US-11-188-298-18451	Sequence 18451, A
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571	23	76.7	253	11	US-11-054-515-1359	Sequence 1359, Ap	644	23	76.7	860	11	US-11-188-298-11604	Sequence 11604, A
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574	23	76.7	255	11	US-11-266-444-2087	Sequence 2087, Ap	647	23	76.7	3353	11	US-11-037-243-64	Sequence 64, Appl1
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576	23	76.7	257	11	US-11-266-444-1640	Sequence 1640, Ap	649	23	76.7	3712	11	US-11-019-711-51	Sequence 51, Appl1
577	23	76.7	269	11	US-11-087-099-983	Sequence 983, App	650	22	73.3	5	9	US-10-932-334-1	Sequence 1, Appl1
578	23	76.7	269	11	US-11-224-726-1	Sequence 1, Appl1	651	22	73.3	5	11	US-11-173-071-5	Sequence 5, Appl1
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581	23	76.7	295	11	US-11-193-205-1	Sequence 1, Appl1	654	22	73.3	5	11	US-11-126-978-1	Sequence 1, Appl1
582	23	76.7	300	11	US-11-188-298-19027	Sequence 19027, A	655	22	73.3	5	11	US-11-177-648-1	Sequence 1, Appl1
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586	23	76.7	312	11	US-11-124-3678-514	Sequence 514, App	659	22	73.3	11	11	US-11-129-741-61	Sequence 416, App
587	23	76.7	312	11	US-11-079-463-7634	Sequence 7634, App	660	22	73.3	14	11	US-11-167-872-61	Sequence 49, Appl1
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597	23	76.7	388	11	US-11-172-740-2131	Sequence 2131, Ap	670	22	73.3	20	11	US-11-054-515-22914	Sequence 22914, Ap
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600	23	76.7	415	11	US-11-087-099-7779	Sequence 7779, App	673	22	73.3	20	11	US-11-247-423-96	Sequence 96, Appl1
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604	23	76.7	430	11	US-11-223-294-54	Sequence 54, Appl1	677	22	73.3	20	11	US-11-247-423-100	Sequence 100, App
605	23	76.7	430	11	US-11-087-099-5817	Sequence 5817, App	678	22	73.3	20	11	US-11-247-423-101	Sequence 101, App

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682	22	73.3	23	11	US-11-166-412-183	Sequence 183, App	755	22	73.3	111	11	US-11-097-812-34	Sequence 34, Appl
683	22	73.3	31	11	US-11-129-741-3671	Sequence 3671, Ap	756	22	73.3	111	11	US-11-097-812-36	Sequence 36, Appl
684	22	73.3	40	9	US-10-895-064-2528	Sequence 2528, Ap	757	22	73.3	111	11	US-11-097-812-106	Sequence 106, Appl
685	22	73.3	40	11	US-11-129-741-2528	Sequence 2528, Ap	758	22	73.3	111	11	US-11-097-812-115	Sequence 115, App
686	22	73.3	48	9	US-10-467-657-738	Sequence 738, App	759	22	73.3	111	11	US-11-097-812-205	Sequence 205, App
687	22	73.3	48	9	US-10-467-657-746	Sequence 746, App	760	22	73.3	111	11	US-11-216-813-77	Sequence 77, Appl
688	22	73.3	48	9	US-10-467-657-838	Sequence 838, App	761	22	73.3	113	11	US-11-156-084-172	Sequence 172, App
689	22	73.3	48	9	US-10-467-657-870	Sequence 870, App	762	22	73.3	113	11	US-11-177-648-7	Sequence 7, Appl1
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692	22	73.3	62	11	US-11-264-096-372	Sequence 372, App	765	22	73.3	113	11	US-11-177-648-13	Sequence 13, Appl
693	22	73.3	64	11	US-11-087-099-1171	Sequence 1171, Ap	766	22	73.3	113	11	US-11-177-648-14	Sequence 14, Appl
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703	22	73.3	95	11	US-11-054-669-91	Sequence 91, Appl	776	22	73.3	113	11	US-11-177-648-89	Sequence 89, Appl
704	22	73.3	95	11	US-11-054-669-92	Sequence 92, Appl	777	22	73.3	113	11	US-11-177-648-91	Sequence 91, Appl
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706	22	73.3	95	11	US-11-084-554-113	Sequence 113, App	779	22	73.3	116	11	US-11-096-046-3	Sequence 3, Appl1
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708	22	73.3	95	11	US-11-061-848-54	Sequence 54, Appl	781	22	73.3	117	11	US-11-004-590-228	Sequence 228, App
709	22	73.3	95	11	US-11-004-590-96	Sequence 96, Appl	782	22	73.3	117	11	US-11-259-232-48	Sequence 48, App
710	22	73.3	95	11	US-11-004-590-97	Sequence 97, Appl	783	22	73.3	117	11	US-11-259-232-49	Sequence 49, Appl
711	22	73.3	95	11	US-11-136-250-104	Sequence 104, App	784	22	73.3	117	11	US-11-126-798-48	Sequence 48, Appl
712	22	73.3	95	11	US-11-136-250-113	Sequence 113, App	785	22	73.3	118	11	US-11-126-798-49	Sequence 49, Appl
713	22	73.3	96	11	US-11-128-900-99	Sequence 99, Appl	786	22	73.3	118	11	US-11-079-463-6566	Sequence 6566, Ap
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715	22	73.3	98	11	US-11-054-669-33	Sequence 33, Appl	788	22	73.3	120	9	US-10-932-334-72	Sequence 72, Appl
716	22	73.3	98	11	US-11-084-554-47	Sequence 47, Appl	789	22	73.3	120	11	US-11-173-071-2	Sequence 2, Appl1
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718	22	73.3	98	11	US-11-136-250-47	Sequence 47, Appl	791	22	73.3	121	11	US-11-108-135-24	Sequence 24, Appl
719	22	73.3	101	11	US-11-049-536-34	Sequence 34, Appl	792	22	73.3	121	11	US-11-108-135-28	Sequence 28, Appl
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721	22	73.3	102	9	US-10-816-768-45	Sequence 45, Appl	794	22	73.3	121	11	US-11-126-978-28	Sequence 28, Appl
722	22	73.3	102	11	US-11-326-555-11	Sequence 11, Appl	795	22	73.3	122	9	US-10-932-334-73	Sequence 73, Appl
723	22	73.3	103	9	US-10-771-257-106	Sequence 106, App	796	22	73.3	123	9	US-10-932-334-87	Sequence 87, Appl
724	22	73.3	104	11	US-11-250-411-105	Sequence 105, App	797	22	73.3	123	9	US-10-932-334-88	Sequence 88, Appl
725	22	73.3	104	11	US-11-250-411-107	Sequence 107, App	798	22	73.3	123	9	US-10-932-334-92	Sequence 92, Appl
726	22	73.3	105	11	US-11-250-411-109	Sequence 109, App	799	22	73.3	123	9	US-10-793-626-56	Sequence 56, Appl
727	22	73.3	105	11	US-11-250-411-110	Sequence 110, App	800	22	73.3	124	9	US-10-932-334-7	Sequence 7, Appl1
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729	22	73.3	106	11	US-11-174-186-1	Sequence 1, Appl1	802	22	73.3	124	9	US-10-932-334-70	Sequence 70, Appl
730	22	73.3	106	11	US-11-174-186-8	Sequence 8, Appl1	803	22	73.3	125	9	US-10-469-469-32	Sequence 32, Appl
731	22	73.3	106	11	US-11-174-186-9	Sequence 9, Appl1	804	22	73.3	126	11	US-11-250-411-94	Sequence 94, Appl
732	22	73.3	106	11	US-11-174-186-10	Sequence 10, Appl	805	22	73.3	126	11	US-11-250-411-96	Sequence 96, Appl
733	22	73.3	106	11	US-11-174-186-11	Sequence 11, Appl	806	22	73.3	127	9	US-10-721-763-35	Sequence 35, Appl
734	22	73.3	106	11	US-11-174-186-12	Sequence 12, Appl	807	22	73.3	128	11	US-11-173-071-12	Sequence 12, Appl
735	22	73.3	106	11	US-11-174-186-13	Sequence 13, Appl	808	22	73.3	128	11	US-11-173-071-14	Sequence 14, Appl
736	22	73.3	106	11	US-11-174-186-14	Sequence 14, Appl	809	22	73.3	130	11	US-11-090-331-4	Sequence 4, Appl1
737	22	73.3	106	11	US-11-174-186-15	Sequence 15, Appl	810	22	73.3	130	11	US-11-072-512-3731	Sequence 3731, Ap
738	22	73.3	106	11	US-11-174-186-16	Sequence 16, Appl	811	22	73.3	135	11	US-11-859-232-37	Sequence 37, App
739	22	73.3	107	10	US-11-239-308-24	Sequence 24, Appl	812	22	73.3	136	9	US-10-644-807-234	Sequence 234, App
740	22	73.3	107	10	US-11-239-308-26	Sequence 26, Appl	813	22	73.3	138	11	US-11-090-331-8	Sequence 8, Appl1
741	22	73.3	107	11	US-11-004-590-236	Sequence 236, App	814	22	73.3	138	11	US-11-079-463-7376	Sequence 7376, Ap
742	22	73.3	108	11	US-11-102-512-53	Sequence 53, Appl	815	22	73.3	138	11	US-11-079-463-8678	Sequence 8678, Ap
743	22	73.3	108	11	US-11-221-811-45	Sequence 45, Appl	816	22	73.3	139	8	US-10-370-859-55	Sequence 55, Appl
744	22	73.3	110	11	US-11-097-812-96	Sequence 96, Appl	817	22	73.3	140	11	US-11-193-512-27	Sequence 27, Appl
745	22	73.3	110	11	US-11-097-812-98	Sequence 98, Appl	818	22	73.3	140	11	US-11-193-512-74	Sequence 74, Appl
746	22	73.3	110	11	US-11-097-812-114	Sequence 114, App	819	22	73.3	140	11	US-11-193-512-76	Sequence 76, Appl
747	22	73.3	110	11	US-11-097-812-172	Sequence 172, App	820	22	73.3	140	11	US-11-193-512-78	Sequence 78, Appl
748	22	73.3	111	10	US-11-219-563-77	Sequence 77, Appl	821	22	73.3	140	11	US-11-193-512-83	Sequence 83, Appl
749	22	73.3	111	10	US-11-097-812-17	Sequence 17, Appl	822	22	73.3	143	9	US-10-932-334-52	Sequence 52, Appl
750	22	73.3	111	11	US-11-097-812-20	Sequence 20, Appl	823	22	73.3	144	11	US-11-169-041-150	Sequence 150, App
751	22	73.3	111	11	US-11-097-812-21	Sequence 21, Appl	824	22	73.3	150	11	US-11-096-568A-24935	Sequence 24935, A

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826	22	73.3	155	11	US-11-128-900-20	Sequence 20, App	899	22	73.3	251	11	US-11-266-444-272	Sequence 272, App
827	22	73.3	155	11	US-11-128-900-112	Sequence 112, App	900	22	73.3	251	11	US-11-266-444-874	Sequence 874, App
828	22	73.3	156	11	US-11-096-568A-169	Sequence 169, App	901	22	73.3	251	11	US-11-266-444-876	Sequence 876, App
829	22	73.3	161	9	US-10-703-799B-22	Sequence 22, App	902	22	73.3	251	11	US-11-266-444-1046	Sequence 1046, App
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831	22	73.3	165	11	US-11-055-822-678	Sequence 678, App	904	22	73.3	251	11	US-11-266-444-1053	Sequence 1053, App
832	22	73.3	167	11	US-11-055-822-676	Sequence 676, App	905	22	73.3	251	11	US-11-266-444-1058	Sequence 1058, App
833	22	73.3	179	9	US-10-703-799B-20	Sequence 20, App	906	22	73.3	251	11	US-11-266-444-1060	Sequence 1060, App
834	22	73.3	187	9	US-10-506-454-610	Sequence 610, App	907	22	73.3	251	11	US-11-266-444-1061	Sequence 1061, App
835	22	73.3	187	11	US-11-096-568A-168	Sequence 168, App	908	22	73.3	251	11	US-11-266-444-1063	Sequence 1063, App
836	22	73.3	189	11	US-11-096-568A-1824	Sequence 1824, App	909	22	73.3	251	11	US-11-266-444-1066	Sequence 1066, App
837	22	73.3	192	11	US-11-096-568A-1697	Sequence 1697, App	910	22	73.3	251	11	US-11-266-444-1067	Sequence 1067, App
838	22	73.3	199	11	US-11-079-463-5975	Sequence 5975, App	911	22	73.3	251	11	US-11-266-444-1080	Sequence 1080, App
839	22	73.3	200	11	US-11-096-568A-784	Sequence 784, App	912	22	73.3	251	11	US-11-266-444-1081	Sequence 1081, App
840	22	73.3	201	11	US-11-096-568A-783	Sequence 783, App	913	22	73.3	251	11	US-11-266-444-1083	Sequence 1083, App
841	22	73.3	204	11	US-11-096-568A-13598	Sequence 13598, A	914	22	73.3	251	11	US-11-266-444-1083	Sequence 1083, App
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843	22	73.3	213	11	US-11-174-186-42	Sequence 42, App	916	22	73.3	252	11	US-11-096-568A-1822	Sequence 1822, App
844	22	73.3	213	11	US-11-102-621-118	Sequence 118, App	917	22	73.3	253	11	US-11-054-515-1418	Sequence 1418, App
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847	22	73.3	215	11	US-11-124-367A-381	Sequence 381, App	920	22	73.3	253	11	US-11-266-444-1418	Sequence 1418, App
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853	22	73.3	226	11	US-11-096-568A-782	Sequence 782, App	926	22	73.3	256	11	US-11-054-515-907	Sequence 907, App
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866	22	73.3	242	11	US-11-266-444-2099	Sequence 2099, App	939	22	73.3	275	11	US-11-096-568A-15197	Sequence 15197, A
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893	22	73.3	251	11	US-11-054-515-1081	Sequence 1081, App	966	22	73.3	315	11	US-11-087-099-7938	Sequence 7938, App
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974 22 73.3 320 11 US-11-112-882-76 Sequence 76, App
975 22 73.3 321 11 US-11-096-568A-7416 Sequence 7416, App
976 22 73.3 323 11 US-11-098-686-10185 Sequence 10185, A
977 22 73.3 324 11 US-11-151-762-5 Sequence 5, Appl
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979 22 73.3 325 11 US-11-079-463-7610 Sequence 7610, App
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983 22 73.3 336 11 US-11-096-568A-13596 Sequence 13596, A
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985 22 73.3 338 11 US-11-096-568A-3289 Sequence 3289, App
986 22 73.3 342 11 US-11-096-568A-7803 Sequence 7803, App
987 22 73.3 344 11 US-11-087-099-6760 Sequence 6760, App
988 22 73.3 345 11 US-11-079-463-5441 Sequence 5441, App
989 22 73.3 346 10 US-11-301-554-329 Sequence 329, App
990 22 73.3 346 11 US-11-186-284-189 Sequence 189, App
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992 22 73.3 346 11 US-11-054-281-96 Sequence 96, Appl
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994 22 73.3 348 11 US-11-054-281-69 Sequence 69, Appl
995 22 73.3 348 11 US-11-054-281-98 Sequence 98, Appl
996 22 73.3 348 11 US-11-054-281-99 Sequence 99, Appl
997 22 73.3 349 11 US-11-087-099-11339 Sequence 11339, A
998 22 73.3 349 11 US-11-086-568A-3288 Sequence 3288, App
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ALIGNMENTS

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RESULT 1
US-11-096-074-50
; Sequence 50, Application US/11096074
; Publication No. US20050260193A1
; GENERAL INFORMATION:
; APPLICANT: LIEBERBURG, IVAN
; TITLE OF INVENTION: STEROID SPARING AGENTS AND METHODS OF USING SAME
; FILE REFERENCE: 034008-112
; CURRENT APPLICATION NUMBER: US/11/096,074
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: 60/558,120
; PRIOR FILING DATE: 2004-04-01
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 50
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: humanized antibody
US-11-096-074-50
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Query Match 100.0%; Score 30; DB 11; Length 116;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy 1 SYTH 5
Db 31 SYTH 35
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US-11-095-822-50
; Sequence 50, Application US/11095822
; Publication No. US2006004019A1
; GENERAL INFORMATION:
; APPLICANT: LIEBERBURG, IVAN
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; TITLE OF INVENTION: STEROID SPARING AGENTS AND METHODS OF USING SAME
; FILE REFERENCE: 002010-872
; CURRENT APPLICATION NUMBER: US/11/095,822
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: 60/558,121
; PRIOR FILING DATE: 2004-04-01
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 50
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: humanized antibody
US-11-095-822-50
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Query Match 100.0%; Score 30; DB 11; Length 116;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy 1 SYTH 5
Db 31 SYTH 35
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RESULT 3
US-10-507-662-30
; Sequence 30, Application US/10507662
; Publication No. US20050255102A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; FILE REFERENCE: A136PCT
; CURRENT APPLICATION NUMBER: US/10/507,662
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: 60/364,991
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 60/426,286
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-507-662-30
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Query Match 100.0%; Score 30; DB 9; Length 118;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy 1 SYTH 5
Db 31 SYTH 35
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RESULT 4
US-10-507-662-31
; Sequence 31, Application US/10507662
; Publication No. US20050255102A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; FILE REFERENCE: A136PCT
; CURRENT APPLICATION NUMBER: US/10/507,662
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: 60/364,991
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 60/426,286
; PRIOR FILING DATE: 2002-11-13
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NUMBER OF SEQ ID NOS: 64
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 31
LENGTH: 118
TYPE: PRT
ORGANISM: Homo sapiens
US-10-507-662-31

Query Match 100.0%; Score 30; DB 9; Length 118;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
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DB 31 SYTH 35

RESULT 5
US-10-507-662-34
Sequence 34, Application US/10507662
Publication No. US20050255102A1
GENERAL INFORMATION:
APPLICANT: BIOGEN, INC.
TITLE OF INVENTION: ANTI-ALPHA-V BETA-6 ANTIBODIES
FILE REFERENCE: A136PCT
CURRENT APPLICATION NUMBER: US/10/507,662
CURRENT FILING DATE: 2004-09-13
PRIOR APPLICATION NUMBER: 60/364,991
PRIOR FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: 60/426,286
PRIOR FILING DATE: 2002-11-13
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 34
LENGTH: 118
TYPE: PRT
ORGANISM: Homo sapiens
US-10-507-662-34

Query Match 100.0%; Score 30; DB 9; Length 118;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
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DB 33 SYTH 37

RESULT 6
US-10-507-662-35
Sequence 35, Application US/10507662
Publication No. US20050255102A1
GENERAL INFORMATION:
APPLICANT: BIOGEN, INC.
TITLE OF INVENTION: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
FILE REFERENCE: A136PCT
CURRENT APPLICATION NUMBER: US/10/507,662
CURRENT FILING DATE: 2004-09-13
PRIOR APPLICATION NUMBER: 60/364,991
PRIOR FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: 60/426,286
PRIOR FILING DATE: 2002-11-13
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 35
LENGTH: 118
TYPE: PRT
ORGANISM: Homo sapiens
US-10-507-662-35

Query Match 100.0%; Score 30; DB 9; Length 118;

Best Local Similarity 100.0%; Pred. No. 28;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
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DB 31 SYTH 35

RESULT 7
US-10-507-662-36
Sequence 36, Application US/10507662
Publication No. US20050255102A1
GENERAL INFORMATION:
APPLICANT: BIOGEN, INC.
TITLE OF INVENTION: ANTI-ALPHA-V BETA-6 ANTIBODIES
FILE REFERENCE: A136PCT
CURRENT APPLICATION NUMBER: US/10/507,662
CURRENT FILING DATE: 2004-09-13
PRIOR APPLICATION NUMBER: 60/364,991
PRIOR FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: 60/426,286
PRIOR FILING DATE: 2002-11-13
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 36
LENGTH: 118
TYPE: PRT
ORGANISM: Homo sapiens
US-10-507-662-36

Query Match 100.0%; Score 30; DB 9; Length 118;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
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DB 31 SYTH 35

RESULT 8
US-10-946-836A-14
Sequence 14, Application US/10946836A
Publication No. US20060009382A1
GENERAL INFORMATION:
APPLICANT: Tegenero AG
APPLICANT: Hanke, Thomas
TITLE OF INVENTION: USE OF A CD28 BINDING PHARMACEUTICAL SUBSTANCE FOR MAKING A
FILE REFERENCE: 7003/25, TEG/US/0407
CURRENT APPLICATION NUMBER: US/10/946,836A
CURRENT FILING DATE: 2004-09-22
PRIOR APPLICATION NUMBER: DE 103 45 008.4
PRIOR FILING DATE: 2003-09-22
PRIOR APPLICATION NUMBER: DE 103 49 371.9
PRIOR FILING DATE: 2003-10-20
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn version 3.2
SEQ ID NO 14
LENGTH: 120
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: monoclonal antibody 5.11A partial sequence
US-10-946-836A-14

Query Match 100.0%; Score 30; DB 9; Length 120;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
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Db 31 SYTH 35

RESULT 9
US-10-946-836A-19
; Sequence 19, Application US/10946836A
; Publication No. US20060009382A1
; GENERAL INFORMATION:
; APPLICANT: Tegenero AG
; APPLICANT: Hanke, Thomas
; APPLICANT: Lin, Chia-Huey
; TITLE OF INVENTION: USE OF A CD28 BINDING PHARMACEUTICAL SUBSTANCE FOR MAKING A
; FILE REFERENCE: 7003/25 TEG/US/0407
; CURRENT APPLICATION NUMBER: US/10/946,836A
; CURRENT FILING DATE: 2004-09-22
; PRIOR APPLICATION NUMBER: DE 103 45 008.4
; PRIOR FILING DATE: 2003-09-22
; PRIOR APPLICATION NUMBER: DE 103 49 371.9
; PRIOR FILING DATE: 2003-10-20
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: monoclonal antibody 5.11A partial sequence
US-10-946-836A-19

Query Match 100.0%; Score 30; DB 9; Length 120;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
Db 31 SYTH 35

RESULT 10
US-10-988-207-14
; Sequence 14, Application US/10988207
; Publication No. US20060008457A1
; GENERAL INFORMATION:
; APPLICANT: Tegenero AG
; APPLICANT: Hanke, Thomas
; TITLE OF INVENTION: USE OF AN EFFECTIVE SUBSTANCE BINDING TO CD28 FOR PRODUCING A
; FILE REFERENCE: TEG/US/0409
; CURRENT APPLICATION NUMBER: US/10/988,207
; CURRENT FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: DE 103 52 900.4
; PRIOR FILING DATE: 2003-11-11
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: mab 5.11A partial sequence
US-10-988-207-14

Query Match 100.0%; Score 30; DB 9; Length 120;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
Db 31 SYTH 35

RESULT 11

US-10-988-207-19
; Sequence 19, Application US/10988207
; Publication No. US20060008457A1
; GENERAL INFORMATION:
; APPLICANT: Tegenero AG
; APPLICANT: Hanke, Thomas
; TITLE OF INVENTION: USE OF AN EFFECTIVE SUBSTANCE BINDING TO CD28 FOR PRODUCING A
; FILE REFERENCE: TEG/US/0409
; CURRENT APPLICATION NUMBER: US/10/988,207
; CURRENT FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: DE 103 52 900.4
; PRIOR FILING DATE: 2003-11-11
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: mab 5.11A partial sequence
US-10-988-207-19

Query Match 100.0%; Score 30; DB 9; Length 120;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
Db 31 SYTH 35

RESULT 12
US-10-988-207-26
; Sequence 26, Application US/10988207
; Publication No. US20060008457A1
; GENERAL INFORMATION:
; APPLICANT: Tegenero AG
; APPLICANT: Hanke, Thomas
; TITLE OF INVENTION: USE OF AN EFFECTIVE SUBSTANCE BINDING TO CD28 FOR PRODUCING A
; FILE REFERENCE: TEG/US/0409
; CURRENT APPLICATION NUMBER: US/10/988,207
; CURRENT FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: DE 103 52 900.4
; PRIOR FILING DATE: 2003-11-11
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: mab TGN1412 variable region heavy chain
US-10-988-207-26

Query Match 100.0%; Score 30; DB 9; Length 120;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
Db 31 SYTH 35

RESULT 13
US-11-054-515-2089
; Sequence 2089, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3

```

; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2089
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2089
```

```

Query Match          100.0%; Score 30; DB 11; Length 245;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 SYTH 5
        |||||
Db      31 SYTH 35
```

```

RESULT 14
US-11-266-444-2089
; Sequence 2089, Application US/11266444
; Publication No. US20060062789A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulat
; FILE REFERENCE: PF523P1D1
; CURRENT APPLICATION NUMBER: US/11/266,444
; CURRENT FILING DATE: 2005-11-04
; PRIOR APPLICATION NUMBER: 09/880,746
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2089
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-266-444-2089
```

```

Query Match          100.0%; Score 30; DB 11; Length 245;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy      1 SYTH 5
        |||||
Db      31 SYTH 35
```

```

RESULT 15
US-11-054-515-2090
; Sequence 2090, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2090
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2090
```

```

Query Match          100.0%; Score 30; DB 11; Length 258;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 SYTH 5
        |||||
Db      31 SYTH 35
```

```

RESULT 16
US-11-266-444-2090
; Sequence 2090, Application US/11266444
; Publication No. US20060062789A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulato
; FILE REFERENCE: PF523P1D1
; CURRENT APPLICATION NUMBER: US/11/266,444
; CURRENT FILING DATE: 2005-11-04
; PRIOR APPLICATION NUMBER: 09/880,746
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
```

;; PRIOR FILING DATE: 2001-05-25
;; NUMBER OF SEQ ID NOS: 3239
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 2090
;; LENGTH: 258
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-266-444-2090

Query Match 100.0%; Score 30; DB 11; Length 258;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
|||
Db 31 SYTH 35

RESULT 17
US-11-188-298-3002
; Sequence 3002, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 3002
; LENGTH: 774
; TYPE: PRT
; ORGANISM: Schizosaccharomyces pombe
US-11-188-298-3002

Query Match 100.0%; Score 30; DB 11; Length 774;
Best Local Similarity 100.0%; Pred. No. 1,5e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
|||
Db 668 SYTH 672

RESULT 18
US-10-895-064-1817
; Sequence 1817, Application US/10895064
; Publication No. US20060018923A1
; GENERAL INFORMATION:
; APPLICANT: PEIRIS, JOSEPH S.M.
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: GUAN, YI
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: NICHOLLS, JOHN M.
; APPLICANT: LEUNG, FREDERICK C.
; TITLE OF INVENTION: A NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT INFECTION AND USES
; FILE REFERENCE: V0690.0031
; CURRENT APPLICATION NUMBER: US/10/895,064
; CURRENT FILING DATE: 2004-07-21
; NUMBER OF SEQ ID NOS: 2918
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1817
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Corononavirius-HKU1
US-10-895-064-1817

Query Match 96.7%; Score 29; DB 9; Length 61;
Best Local Similarity 80.0%; Pred. No. 25;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 SYTH 5
|||
Db 26 SYTH 30

RESULT 19
US-11-129-741-1817
; Sequence 1817, Application US/11129741
; Publication No. US20060034853A1
; GENERAL INFORMATION:
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: MOO, CHIU YAT PATRICK
; APPLICANT: LAU, KAR PUI SUSANNA
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: PEIRIS, JOSEPH S.M.
; APPLICANT: GUAN, YI
; TITLE OF INVENTION: A NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT
; FILE REFERENCE: V0690.0044
; CURRENT APPLICATION NUMBER: US/11/129,741
; CURRENT FILING DATE: 2005-05-16
; PRIOR APPLICATION NUMBER: 10/895,064
; PRIOR FILING DATE: 2004-07-21
; NUMBER OF SEQ ID NOS: 4257
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1817
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Corononavirius-HKU1
US-11-129-741-1817

Query Match 96.7%; Score 29; DB 11; Length 61;
Best Local Similarity 80.0%; Pred. No. 25;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
|||
Db 26 SYTH 30

RESULT 20
US-11-054-515-1406
; Sequence 1406, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Bly5
; FILE REFERENCE: PFS23P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17

```
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1406
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1406
```

```
Query Match      96.7%; Score 29; DB 11; Length 243;
Best Local Similarity 80.0%; Pred. No. 85;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 SYTH 5
      |||:|
Db      31 SYTH 35
```

```
RESULT 21
US-11-266-444-1406
; Sequence 1406, Application US/11266444
; Publication No. US20060062789A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulat
```

```
; FILE REFERENCE: PF523P1D1
; CURRENT APPLICATION NUMBER: US/11/266,444
; PRIOR FILING DATE: 2005-11-04
; PRIOR APPLICATION NUMBER: 09/880,746
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patentn Ver. 2.0
; SEQ ID NO 1406.
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-266-444-1406
```

```
Query Match      96.7%; Score 29; DB 11; Length 243;
Best Local Similarity 80.0%; Pred. No. 85;
```

```
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 SYTH 5
      |||:|
Db      31 SYTH 35
```

```
RESULT 22
US-11-079-463-7470
; Sequence 7470, Application US/11079463
; Publication No. US20060073161A1
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES FRA
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: PATH00-03D1V2
; CURRENT APPLICATION NUMBER: US/11/079,463
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/128,705
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 09/540,209
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 10444
; SEQ ID NO 7470
```

```
; LENGTH: 244
; TYPE: PRT
; ORGANISM: B.fragilis
US-11-079-463-7470
```

```
Query Match      96.7%; Score 29; DB 11; Length 244;
Best Local Similarity 80.0%; Pred. No. 86;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 SYTH 5
      |||:|
Db      62 SYTH 66
```

```
RESULT 23
US-11-054-515-1384
; Sequence 1384, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
```

```
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1384
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1384
```

```
Query Match      96.7%; Score 29; DB 11; Length 247;
Best Local Similarity 80.0%; Pred. No. 86;
```

```
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 SYTH 5
      |||:|
Db      31 SYTH 35
```

```
RESULT 24
US-11-266-444-1384
; Sequence 1384, Application US/11266444
; Publication No. US20060062789A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulator
; FILE REFERENCE: PF523P1D1
; CURRENT APPLICATION NUMBER: US/11/266,444
; PRIOR FILING DATE: 2005-11-04
; PRIOR APPLICATION NUMBER: 09/880,746
; PRIOR FILING DATE: 2001-06-15
```

PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1384
LENGTH: 247
TYPE: PRT
ORGANISM: Homo sapiens
US-11-266-444-1384

Query Match 96.7%; Score 29; DB 11; Length 247;
Best Local Similarity 80.0%; Pred. No. 86;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYTH 5
|||:
Db 31 SYTH 35

RESULT 25
US-10-624-932-26
Sequence 26, Application US/10624932
Publication No. US20040096877A1
GENERAL INFORMATION:
APPLICANT: Taupier, Raymond
APPLICANT: Padigaru, Muralidhara
APPLICANT: Rastelli, Luca
APPLICANT: Spaderna, Steven
APPLICANT: Shinkets, Richard
APPLICANT: Zehusen, Bryan
APPLICANT: Spytek, Kimberly
APPLICANT: Shenoy, Suresh
APPLICANT: Li, Li
APPLICANT: Gusev, Vladimir
APPLICANT: Grose, William
APPLICANT: Alsobrook, John
APPLICANT: Lepley, Denise
APPLICANT: Burgess, Catherine
APPLICANT: Gerlach, Valerie
APPLICANT: Ellerman, Karen
APPLICANT: Macdougall, John
APPLICANT: Stone, David
APPLICANT: Smitheon, Glenda
TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-074 US
CURRENT APPLICATION NUMBER: US/10/624,932
CURRENT FILING DATE: 2003-07-21
PRIOR APPLICATION NUMBER: US/09/918,779
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/221,409
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/222,840
PRIOR FILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: 60/223,752
PRIOR FILING DATE: 2000-08-08
PRIOR APPLICATION NUMBER: 60/223,762
PRIOR FILING DATE: 2000-08-08
PRIOR APPLICATION NUMBER: 60/223,770
PRIOR FILING DATE: 2000-08-08
PRIOR APPLICATION NUMBER: 60/223,769
PRIOR FILING DATE: 2000-08-08
PRIOR APPLICATION NUMBER: 60/225,146
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/225,392
PRIOR FILING DATE: 2000-08-15

PRIOR APPLICATION NUMBER: 60/225,470
PRIOR FILING DATE: 2000-08-15
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 26
LENGTH: 1210
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1185)
OTHER INFORMATION: wherein Xaa is any amino acid as defined in the
OTHER INFORMATION: specification
US-10-624-932-26

Query Match 96.7%; Score 29; DB 9; Length 1210;
Best Local Similarity 80.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYTH 5
|||:
Db 617 SYTH 621

RESULT 26
US-11-039-398-14
Sequence 14, Application US/11039398
Publication No. US20050267297A1
GENERAL INFORMATION:
APPLICANT: Friddle, Carl Johan
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Hilbun, D. Wade
APPLICANT: Hilbun, Erin
APPLICANT: Nepomichny, Boris
TITLE OF INVENTION: Novel Human Proteases and
FILE REFERENCE: LEX-0221-USA
CURRENT APPLICATION NUMBER: US/11/039,398
CURRENT FILING DATE: 2005-01-20
PRIOR APPLICATION NUMBER: US/09/938,330
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: US 60/227,104
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: US 60/233,796
PRIOR FILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14
LENGTH: 1213
TYPE: PRT
ORGANISM: homo sapiens
US-11-039-398-14
Query Match 96.7%; Score 29; DB 11; Length 1213;
Best Local Similarity 80.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYTH 5
|||:
Db 623 SYTH 627

RESULT 27
US-11-039-398-12
Sequence 12, Application US/11039398
Publication No. US20050267297A1
GENERAL INFORMATION:
APPLICANT: Friddle, Carl Johan
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Walke, D. Wade
APPLICANT: Hilbun, Erin


```
; APPLICANT: Nepomichy, Boris
; APPLICANT: Hu, Yi
; TITLE OF INVENTION: Novel Human Proteases and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0221-USA
; CURRENT APPLICATION NUMBER: US/11/039,398
; CURRENT FILING DATE: 2005-01-20
; PRIOR APPLICATION NUMBER: US/09/938,330
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US 60/227,104
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 60/233,796
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 1216
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-039-398-12
```

```
Query Match          96.7%; Score 29; DB 11; Length 1216;
Best Local Similarity 80.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 SYTH 5
        |||:|
Db      623 SYTH 627
```

```
RESULT 28
US-11-039-398-10
; Sequence 10, Application US/11039398
; Publication No. US20050267297A1
; GENERAL INFORMATION:
; APPLICANT: Friddle, Carl Johan
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Walke, D. Wade
; APPLICANT: Hilbun, Erin
; APPLICANT: Nepomichy, Boris
; APPLICANT: Hu, Yi
; TITLE OF INVENTION: Novel Human Proteases and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0221-USA
; CURRENT APPLICATION NUMBER: US/11/039,398
; CURRENT FILING DATE: 2005-01-20
; PRIOR APPLICATION NUMBER: US/09/938,330
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US 60/227,104
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 60/233,796
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 1219
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-039-398-10
```

```
Query Match          96.7%; Score 29; DB 11; Length 1219;
Best Local Similarity 80.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 SYTH 5
        |||:|
Db      623 SYTH 627
```

```
RESULT 29
US-11-039-398-8
; Sequence 8, Application US/11039398
; Publication No. US20050267297A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Friddle, Carl Johan
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Walke, D. Wade
; APPLICANT: Hilbun, Erin
; APPLICANT: Nepomichy, Boris
; APPLICANT: Hu, Yi
; TITLE OF INVENTION: Novel Human Proteases and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0221-USA
; CURRENT APPLICATION NUMBER: US/11/039,398
; CURRENT FILING DATE: 2005-01-20
; PRIOR APPLICATION NUMBER: US/09/938,330
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US 60/227,104
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 60/233,796
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 1222
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-039-398-8
```

```
Query Match          96.7%; Score 29; DB 11; Length 1222;
Best Local Similarity 80.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 SYTH 5
        |||:|
Db      623 SYTH 627
```

```
RESULT 30
US-11-039-398-18
; Sequence 18, Application US/11039398
; Publication No. US20050267297A1
; GENERAL INFORMATION:
; APPLICANT: Friddle, Carl Johan
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Walke, D. Wade
; APPLICANT: Hilbun, Erin
; APPLICANT: Nepomichy, Boris
; APPLICANT: Hu, Yi
; TITLE OF INVENTION: Novel Human Proteases and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0221-USA
; CURRENT APPLICATION NUMBER: US/11/039,398
; CURRENT FILING DATE: 2005-01-20
; PRIOR APPLICATION NUMBER: US/09/938,330
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US 60/227,104
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 60/233,796
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 1232
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-039-398-18
```

```
Query Match          96.7%; Score 29; DB 11; Length 1232;
Best Local Similarity 80.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 SYTH 5
        |||:|
Db      623 SYTH 627
```

```
RESULT 31
US-11-039-398-16
; Sequence 16, Application US/11039398
; Publication No. US20050267297A1
; GENERAL INFORMATION:
; APPLICANT: Friddele, Carl Johan
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Walke, D. Wade
; APPLICANT: Hilbun, Erin
; APPLICANT: Nepomnichy, Boris
; APPLICANT: Hu, Yi
; TITLE OF INVENTION: Novel Human Proteases and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0221-USA
; CURRENT APPLICATION NUMBER: US/11/039,398
; CURRENT FILING DATE: 2005-01-20
; PRIOR APPLICATION NUMBER: US/09/938,330
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US 60/227,104
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 60/233,796
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 1235
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-039-398-16
```

```
Query Match          96.7%; Score 29; DB 11; Length 1235;
Best Local Similarity 80.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 SYTH 5
Db 623 SYTH 627

RESULT 32
US-11-039-398-22
; Sequence 22, Application US/11039398
; Publication No. US20050267297A1
; GENERAL INFORMATION:
; APPLICANT: Friddele, Carl Johan
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Walke, D. Wade
; APPLICANT: Hilbun, Erin
; APPLICANT: Nepomnichy, Boris
; APPLICANT: Hu, Yi
; TITLE OF INVENTION: Novel Human Proteases and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0221-USA
; CURRENT APPLICATION NUMBER: US/11/039,398
; CURRENT FILING DATE: 2005-01-20
; PRIOR APPLICATION NUMBER: US/09/938,330
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US 60/227,104
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 60/233,796
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 1249
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-039-398-22
```

```
Query Match          96.7%; Score 29; DB 11; Length 1249;
Best Local Similarity 80.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 SYTH 5
Db 623 SYTH 627
```

```
RESULT 33
US-11-039-398-20
; Sequence 20, Application US/11039398
; Publication No. US20050267297A1
; GENERAL INFORMATION:
; APPLICANT: Friddele, Carl Johan
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Walke, D. Wade
; APPLICANT: Hilbun, Erin
; APPLICANT: Nepomnichy, Boris
; APPLICANT: Hu, Yi
; TITLE OF INVENTION: Novel Human Proteases and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0221-USA
; CURRENT APPLICATION NUMBER: US/11/039,398
; CURRENT FILING DATE: 2005-01-20
; PRIOR APPLICATION NUMBER: US/09/938,330
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US 60/227,104
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 60/233,796
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 1252
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-039-398-20
```

```
Query Match          96.7%; Score 29; DB 11; Length 1252;
Best Local Similarity 80.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 SYTH 5
Db 623 SYTH 627
```

```
RESULT 34
US-11-096-568A-4404
; Sequence 4404, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Theby2
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 4404
; LENGTH: 62
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(62)
; OTHER INFORMATION: Ceres Seq. ID no. 13637456
US-11-096-568A-4404
```

```
Query Match          93.3%; Score 28; DB 11; Length 62;
Best Local Similarity 80.0%; Pred. No. 39;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 SYTH 5
Db 623 SYTH 627
```

Db 28 SYTIL 32

RESULT 35

US-11-096-568A-4402
; Sequence 4402, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 4402
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(74)
; OTHER INFORMATION: Ceres Seq. ID no. 13637454
US-11-096-568A-4402

Query Match 93.3%; Score 28; DB 11; Length 74;

Best Local Similarity 80.0%; Pred. No. 46;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTIL 5

Db 40 SYTIL 44

RESULT 36

US-10-507-662-32
; Sequence 32, Application US/10507662
; Publication No. US20050255102A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; FILE REFERENCE: A136PCT
; CURRENT APPLICATION NUMBER: US/10/507,662
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: 60/364,991
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 60/426,286
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-507-662-32

Query Match 93.3%; Score 28; DB 9; Length 118;

Best Local Similarity 80.0%; Pred. No. 70;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTIL 5

Db 31 SYTIL 35

RESULT 37

US-10-507-662-33
; Sequence 33, Application US/10507662
; Publication No. US20050255102A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA

; TITLE OF INVENTION: ANTI-ALPHA-V BETA-6 ANTIBODIES

; FILE REFERENCE: A136PCT
; CURRENT APPLICATION NUMBER: US/10/507,662
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: 60/364,991
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 60/426,286
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-507-662-33

Query Match 93.3%; Score 28; DB 9; Length 118;

Best Local Similarity 80.0%; Pred. No. 70;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTIL 5

Db 31 SYTIL 35

RESULT 38

US-11-054-515-1967
; Sequence 1967, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunologically Bind Blys
; FILE REFERENCE: P523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1967
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1967

Query Match 93.3%; Score 28; DB 11; Length 256;

Best Local Similarity 80.0%; Pred. No. 1,440;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTIL 5

Db 31 SYTIL 35

RESULT 39

US-11-054-515-1967
; Sequence 1967, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunologically Bind Blys
; FILE REFERENCE: P523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1967
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1967

Query Match 93.3%; Score 28; DB 11; Length 256;

Best Local Similarity 80.0%; Pred. No. 1,440;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTIL 5

Db 31 SYTIL 35

US-11-266-444-1967
; Sequence 1967, Application US/11266444
; Publication No. US2006062789A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that immunospecifically bind to B lymphocyte stimulac
; FILE REFERENCE: P5523P1D1
; CURRENT APPLICATION NUMBER: US/11/266,444
; CURRENT FILING DATE: 2005-11-04
; PRIOR APPLICATION NUMBER: 09/880,746
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1967
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-266-444-1967

Query Match 93.3%; Score 28; DB 11; Length 256;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYTH 5
|||:
Db 31 SYTH 35

RESULT 40
US-10-467-657-8598
; Sequence 8598, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 8598
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8598

Query Match 93.3%; Score 28; DB 9; Length 288;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYTH 5
|||:
Db 149 SYTH 153

RESULT 41
US-10-510-229-86

; Sequence 86, Application US/10510229
; Publication No. US20060083735A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Yoram
; APPLICANT: Cohen, Cyril J.
; TITLE OF INVENTION: ANTIGEN-PRESENTING COMPLEX-BINDING COMPOSITIONS AND USES THEREOF
; FILE REFERENCE: 28429
; CURRENT APPLICATION NUMBER: US/10/510,229
; CURRENT FILING DATE: 2004-10-13
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 86
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURES:
; OTHER INFORMATION: Sequence of complementarity determining region of Fab
US-10-510-229-86

Query Match 90.0%; Score 27; DB 9; Length 5;
Best Local Similarity 80.0%; Pred. No. 1.9e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYTH 5
|||:
Db 1 SYTH 5

RESULT 42
US-11-125-837-10
; Sequence 10, Application US/11125837
; Publication No. US20050266003A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Kong-Hwa
; APPLICANT: Chang, Chung Nan
; APPLICANT: Chen, Pei-Jiun
; APPLICANT: Huang, Chiu-Chen
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 13062-011001
; CURRENT APPLICATION NUMBER: US/11/125,837
; CURRENT FILING DATE: 2005-05-10
; PRIOR APPLICATION NUMBER: US 60/569,892
; PRIOR FILING DATE: 2004-05-10
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-125-837-10

Query Match 90.0%; Score 27; DB 11; Length 5;
Best Local Similarity 80.0%; Pred. No. 1.9e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYTH 5
|||:
Db 1 SYTH 5

RESULT 43
US-11-201-825-34
; Sequence 34, Application US/11201825
; Publication No. US20060034831A1
; GENERAL INFORMATION:
; APPLICANT: TOBIN, JAMES F.
; TITLE OF INVENTION: COMBINATION THERAPY FOR DIABETES, OBESITY, AND
; TITLE OF INVENTION: CARDIOVASCULAR DISEASES USING GDF-8 INHIBITORS
; FILE REFERENCE: 08702.0106-00000
; CURRENT APPLICATION NUMBER: US/11/201,825
; CURRENT FILING DATE: 2005-08-11
; PRIOR APPLICATION NUMBER: 60/600,784

;; PRIOR FILING DATE: 2004-08-12
;; NUMBER OF SEQ ID NOS: 77
;; SOFTWARE: PatentIn Ver. 3.2
;; SEQ ID NO 34
;; LENGTH: 5
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-201-825-34

Query Match 90.0%; Score 27; DB 11; Length 5;
Best Local Similarity 80.0%; Pred. No. 1.9e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
 :||||
Db 6 AYYH 10

RESULT 44
US-11-194-989-3
; Sequence 3, Application US/1194989
; Publication No. US20060057701A1
; GENERAL INFORMATION:
; APPLICANT: ROSENTHAL, Arnon
; APPLICANT: PONS, Jaume
; APPLICANT: HO, Wei-Hsien
; APPLICANT: GRIMM, Jan Markus
; TITLE OF INVENTION: ANTIBODIES DIRECTED AGAINST AMYLOID-BETA
; TITLE OF INVENTION: PEPTIDE AND METHODS USING SAME
; FILE REFERENCE: 514712002300
; CURRENT APPLICATION NUMBER: US/11/194,989
; PRIOR FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US 60/676,093
; PRIOR FILING DATE: 2005-04-29
; PRIOR APPLICATION NUMBER: US 60/653,197
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: US 60/592,494
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-11-194-989-3

Query Match 90.0%; Score 27; DB 11; Length 10;
Best Local Similarity 80.0%; Pred. No. 12;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
 :||||
Db 6 AYYH 10

RESULT 45
US-11-195-207-3
; Sequence 3, Application US/1195207
; Publication No. US20060057702A1
; GENERAL INFORMATION:
; APPLICANT: ROSENTHAL, Arnon
; APPLICANT: PONS, Jaume
; APPLICANT: HO, Wei-Hsien
; APPLICANT: GRIMM, Jan Markus
; TITLE OF INVENTION: ANTIBODIES DIRECTED AGAINST AMYLOID-BETA
; FILE REFERENCE: 514712002301
; CURRENT APPLICATION NUMBER: US/11/195,207
; PRIOR FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US 60/676,093
; PRIOR FILING DATE: 2005-04-29

;; PRIOR APPLICATION NUMBER: US 60/653,197
;; PRIOR FILING DATE: 2005-02-14
;; PRIOR APPLICATION NUMBER: US 60/592,494
;; PRIOR FILING DATE: 2004-07-30
;; NUMBER OF SEQ ID NOS: 53
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 3
;; LENGTH: 10
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Synthetic construct
US-11-195-207-3

Query Match 90.0%; Score 27; DB 11; Length 10;
Best Local Similarity 80.0%; Pred. No. 12;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
 :||||
Db 6 AYYH 10

RESULT 46
US-11-004-399-2005
; Sequence 2005, Application US/11004399
; Publication No. US20060053516A1
; GENERAL INFORMATION:
; APPLICANT: Chye, Mee Lee
; APPLICANT: Li, Hong Ye
; APPLICANT: Ramalingam, Sathiskumar
; APPLICANT: Poon, Leo Lit Man
; APPLICANT: Peiris, Joseph Sriyal Malik
; TITLE OF INVENTION: Genetically Modified Plants Comprising SARS-CoV Viral Nucleotide
; FILE REFERENCE: 2587/73166/RDK
; CURRENT APPLICATION NUMBER: US/11/004,399
; PRIOR FILING DATE: 2004-12-03
; PRIOR APPLICATION NUMBER: US 60/527,637
; PRIOR FILING DATE: 2003-12-03
; NUMBER OF SEQ ID NOS: 4043
; SOFTWARE: PatentIn Version 3.1
; SEQ ID NO 2005
; LENGTH: 31
; TYPE: PRT
; ORGANISM: SARS-CoV Virus
US-11-004-399-2005

Query Match 90.0%; Score 27; DB 11; Length 31;
Best Local Similarity 80.0%; Pred. No. 33;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTH 5
 :||||
Db 6 SYWH 10

RESULT 47
US-11-221-902-58
; Sequence 58, Application US/11221902
; Publication No. US20060088522A1
; GENERAL INFORMATION:
; APPLICANT: Myeth
; TITLE OF INVENTION: HUMANIZED ANTI-574 ANTIBODIES AND ANTI-574/CALICHEAMICIN CONUGATE
; FILE REFERENCE: 040000-0317285
; CURRENT APPLICATION NUMBER: US/11/221,902
; PRIOR FILING DATE: 2005-09-09
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Version 3.3
; SEQ ID NO 58
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens

US-11-221-902-58

Query Match 90.0%; Score 27; DB 10; Length 98;
Best Local Similarity 80.0%; Pred. No. 94;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYTH 5
|||:
Db 31 SYTH 35

RESULT 48

US-11-054-669-7
; Sequence 7, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
; FILE REFERENCE: 30219/US/3
; CURRENT APPLICATION NUMBER: US/11/054,669
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 10/194,975
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-669-7

Query Match 90.0%; Score 27; DB 11; Length 98;
Best Local Similarity 80.0%; Pred. No. 94;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYTH 5
|||:
Db 31 SYTH 35

RESULT 49

US-11-084-554-20
; Sequence 20, Application US/11084554
; Publication No. US20050260679A1
; GENERAL INFORMATION:
; APPLICANT: Kelleman, Sirid-Ai
; APPLICANT: Green, Larry L.
; APPLICANT: Korver, Wouter
; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
; FILE REFERENCE: AGENIX.100A
; CURRENT APPLICATION NUMBER: US/11/084,554
; CURRENT FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: 60/554,372
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/574,661
; PRIOR FILING DATE: 2004-05-24
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-084-554-20

Query Match 90.0%; Score 27; DB 11; Length 98;
Best Local Similarity 80.0%; Pred. No. 94;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYTH 5
|||:
Db 31 SYTH 35

Db 31 SYTH 35

RESULT 50
US-11-004-590-7
; Sequence 7, Application US/11004590
; Publication No. US2006000883A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; APPLICANT: Desjarlais, John R.
; APPLICANT: Hammond, Phillip W.
; TITLE OF INVENTION: METHODS OF GENERATING VARIANT PROTEINS WITH INCREASED HOST STRING
; CONTENT AND COMPOSITIONS THEREOF
; FILE REFERENCE: 185832/US/5
; CURRENT APPLICATION NUMBER: US/11/004,590
; CURRENT FILING DATE: 2004-12-03
; PRIOR APPLICATION NUMBER: US 60/527,167
; PRIOR FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: US 60/581,613
; PRIOR FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US 60/601,665
; PRIOR FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: US 60/619,483
; PRIOR FILING DATE: 2004-10-14
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-004-590-7

Query Match 90.0%; Score 27; DB 11; Length 98;
Best Local Similarity 80.0%; Pred. No. 94;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYTH 5
|||:
Db 31 SYTH 35

Search completed: May 4, 2006, 13:54:27
Job time : 10.7937 secs

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OM protein - protein search, using sw model

Run on: May 4, 2006, 12:46:10 ; Search time 151.111 Seconds
(without alignments)
49.430 Million cell updates/sec

Title: US-10-700-632-2

Perfect score: 89

Sequence: 1 VIYPGNDISYNOKFXG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_21:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	88	98.9	17	8	AD032141 Mouse ant
2	88	98.9	17	8	AD032086 Mouse ant
3	88	98.9	117	8	AD032157 Mouse ant
4	88	98.9	118	8	AD032091 Mouse ant
5	88	98.9	118	8	AD032093 Humanised
6	73	82.0	17	3	AAV80140 Chimeric
7	73	82.0	17	3	AAV80140 Chimeric
8	73	82.0	17	4	AAO14423 Human CDR
9	73	82.0	17	6	ABH82655 CDR2 frag
10	73	82.0	106	2	AAV91365 Anti-proc
11	73	82.0	114	8	AD032164 Mouse ant
12	73	82.0	116	2	AAV64224 Anti-(6-4
13	73	82.0	127	9	AAE88769 Murine SA
14	73	82.0	136	2	AAV14153 Ig heavy
15	73	82.0	219	7	AD079230 OC125-3.1
16	73	82.0	248	7	AD032327 Mouse scf
17	73	82.0	615	7	AD032341 Fusion pr
18	72	80.9	17	7	AD066265 Mouse pro
19	72	80.9	17	8	ADP94575 Humanised
20	72	80.9	17	8	ADP79604 Murine 2H
21	72	80.9	17	8	ADH80237 CD20 bind
22	72	80.9	17	8	ADW47106 Anti-CD20
23	72	80.9	17	9	ADW21313 Mouse ant
24	72	80.9	120	7	ADJ94601 Mouse ant

25	72	80.9	121	7	ADJ94605 Chimeric
26	72	80.9	121	7	ADJ94609 Humanised
27	72	80.9	121	7	ADJ94608 Humanised
28	72	80.9	121	7	ADJ94607 Chimeric
29	72	80.9	121	9	ADW03412 Murine an
30	72	80.9	121	9	ADJ16288 Vhd antib
31	72	80.9	121	9	ADJ16286 2B8 antib
32	72	80.9	121	9	ADJ16329 Modified
33	72	80.9	121	9	ADJ16287 Vhc antib
34	72	80.9	122	6	AAO27203 Chimeric
35	72	80.9	122	8	ADP79573 Murine 2H
36	72	80.9	122	8	ADP79574 Humanised
37	72	80.9	122	8	ADJ33302 Anti-CD20
38	72	80.9	122	9	ADV21492 Human ant
39	72	80.9	122	9	ADW03408 Humanised
40	72	80.9	122	9	ADW21310 Mouse ant
41	72	80.9	122	9	ADW21309 Mouse ant
42	72	80.9	122	9	ADX00803 Humanized
43	72	80.9	122	9	ADY21867 Human ant
44	72	80.9	122	9	ADJ16331 Modified
45	72	80.9	122	9	ADJ16294 Lue16 ant
46	72	80.9	122	9	ADJ16295 Vhy light
47	72	80.9	122	9	ADY62623 Humanized
48	72	80.9	122	9	ADZ83548 CD20 VH
49	72	80.9	122	9	ADZ83548 Humanized
50	72	80.9	122	9	ADZ83548 Humanized
51	72	80.9	123	6	AAO27195 Chimeric
52	72	80.9	123	6	AAO27201 Murine an
53	72	80.9	123	9	ADW47048 Heavy cha
54	72	80.9	123	9	ADW47042 Heavy cha
55	72	80.9	140	1	ADP94780 2 H7 VH g
56	72	80.9	140	2	AAV55215 Murine va
57	72	80.9	140	2	AAW10242 Heavy cha
58	72	80.9	140	2	AAW10588 2H7 antib
59	72	80.9	140	2	AAW16343 2H7 heavy
60	72	80.9	140	2	AAW89540 Mouse ant
61	72	80.9	140	4	AAV98092 2H7 heavy
62	72	80.9	140	6	ABR55873 Anti-CD20
63	72	80.9	140	6	ABU08394 Murine ant
64	72	80.9	140	7	AD066270 Mouse ant
65	72	80.9	140	7	AD065027 Immunoglo
66	72	80.9	140	7	AD085690 Murine im
67	72	80.9	140	7	AD073084 Murine FU
68	72	80.9	140	7	AD060661 Protein r
69	72	80.9	140	7	ADJ94616 Human ant
70	72	80.9	140	7	ADJ94618 Human ant
71	72	80.9	140	8	ADN49734 Mature va
72	72	80.9	140	8	ADU74410 Mouse ant
73	72	80.9	140	9	ADV92492 2B8 heavy
74	72	80.9	140	9	ADV92492 Novel chi
75	72	80.9	140	9	ADV92492 Novel chi
76	72	80.9	253	8	ADP79580 Chimeric
77	72	80.9	266	5	ADG31021 Mouse sin
78	72	80.9	266	7	AD025450 Binding d
79	72	80.9	266	7	AD042725 Synthetic
80	72	80.9	266	9	ADP95393 Mouse 2H7
81	72	80.9	266	9	ADP94427 Mouse ant
82	72	80.9	267	9	ADY21839 Human ant
83	72	80.9	268	9	ADY21859 Human ant
84	72	80.9	268	9	ADY21861 Human ant
85	72	80.9	268	9	ADY21869 Human ant
86	72	80.9	268	9	ADY21837 Human ant
87	72	80.9	360	5	AAE27924 Human CH2
88	72	80.9	360	6	ABH82833 Antibody
89	72	80.9	368	9	ADW77074 Heavy cha
90	72	80.9	412	4	AAV30694 A fusion
91	72	80.9	412	6	ABJ39009 B9E9 scFv
92	72	80.9	422	5	ABG31032 Synthetic
93	72	80.9	422	7	AD025591 Binding d
94	72	80.9	422	7	ADD25473 Binding d
95	72	80.9	422	7	ADW42748 2H7scFV-C
96	72	80.9	422	9	ABE95416 Mouse 2H7
97	72	80.9	422	9	ABE94450 Mouse ant

98	72	80.9	423	4	AB30695	AB30695 A fusion	171	72	80.9	500	9	ADY21783	ADY21783 Antibody
99	72	80.9	423	6	AB39010	Abj39010 B99 scFv	172	72	80.9	500	9	ADY21891	ADY21891 Antibody
100	72	80.9	426	9	ADY22144	Ady22144 Antibody	173	72	80.9	500	9	ADY21764	ADY21764 Antibody
101	72	80.9	426	9	AB95423	Aeb95423 Mouse 2H7	174	72	80.9	500	9	ADY21793	ADY21793 Antibody
102	72	80.9	426	9	AB94457	Aeb94457 Mouse ant	175	72	80.9	500	9	ADY21915	ADY21915 Antibody
103	72	80.9	451	8	ADL92472	Adl92472 Antibody	176	72	80.9	500	9	ADY21997	ADY21997 Antibody
104	72	80.9	451	8	ADL92473	Adl92473 Improved	177	72	80.9	500	9	ADY21787	ADY21787 Antibody
105	72	80.9	451	8	ADU68155	Adu68155 Novel var	178	72	80.9	500	9	ADY21931	ADY21931 Antibody
106	72	80.9	451	8	ADU68154	Adu68154 Novel var	179	72	80.9	500	9	ADY21993	ADY21993 Antibody
107	72	80.9	452	8	ADS33304	AdS33304 Anti-CD20	180	72	80.9	500	9	ADY21683	ADY21683 Antibody
108	72	80.9	452	8	ADM03410	AdM03410 Humanized	181	72	80.9	500	9	ADY21785	ADY21785 Antibody
109	72	80.9	452	9	ADM03411	AdM03411 Humanized	182	72	80.9	500	9	ADY21789	ADY21789 Antibody
110	72	80.9	452	9	ABE27728	Aeb27728 Humanized	183	72	80.9	500	9	ADY21653	ADY21653 Antibody
111	72	80.9	452	9	ABE17638	Aeb17638 Heavy cha	184	72	80.9	500	9	ADY21933	ADY21933 Antibody
112	72	80.9	470	3	AB08026	Aab08026 A dimeric	185	72	80.9	500	9	ADY21760	ADY21760 Antibody
113	72	80.9	470	5	AAE27923	Aae27923 Human C2B	186	72	80.9	500	9	ADY21781	ADY21781 Antibody
114	72	80.9	470	6	ABE82832	AbE82832 Antibody	187	72	80.9	500	9	ADY21791	ADY21791 Antibody
115	72	80.9	470	6	ADV92496	Adv92496 Anti-CD20	188	72	80.9	500	9	ADY21871	ADY21871 Antibody
116	72	80.9	470	8	ADV98559	Adv98559 Novel chi	189	72	80.9	500	9	ADY21889	ADY21889 Antibody
117	72	80.9	471	8	ADP79584	Adp79584 2H7 v16 H	190	72	80.9	500	9	ADY21909	ADY21909 Antibody
118	72	80.9	471	8	ADP79585	Adp79585 2H7 v31 L	191	72	80.9	500	9	ADY21917	ADY21917 Antibody
119	72	80.9	471	8	ADM03399	AdM03399 Human ant	192	72	80.9	500	9	ADY21925	ADY21925 Antibody
120	72	80.9	471	9	ADM03406	AdM03406 Human ant	193	72	80.9	500	9	ADY21901	ADY21901 Antibody
121	72	80.9	471	9	ADM21319	AdM21319 Mouse ant	194	72	80.9	500	9	ADY21995	ADY21995 Antibody
122	72	80.9	471	9	ADM21320	AdM21320 Mouse ant	195	72	80.9	500	9	ADY21893	ADY21893 Antibody
123	72	80.9	471	9	ADX00805	AdX00805 Humanized	196	72	80.9	500	9	ADY21762	ADY21762 Antibody
124	72	80.9	471	9	ADY62625	AdY62625 Humanized	197	72	80.9	500	9	ADY21756	ADY21756 Antibody
125	72	80.9	482	5	ABG31031	Abg31031 Synthetic	198	72	80.9	500	9	ADY21755	ADY21755 Antibody
126	72	80.9	482	7	ADD25472	Add25472 Binding d	199	72	80.9	500	9	ADY21923	ADY21923 Antibody
127	72	80.9	482	7	ADD25589	Add25589 Binding d	200	72	80.9	500	9	ADY21779	ADY21779 Antibody
128	72	80.9	482	7	ADM42747	Adm42747 2H7-CD154	201	72	80.9	500	9	ADY21907	ADY21907 Antibody
129	72	80.9	482	7	ABE95415	Aeb95415 Mouse 2H7	202	72	80.9	501	9	ADY21855	ADY21855 Antibody
130	72	80.9	482	9	ABE94449	Aeb94449 Mouse ant	203	72	80.9	501	9	ADY21853	ADY21853 Antibody
131	72	80.9	486	9	ADY22142	Ady22142 Antibody	204	72	80.9	502	7	ADD25744	ADD25744 Antibody
132	72	80.9	486	9	ABE95425	Aeb95425 Mouse 2H7	205	72	80.9	502	9	ADY21701	ADY21701 Antibody
133	72	80.9	486	9	ABE94456	Aeb94456 Mouse ant	206	72	80.9	502	9	ADY22140	ADY22140 Antibody
134	72	80.9	490	9	ADV21539	Adv21539 Mouse ant	207	72	80.9	502	9	ABE95424	ABE95424 Antibody
135	72	80.9	491	9	ADZ83606	Adz83606 CD3 speci	208	72	80.9	502	9	ABE94458	ABE94458 Antibody
136	72	80.9	491	9	ADZ83598	Adz83598 CD3 speci	209	72	80.9	503	7	ADD25676	ADD25676 Antibody
137	72	80.9	491	9	ADZ83602	Adz83602 CD3 speci	210	72	80.9	503	5	ABG31028	ABG31028 Antibody
138	72	80.9	491	9	ADZ83596	Adz83596 CD3 speci	211	72	80.9	505	7	ADD25723	ADD25723 Antibody
139	72	80.9	491	9	ADZ83604	Adz83604 CD3 speci	212	72	80.9	505	7	ADD25457	ADD25457 Antibody
140	72	80.9	491	9	ADZ83600	Adz83600 CD3 speci	213	72	80.9	505	7	ADY21649	ADY21649 Antibody
141	72	80.9	496	9	ADV21537	Adv21537 Mature fo	214	72	80.9	505	7	ADM42732	ADM42732 Antibody
142	72	80.9	498	7	ADD25674	Add25674 Binding d	215	72	80.9	505	9	ADY21685	ADY21685 Antibody
143	72	80.9	498	7	ADY21547	Ady21547 Antibody	216	72	80.9	505	9	ABE95400	ABE95400 Antibody
144	72	80.9	499	5	ABG31026	Abg31026 Synthetic	217	72	80.9	505	9	ABE94434	ABE94434 Antibody
145	72	80.9	499	5	ABG31027	Abg31027 Synthetic	218	72	80.9	507	9	ADY21879	ADY21879 Antibody
146	72	80.9	499	5	ABG31025	Abg31025 Synthetic	219	72	80.9	514	9	ADD25675	ADD25675 Antibody
147	72	80.9	499	7	ADD25587	Add25587 Binding d	220	72	80.9	516	9	ADY21649	ADY21649 Antibody
148	72	80.9	499	7	ADD25454	Add25454 Binding d	221	72	80.9	516	7	ADD25738	ADD25738 Antibody
149	72	80.9	499	7	ADD25456	Add25456 Binding d	222	72	80.9	516	9	ADY21877	ADY21877 Antibody
150	72	80.9	499	7	ADD25455	Add25455 Binding d	223	72	80.9	516	9	ADY21696	ADY21696 Antibody
151	72	80.9	499	7	ADM42731	Adm42731 2H7scFv-I	224	72	80.9	520	7	ADD25725	ADD25725 Antibody
152	72	80.9	499	7	ADM42729	Adm42729 2H7scFv-I	225	72	80.9	520	9	ADY21687	ADY21687 Antibody
153	72	80.9	499	7	ADM42730	Adm42730 2H7scFv-I	226	72	80.9	551	9	ADY22067	ADY22067 Antibody
154	72	80.9	499	9	ABE95397	Aeb95397 Mouse hum	227	72	80.9	592	7	ADD25773	ADD25773 Antibody
155	72	80.9	499	9	ABE95398	Aeb95398 Mouse hum	228	72	80.9	592	7	ADY21754	ADY21754 Antibody
156	72	80.9	499	9	ABE95399	Aeb95399 Mouse hum	229	72	80.9	593	9	ADY21873	ADY21873 Antibody
157	72	80.9	499	9	ABE94431	Aeb94431 Mouse ant	230	72	80.9	599	9	ADY21875	ADY21875 Antibody
158	72	80.9	499	9	ABE94433	Aeb94433 Mouse ant	231	72	80.9	626	9	ADV92500	ADV92500 Antibody
159	72	80.9	499	9	ABE94432	Aeb94432 Mouse ant	232	72	80.9	626	9	ADV98563	ADV98563 Antibody
160	72	80.9	499	9	ABE94436	Aeb94436 Mouse ant	233	72	80.9	633	3	AAE84965	AAE84965 Amino aci
161	72	80.9	500	7	ADD25826	Add25826 Binding d	234	72	80.9	641	9	ADV92502	ADV92502 Antibody
162	72	80.9	500	7	ADD25837	Add25837 Binding d	235	72	80.9	641	9	ADV98565	ADV98565 Novel chi
163	72	80.9	500	7	ADD25713	Add25713 Binding d	236	72	80.9	657	9	ADY92504	ADY92504 FL/Fc/CD2
164	72	80.9	500	7	ADD25836	Add25836 Binding d	237	72	80.9	657	9	ADV98567	ADV98567 Novel chi
165	72	80.9	500	7	ADD25824	Add25824 Binding d	238	72	80.9	768	7	ADD25789	ADD25789 Binding d
166	72	80.9	500	7	ADD25827	Add25827 Binding d	239	72	80.9	768	9	ADY21740	ADY21740 Antibody
167	72	80.9	500	7	ADD25835	Add25835 Binding d	240	72	79.8	118	9	ADH85026	ADH85026 Monoclonal
168	72	80.9	500	7	ADD25828	Add25828 Binding d	241	72	79.8	140	1	AAE70627	AAE70627 Sequence
169	72	80.9	500	7	ADD25679	Add25679 Binding d	242	72	78.7	128	9	AEA88768	AEA88768 Murine SA
170	72	80.9	500	7	ADD25791	Add25791 Binding d	243	72	78.7	131	9	AEA88771	AEA88771 Murine SA

244	70	78.7	470	8	ADM72031	Adm72031	Chimeric	317	62	69.7	98	9	ADM86104	Adm86104	Novel	Cyt
245	69	77.5	118	2	AAW27122	AAW27122	Murine an	318	62	69.7	153	2	AAW27120	AAW27120	Murine mo	
246	68	76.4	17	9	ADM47109	Adm47109	Anti-CD20	319	62	69.7	153	2	AAW87594	AAW87594	Antibody	
247	68	76.4	113	8	ADO32162	Ado32162	Mouse ant	320	62	69.7	153	6	AAO16293	AAO16293	Mouse 11D	
248	68	76.4	114	3	AAV51263	AAV51263	Monoclonal	321	62	69.7	291	4	AAW20443	AAW20443	Antibody	
249	68	76.4	120	2	AAW19915	AAW19915	Heavy cha	322	62	69.7	322	4	AAW20440	AAW20440	Antibody	
250	68	76.4	122	9	ADM47050	Adm47050	Heavy cha	323	62	69.7	729	4	AAW20439	AAW20439	Antibody	
251	68	76.4	123	9	ADXL6298	Adxl6298	IH4 heavy	324	61	68.5	17	9	ADM47108	ADM47108	Anti-CD20	
252	68	76.4	133	1	AAW90844	AAW90844	Predicted	325	61	68.5	117	2	ADM86082	ADM86082	Mouse DS6	
253	68	76.4	133	2	AAW04384	AAW04384	Colon Can	326	61	68.5	117	2	AAW04381	AAW04381	Variable	
254	68	76.4	133	2	AAW38313	AAW38313	Sequence	327	61	68.5	117	2	AAW38310	AAW38310	Sequence	
255	68	76.4	133	2	AAW50686	AAW50686	Human C8	328	61	68.5	117	2	AAW50683	AAW50683	Human CH	
256	68	76.4	133	2	AAW57177	AAW57177	Amino aci	329	61	68.5	117	2	AAW57175	AAW57175	Amino ac	
257	68	76.4	133	3	AAW57048	AAW57048	Amino aci	330	61	68.5	117	3	AAW57046	AAW57046	Human Vh	
258	68	76.4	133	3	AAW90723	AAW90723	Amino aci	331	61	68.5	117	3	AAW90714	AAW90714	VHalphaTA	
259	68	76.4	133	3	AAW90716	AAW90716	CC83 VH r	332	61	68.5	117	4	AAW02133	AAW02133	Mouse par	
260	68	76.4	133	4	AAW02142	AAW02142	Mouse ant	333	61	68.5	117	6	ADBL7717	ADBL7717	Heavy cha	
261	68	76.4	133	4	AAW02135	AAW02135	Mouse par	334	61	68.5	117	7	ADG46837	ADG46837	Mouse Vha	
262	68	76.4	133	6	ADBL7720	Adbl7720	Heavy cha	335	61	68.5	117	7	ADK66814	ADK66814	Mouse VH	
263	68	76.4	133	7	ADG46840	Adg46840	Mouse CC8	336	61	68.5	117	9	ADM86091	ADM86091	Mouse DS6	
264	68	76.4	133	7	ADK66842	Adk66842	Mouse CC4	337	61	68.5	117	9	ADM86090	ADM86090	Mouse DS6	
265	68	76.4	133	7	ADK66818	Adk66818	Mouse CC8	338	61	68.5	117	9	ADM86089	ADM86089	Mouse DS6	
266	68	76.4	134	2	AAW04385	AAW04385	Colon Can	339	61	68.5	122	9	ADM47046	ADM47046	Heavy cha	
267	68	76.4	134	2	AAW38314	AAW38314	Sequence	340	61	68.5	132	4	AAW62049	AAW62049	Mouse mon	
268	68	76.4	134	2	AAW50687	AAW50687	Human CC9	341	61	68.5	137	9	ADW71825	ADW71825	Human 3F4	
269	68	76.4	134	2	AAW57186	AAW57186	Amino aci	342	61	68.5	233	9	ADV26033	ADV26033	3F4Vh/hG4	
270	68	76.4	134	3	AAW57050	AAW57050	Amino aci	343	61	68.5	235	9	ADV26035	ADV26035	3F4Vh/G2G	
271	68	76.4	134	3	AAW90718	AAW90718	CC92 VH r	344	61	68.5	248	7	ADG32323	ADG32323	Mouse scf	
272	68	76.4	134	4	AAW02137	AAW02137	Mouse par	345	61	68.5	317	7	ADG32360	ADG32360	Precursor	
273	68	76.4	134	6	ADBL7721	Adbl7721	Heavy cha	346	61	68.5	463	7	AAW14939	AAW14939	3F4 (Chim	
274	68	76.4	134	7	ADG46841	Adg46841	Mouse CC9	347	61	68.5	463	2	AAW14940	AAW14940	3F4 (Chim	
275	68	76.4	134	7	ADK66822	Adk66822	Mouse CC9	348	61	68.5	464	2	AAW14941	AAW14941	3F4 Human	
276	68	76.4	150	2	AAW20184	AAW20184	Sequence	349	61	68.5	464	2	AAW14938	AAW14938	Murine an	
277	68	76.4	208	4	AAW31418	AAW31418	Protein u	350	61	68.5	465	2	AAW66758	AAW66758	Anti-toba	
278	68	76.4	237	4	AAW31419	AAW31419	Protein u	351	60	67.4	17	8	ADU80239	ADU80239	CD20 bind	
279	68	76.4	238	4	AAW31420	AAW31420	Protein u	352	60	67.4	17	8	ADY59133	ADY59133	Anti-Tag-	
280	68	76.4	242	4	AAW31422	AAW31422	Protein u	353	60	67.4	118	8	ADE25828	ADE25828	Anti-alpha	
281	68	76.4	271	2	AAW20185	AAW20185	Sequence	354	60	67.4	244	5	AAW77830	AAW77830	Nucleotid	
282	68	76.4	271	4	AAW31423	AAW31423	Protein u	355	60	67.4	355	2	AAW35133	AAW35133	R. Pipien	
283	68	76.4	272	4	AAW31424	AAW31424	Protein u	356	60	67.4	669	5	ABB77831	ABB77831	Sequence	
284	68	76.4	661	4	AAW31429	AAW31429	Shed anti	357	60	67.4	956	3	AAW36460	AAW36460	ScFv-GaLy	
285	67	75.3	17	8	ADU80241	ADU80241	CD20 bind	358	59	66.3	17	3	AAW77586	AAW77586	Anti-huma	
286	67	75.3	120	8	ADL26666	ADL26666	Mouse ant	359	59	66.3	17	3	AAW95239	AAW95239	Humanised	
287	67	75.3	121	8	ADU80275	ADU80275	CD20 bind	360	59	66.3	17	4	AAW78855	AAW78855	Anti-huma	
288	67	75.3	140	2	AAW41070	AAW41070	Mouse 2H7	361	59	66.3	17	8	ADL11878	ADL11878	CDR-1 hea	
289	67	75.3	140	2	AAW47513	AAW47513	Mouse 2H7	362	59	66.3	17	9	ADY59155	ADY59155	Anti-Tag-	
290	67	75.3	140	2	AAW47520	AAW47520	Mouse 2H7	363	59	66.3	17	9	ADZ58520	ADZ58520	VEGF rece	
291	66	74.2	122	9	AAW86135	AAW86135	Novel cyt	364	59	66.3	17	9	ADZ48265	ADZ48265	Pharmacu	
292	66	74.2	273	2	AAW52865	AAW52865	Anti-Infl	365	59	66.3	42	2	AAW31609	AAW31609	Mucin Th	
293	65	73.0	17	9	ADZ45359	ADZ45359	Murine fa	366	59	66.3	46	2	AAW31606	AAW31606	Mucin Th	
294	65	73.0	119	9	ADZ45357	ADZ45357	Murine fa	367	59	66.3	75	2	AAW31607	AAW31607	Mucin Th	
295	65	73.0	133	9	AAW88772	AAW88772	Murine SA	368	59	66.3	90	2	AAW31608	AAW31608	Mucin Th	
296	65	73.0	226	9	AAW88770	AAW88770	Murine SA	369	59	66.3	90	2	AAW31605	AAW31605	Mucin Th	
297	64	71.9	17	9	ADW47107	ADW47107	Anti-CD20	370	59	66.3	115	2	AAW36965	AAW36965	CC49 V-the	
298	64	71.9	111	9	ADW69518	ADW69518	Mouse ICA	371	59	66.3	115	2	AAW42261	AAW42261	Murine an	
299	64	71.9	120	8	ADG25803	ADG25803	Anti-CD30	372	59	66.3	115	2	AAW42264	AAW42264	Humanised	
300	64	71.9	122	9	ADW47044	ADW47044	Heavy cha	373	59	66.3	115	2	AAW42263	AAW42263	Humanised	
301	64	71.9	216	6	ABP96776	ABP96776	TSH recep	374	59	66.3	115	2	AAW42265	AAW42265	Humanised	
302	64	71.9	216	6	ABP96775	ABP96775	TSH recep	375	59	66.3	115	2	AAW42266	AAW42266	Humanised	
303	64	71.9	257	8	AAW09777	AAW09777	Antiviral	376	59	66.3	115	2	AAW97178	AAW97178	Monoclonal	
304	64	71.9	257	8	ADV20696	ADV20696	scFv-3a-2	377	59	66.3	115	2	AAW05760	AAW05760	Anti-TIG-	
305	63	70.8	304	5	ADW69520	ADW69520	Mouse ICA	378	59	66.3	115	5	AAW95244	AAW95244	Humanised	
306	63	70.8	13	5	ADG67319	ADG67319	Human ant	379	59	66.3	115	5	AAW78314	AAW78314	Murine CC	
307	63	70.8	17	3	AAW74932	AAW74932	H-CDR-2 o	380	59	66.3	115	5	AAW78316	AAW78316	Humanised	
308	63	70.8	17	3	AAW78323	AAW78323	Anti-zeta	381	59	66.3	115	5	AAW78318	AAW78318	Humanised	
309	63	70.8	19	7	ADW78552	ADW78552	Rat F9/97-	382	59	66.3	115	5	AAW78324	AAW78324	Human CC4	
310	63	70.8	119	7	AAW74940	AAW74940	Immunoglo	383	59	66.3	115	5	AAW78317	AAW78317	Humanised	
311	63	70.8	119	7	ADW78578	ADW78578	Rat F9/97-	384	59	66.3	115	5	AAW78319	AAW78319	Humanised	
312	63	70.8	123	3	AAW78325	AAW78325	Anti-zeta	385	59	66.3	115	6	ABU09362	ABU09362	Heavy mo	
313	63	70.8	133	2	AAW74960	AAW74960	Anti-idio	386	59	66.3	115	6	ABU09369	ABU09369	Heavy cha	
314	63	70.8	135	2	AAW74961	AAW74961	Anti-idio	387	59	66.3	115	6	ABU09368	ABU09368	Heavy cha	
315	63	70.8	436	3	AAW91026	AAW91026	Apoptodod	388	59	66.3	115	6	ABU09364	ABU09364	Humanised	
316	63	70.8	532	3	AAW78328	AAW78328	Bispecifi	389	59	66.3	115	6	ABU10139	ABU10139	Humanised	

390	59	66.3	115	6	ABU10143	ABU10143	Murine TA	463	59	66.3	238	3	AAy57255	AAy57255 4-4-20 V1
391	59	66.3	115	6	ABU10144	ABU10144	Humanised	464	59	66.3	238	3	AAy27680	AAy27680 Bivalent
392	59	66.3	115	6	ABU10137	ABU10137	Murine TA	465	59	66.3	238	3	AAy80925	AAy80925 Single ch
393	59	66.3	115	6	ADB17748	ADB17748	Humanised	466	59	66.3	238	3	AAy54834	AAy54834 Antibody
394	59	66.3	115	6	ADB17746	ADB17746	Native CC	467	59	66.3	238	6	ABU61810	ABU61810 Antigen b
395	59	66.3	115	6	ABU62751	ABU62751	Murine mo	468	59	66.3	240	3	AAW88095	AAW88095 Single-ch
396	59	66.3	115	6	ABU62755	ABU62755	Humanised	469	59	66.3	240	3	AAW807931	AAW807931 A heterob
397	59	66.3	115	6	ABU62760	ABU62760	Murine mo	470	59	66.3	240	3	AAy57250	AAy57250 4-4-20 V1
398	59	66.3	115	6	ABU62754	ABU62754	Humanised	471	59	66.3	240	3	AAy27675	AAy27675 Bivalent
399	59	66.3	115	6	ABU62756	ABU62756	Humanised	472	59	66.3	240	3	AAy80920	AAy80920 Single ch
400	59	66.3	115	6	ABU62761	ABU62761	Heavy cha	473	59	66.3	240	6	ABU61805	ABU61805 Antigen b
401	59	66.3	115	6	ABU62753	ABU62753	Humanised	474	59	66.3	241	3	AAy37645	AAy37645 Multivale
402	59	66.3	115	7	AAE39059	AAE39059	Humanised	475	59	66.3	242	4	AAy31426	AAy31426 Protein u
403	59	66.3	115	7	AAE39061	AAE39061	Humanised	476	59	66.3	244	4	AAy31610	AAy31610 Protein u
404	59	66.3	115	7	AAE39062	AAE39062	Humanised	477	59	66.3	244	4	AAy31425	AAy31425 Protein u
405	59	66.3	115	7	AAE39060	AAE39060	Humanised	478	59	66.3	246	2	AAW81523	AAW81523 Single ch
406	59	66.3	115	7	AAE39057	AAE39057	Murine CC	479	59	66.3	248	2	AAy97382	AAy97382 CC49 VL-P
407	59	66.3	115	7	ADG46868	ADG46868	Humanised	480	59	66.3	249	2	AAW97888	AAW97888 CC49/218
408	59	66.3	115	7	ADG46866	ADG46866	Murine CC	481	59	66.3	251	2	AAy48632	AAy48632 Sequence
409	59	66.3	115	8	ADP71404	ADP71404	Humanised	482	59	66.3	257	2	AAW81524	AAW81524 Single ch
410	59	66.3	115	8	ADP71403	ADP71403	Mouse CC4	483	59	66.3	257	5	AAU75157	AAU75157 CC49/218
411	59	66.3	115	9	ADW77061	ADW77061	Human CC4	484	59	66.3	257	6	ABG73145	ABG73145 CC49/218
412	59	66.3	115	9	ADW77059	ADW77059	Murine CC	485	59	66.3	257	6	ABG73865	ABG73865 CC49/218
413	59	66.3	115	9	ADW77062	ADW77062	Human CC4	486	59	66.3	260	2	AAy38318	AAy38318 Sequence
414	59	66.3	115	9	ADY59202	ADY59202	Anti-Tag-	487	59	66.3	260	2	AAy50691	AAy50691 Human SCF
415	59	66.3	115	9	ADY59150	ADY59150	Anti-Tag-	488	59	66.3	260	2	AAy57182	AAy57182 Amino aci
416	59	66.3	115	9	ADZ48270	ADZ48270	Pharmaceu	489	59	66.3	260	6	ADB17736	ADB17736 SCFVL-11
417	59	66.3	116	2	AAy31604	AAy31604	Mucin Th	490	59	66.3	260	7	ADG46856	ADG46856 SCFVL-fus
418	59	66.3	116	8	ADY74985	ADY74985	Heavy cha	491	59	66.3	262	2	AAy97380	AAy97380 CC49/218
419	59	66.3	117	8	ADY26465	ADY26465	Murine I4	492	59	66.3	262	4	AAy31421	AAy31421 Protein u
420	59	66.3	117	8	ADL11887	ADL11887	Chimera a	493	59	66.3	264	2	AAy97381	AAy97381 PLAP CC49
421	59	66.3	117	8	ADL11892	ADL11892	CDR trans	494	59	66.3	265	9	ADZ48272	ADZ48272 Pharmaceu
422	59	66.3	117	8	ADL11893	ADL11893	CDR trans	495	59	66.3	269	5	AAU75158	AAU75158 CC49/218
423	59	66.3	117	9	ADZ58539	ADZ58539	VEGF rece	496	59	66.3	269	6	ABG73146	ABG73146 CC49/218
424	59	66.3	117	9	ADZ58535	ADZ58535	VEGF rece	497	59	66.3	269	6	ABG73866	ABG73866 CC49/218
425	59	66.3	117	9	ADZ58531	ADZ58531	VEGF rece	498	59	66.3	274	2	AAy38319	AAy38319 Sequence
426	59	66.3	119	6	ABO27172	ABO27172	Mouse ant	499	59	66.3	274	2	AAy50692	AAy50692 Human Hum
427	59	66.3	134	2	AAy04383	AAy04383	Colon Can	500	59	66.3	274	6	ADY57183	ADY57183 Amino aci
428	59	66.3	134	2	AAy38311	AAy38311	Sequence	501	59	66.3	274	6	ADB17738	ADB17738 Hum4 VL-C
429	59	66.3	134	2	AAy38312	AAy38312	Sequence	502	59	66.3	274	7	ADG46858	ADG46858 Hum4 VL-11
430	59	66.3	134	2	AAy50684	AAy50684	Human CC4	503	59	66.3	275	2	AAy49137	AAy49137 Sequence
431	59	66.3	134	2	AAy50685	AAy50685	Human CC4	504	59	66.3	275	2	AAy49139	AAy49139 Sequence
432	59	66.3	134	2	AAy57176	AAy57176	Amino aci	505	59	66.3	280	2	AAy49138	AAy49138 Sequence
433	59	66.3	134	2	AAy57178	AAy57178	Amino aci	506	59	66.3	282	2	AAy48636	AAy48636 Sequence
434	59	66.3	134	3	AAy57047	AAy57047	Amino aci	507	59	66.3	282	2	AAy48635	AAy48635 Sequence
435	59	66.3	134	3	AAy57049	AAy57049	Amino aci	508	59	66.3	284	2	AAy38321	AAy38321 Sequence
436	59	66.3	134	3	AAy90715	AAy90715	CC49 VH r	509	59	66.3	284	2	AAy50694	AAy50694 Plasmid P
437	59	66.3	134	3	AAy90722	AAy90722	CC49 VH r	510	59	66.3	284	7	ADY57185	ADY57185 Amino aci
438	59	66.3	134	3	AAy90717	AAy90717	CC46 VH r	511	59	66.3	284	6	ADB17742	ADB17742 pSC49FLAG
439	59	66.3	134	4	AAU02141	AAU02141	Mouse ant	512	59	66.3	284	7	ADG46862	ADG46862 Hum4 VL-11
440	59	66.3	134	4	AAU02136	AAU02136	Mouse par	513	59	66.3	285	2	AAy48638	AAy48638 Sequence
441	59	66.3	134	4	AAU02134	AAU02134	Mouse par	514	59	66.3	285	2	AAy77045	AAy77045 Heavy cha
442	59	66.3	134	6	ADB17752	ADB17752	Humanised	515	59	66.3	354	5	AAE27926	AAE27926 Human CH2
443	59	66.3	134	6	ADB17719	ADB17719	Heavy cha	516	59	66.3	354	6	ABB82835	ABB82835 Antibody
444	59	66.3	134	6	ADB17718	ADB17718	Heavy cha	517	59	66.3	360	9	ADW77049	ADW77049 Heavy cha
445	59	66.3	134	7	ADG46873	ADG46873	Humanised	518	59	66.3	362	9	ADW77053	ADW77053 Heavy cha
446	59	66.3	134	7	ADG46838	ADG46838	Mouse CC4	519	59	66.3	362	9	ADW77050	ADW77050 Heavy cha
447	59	66.3	134	7	ADG46839	ADG46839	Mouse CC4	520	59	66.3	364	6	ABJ39018	ABJ39018 CC49 sing
448	59	66.3	134	7	ADK66820	ADK66820	Mouse CC4	521	59	66.3	483	2	AAW88099	AAW88099 A protein
449	59	66.3	134	7	ADK66841	ADK66841	Mouse CC4	522	59	66.3	483	3	AAW807935	AAW807935 A divalen
450	59	66.3	134	7	ADK66816	ADK66816	Mouse CC4	523	59	66.3	483	3	AAy57254	AAy57254 Bivalent
451	59	66.3	136	2	AAy04382	AAy04382	Colon Can	524	59	66.3	483	3	AAy27679	AAy27679 Bivalent
452	59	66.3	136	2	AAy77600	AAy77600	Anti-huma	525	59	66.3	483	3	AAy80924	AAy80924 Bivalent
453	59	66.3	136	3	AAy77593	AAy77593	Anti-huma	526	59	66.3	486	6	ABU61809	ABU61809 Protein u
454	59	66.3	136	3	AAy77596	AAy77596	Anti-huma	527	59	66.3	486	2	AAy37649	AAy37649 Sequence
455	59	66.3	136	4	AAy78869	AAy78869	Anti-huma	528	59	66.3	515	9	ADZ48330	ADZ48330 Pharmaceu
456	59	66.3	136	4	AAy78865	AAy78865	Anti-huma	529	59	66.3	515	9	ADZ48331	ADZ48331 Pharmaceu
457	59	66.3	136	4	AAy78862	AAy78862	Anti-huma	530	59	66.3	553	2	AAy56966	AAy56966 CC49 VL-L
458	59	66.3	238	2	AAy37650	AAy37650	Single-ch	531	59	66.3	553	2	AAy56967	AAy56967 CC49 VL-L
459	59	66.3	238	2	AAy55864	AAy55864	4-4-20 VL	532	59	66.3	553	2	AAW97181	AAW97181 A multiva
460	59	66.3	238	2	AAy95438	AAy95438	Linked fu	533	59	66.3	553	2	AAW97180	AAW97180 A multiva
461	59	66.3	238	2	AAW88100	AAW88100	Single ch	534	59	66.3	553	2	AAy05762	AAy05762 CC49 sing
462	59	66.3	238	3	AAy07936	AAy07936	A single-	535	59	66.3	553	2	AAy05763	AAy05763 CC49 sing

536	59	66.3	603	9	ADM44587	Ad444587 Antibody	609	57	64.0	118	8	ADN62630	Adn62630 HIV gp 41
537	59	66.3	621	9	ADM44588	Ad444588 Antibody	610	57	64.0	118	9	AEA44065	Aea44065 Anti-TPO
538	59	66.3	643	9	ADM44592	Ad444592 Antibody	611	57	64.0	118	9	AEA44067	Aea44067 Anti-TPO
539	59	66.3	661	9	ADM44593	Ad444593 Antibody	612	57	64.0	118	9	AEA44061	Aea44061 Anti-TPO
540	58 5	65.7	119	5	ABM07175	Abb07175 Mouse 09	613	57	64.0	119	7	ADG75546	Adg75546 Humanised
541	58	65.2	17	6	ABG74708	Abg74708 Murine hu	614	57	64.0	119	7	ADG75547	Adg75547 Humanised
542	58	65.2	17	7	ABR83155	Abt83155 Hu007 ant	615	57	64.0	119	7	ADG75553	Adg75553 Human H2
543	58	65.2	17	7	ADP84876	Adp84876 Complement	616	57	64.0	119	7	ADG75552	Adg75552 Human H1
544	58	65.2	17	8	ADSI8662	Adsi8662 Peptide s	617	57	64.0	119	9	ADZ45485	Adz45485 Murine fa
545	58	65.2	17	8	ADSI8678	Adsi8678 Peptide s	618	57	64.0	120	8	ADR15133	Adr15133 Mouse ant
546	58	65.2	17	9	ADZ45395	Adz45395 Murine fa	619	57	64.0	121	8	AAr10541	AAr10541 Chimeric
547	58	65.2	111	7	ADC03136	Adc03136 Col on spe	620	57	64.0	121	8	ADJ25647	Adj25647 Mouse act
548	58	65.2	111	7	ADC03140	Adc03140 Col on spe	621	57	64.0	121	9	ADY85053	Ady85053 Human HMG
549	58	65.2	111	7	ADC03142	Adc03142 Col on spe	622	57	64.0	123	3	AAr79877	AAr79877 Anti-BGFR
550	58	65.2	112	7	ADC03148	Adc03148 Col on spe	623	57	64.0	123	3	AAr79877	AAr79877 Anti-BGFR
551	58	65.2	112	7	ADC03144	Adc03144 Col on spe	624	57	64.0	123	4	AAr86110	AAr86110 H. pylori
552	58	65.2	118	2	ADM45393	Adm45393 Murine fa	625	57	64.0	133	4	AAr86074	AAr86074 H. pylori
553	58	65.2	119	2	AAW49814	AAw49814 Murine fa	626	57	64.0	137	9	AAr51615	AAr51615 Human MPl
554	58	65.2	119	2	AAW49813	AAw49813 Murine fa	627	57	64.0	144	9	AAr44094	AAr44094 Anti-TPO
555	58	65.2	119	6	ABR55869	Abt55869 Anti-glyc	628	57	64.0	241	2	AAr09435	AAr09435 Anti-CD19
556	58	65.2	119	6	ABR55868	Abt55868 Human imm	629	57	64.0	242	2	AAr09444	AAr09444 Modified
557	58	65.2	119	8	ADN49726	Adn49726 Variable	630	57	64.0	247	8	ADK42701	Adk42701 1487 scFv
558	58	65.2	119	8	ADN49725	Adn49725 Variable	631	57	64.0	247	8	ADZ79628	Adz79628 Anti-Baci
559	58	65.2	119	8	ADU74402	Adu74402 Mouse ant	632	57	64.0	247	7	ADJ12876	Adj12876 CD28/mela
560	58	65.2	119	8	ADU74401	Adu74401 Human imm	633	56	62.9	13	5	AAr67318	AAr67318 Human ant
561	58	65.2	120	6	ABG74719	Abg74719 Murine hu	634	56	62.9	17	5	AAr05377	AAr05377 Mouse hea
562	58	65.2	120	6	ABG74712	Abg74712 Murine hu	635	56	62.9	17	5	AAr05377	AAr05377 Mouse hea
563	58	65.2	120	6	ABG74703	Abg74703 Murine hu	636	56	62.9	17	7	ABR63921	ABr63921 Murine C5
564	58	65.2	120	7	ABR83159	Abt83159 Hu007 ant	637	56	62.9	17	8	ADJ25677	Adj25677 Mouse arc
565	58	65.2	120	7	ABR83160	Abt83160 Hu007 ant	638	56	62.9	17	8	ADU87709	Adu87709 Mouse Luc
566	58	65.2	138	2	AAr39266	AAr39266 Mouse C4g	639	56	62.9	17	9	ADZ45471	Adz45471 Anti-CD20
567	58	65.2	138	2	AAW49810	AAw49810 Variable	640	56	62.9	17	9	ADZ45471	Adz45471 Murine fa
568	58	65.2	141	2	AAW73292	AAw73292 R6 monocl	641	56	62.9	17	5	AAr15811	AAr15811 Human leu
569	58	65.2	222	2	AAW49817	AAw49817 Fragment	642	56	62.9	112	5	AAr15811	AAr15811 Human mab
570	58	65.2	235	2	AAr39268	AAr39268 Humanised	643	56	62.9	114	9	ADW47068	Adw47068 Heavy cha
571	58	65.2	235	2	AAW49818	AAw49818 Amno aci	644	56	62.9	114	9	ADW47068	Adw47068 Heavy cha
572	58	65.2	267	8	ADP70320	Adp70320 Polioviru	645	56	62.9	115	3	AAr12172	AAr12172 Humanised
573	58	65.2	447	8	ADSI8726	Adsi8726 Amno aci	646	56	62.9	115	3	AAr12169	AAr12169 Humanised
574	58	65.2	448	6	ABR55871	Abt55871 Human imm	647	56	62.9	115	3	AAr12168	AAr12168 Humanised
575	58	65.2	448	6	ADN49728	Adn49728 Human imm	648	56	62.9	115	3	AAr12168	AAr12168 Humanised
576	58	65.2	448	8	ADU74404	Adu74404 Human imm	649	56	62.9	116	8	ADJ11306	Adj11306 Humanised
577	58	65.2	449	2	AAr43339	AAr43339 Complete1	650	56	62.9	116	8	ADJ11302	Adj11302 Humanised
578	58	65.2	449	2	AAW49816	AAw49816 Amno aci	651	56	62.9	116	8	ADJ11304	Adj11304 Humanised
579	58	65.2	450	6	ABG74713	Abg74713 Murine hu	652	56	62.9	118	9	ADZ45469	Adz45469 Murine fa
580	58	65.2	450	8	ADSI8704	Adsi8704 Protein s	653	56	62.9	121	2	AAr74964	AAr74964 Anti-idio
581	58	65.2	450	8	ADSI8710	Adsi8710 Protein s	654	56	62.9	121	2	AAr74964	AAr74964 Anti-idio
582	58	65.2	450	8	ADSI8702	Adsi8702 Protein s	655	56	62.9	121	2	AAr74964	AAr74964 Anti-idio
583	58	65.2	450	8	ADSI8708	Adsi8708 Protein s	656	56	62.9	121	2	AAr74964	AAr74964 Anti-idio
584	58	65.2	450	8	ADSI8708	Adsi8708 Protein s	657	56	62.9	121	2	AAr74964	AAr74964 Anti-idio
585	58	65.2	450	8	ADSI8708	Adsi8708 Protein s	658	56	62.9	121	2	AAr74964	AAr74964 Anti-idio
586	58	65.2	450	8	ADSI8708	Adsi8708 Protein s	659	56	62.9	121	2	AAr74964	AAr74964 Anti-idio
587	58	65.2	450	8	ADSI8708	Adsi8708 Protein s	660	56	62.9	121	2	AAr74964	AAr74964 Anti-idio
588	58	65.2	450	8	ADSI8708	Adsi8708 Protein s	661	56	62.9	121	2	AAr74964	AAr74964 Anti-idio
589	58	65.2	450	8	ADSI8708	Adsi8708 Protein s	662	56	62.9	121	2	AAr74964	AAr74964 Anti-idio
590	58	65.2	450	8	ADSI8708	Adsi8708 Protein s	663	56	62.9	121	2	AAr74964	AAr74964 Anti-idio
591	58	65.2	450	8	ADSI8708	Adsi8708 Protein s	664	56	62.9	121	2	AAr74964	AAr74964 Anti-idio
592	58	65.2	450	8	ADSI8708	Adsi8708 Protein s	665	56	62.9	121	2	AAr74964	AAr74964 Anti-idio
593	58	65.2	450	8	ADSI8708	Adsi8708 Protein s	666	56	62.9	121	2	AAr74964	AAr74964 Anti-idio
594	58	65.2	450	8	ADSI8708	Adsi8708 Protein s	667	56	62.9	121	2	AAr74964	AAr74964 Anti-idio
595	58	65.2	450	8	ADSI8708	Adsi8708 Protein s	668	56	62.9	121	2	AAr74964	AAr74964 Anti-idio
596	58	65.2	450	8	ADSI8708	Adsi8708 Protein s	669	56	62.9	121	2	AAr74964	AAr74964 Anti-idio
597	58	65.2	450	8	ADSI8708	Adsi8708 Protein s	670	56	62.9	121	2	AAr74964	AAr74964 Anti-idio
598	58	65.2	450	8	ADSI8708	Adsi8708 Protein s	671	56	62.9	121	2	AAr74964	AAr74964 Anti-idio
599	58	65.2	450	8	ADSI8708	Adsi8708 Protein s	672	56	62.9	121	2	AAr74964	AAr74964 Anti-idio
600	58	65.2	450	8	ADSI8708	Adsi8708 Protein s	673	56	62.9	121	2	AAr74964	AAr74964 Anti-idio
601	58	65.2	450	8	ADSI8708	Adsi8708 Protein s	674	56	62.9	121	2	AAr74964	AAr74964 Anti-idio
602	58	65.2	450	8	ADSI8708	Adsi8708 Protein s	675	56	62.9	121	2	AAr74964	AAr74964 Anti-idio
603	58	65.2	450	8	ADSI8708	Adsi8708 Protein s	676	56	62.9	121	2	AAr74964	AAr74964 Anti-idio
604	58	65.2	450	8	ADSI8708	Adsi8708 Protein s	677	56	62.9	121	2	AAr74964	AAr74964 Anti-idio
605	58	65.2	450	8	ADSI8708	Adsi8708 Protein s	678	56	62.9	121	2	AAr74964	AAr74964 Anti-idio
606	58	65.2	450	8	ADSI8708	Adsi8708 Protein s	679	56	62.9	121	2	AAr74964	AAr74964 Anti-idio
607	58	65.2	450	8	ADSI8708	Adsi8708 Protein s	680	56	62.9	121	2	AAr74964	AAr74964 Anti-idio
608	58	65.2	450	8	ADSI8708	Adsi8708 Protein s	681	56	62.9	121	2	AAr74964	AAr74964 Anti-idio

682	56	62.9	263	9	AEA41156	Aea41156 Human Ieu	755	55	61.8	222	9	ADW50595	Adw50595 Protein o
683	56	62.9	264	2	AAW35562	AAW35562 HindIII-E	756	55	61.8	246	9	ADW50596	Adw50596 Protein o
684	56	62.9	271	3	AAW23818	AAW23818 Plasmid p	757	55	61.8	248	2	AAW17964	Aaw17964 Mouse scf
685	56	62.9	271	4	AAW67494	AAW67494 Amino aci	758	55	61.8	249	1	AAW60154	Aaw60154 Biosynthe
686	56	62.9	271	5	AAW47632	AAW47632 Murine aci	759	55	61.8	264	7	ADW25839	Adw25839 Binding d
687	56	62.9	271	5	ABG97809	ABG97809 Mouse MAB	760	55	61.8	266	9	ADW21811	Adw21811 Single ch
688	56	62.9	271	5	ABG35312	ABG35312 Thrombopo	761	55	61.8	274	2	AAW44228	Aaw44228 Chimeric
689	56	62.9	274	2	AAW09819	AAW09819 VHA715-1i	762	55	61.8	290	9	ABR30749	AbR30749 CD20 EC d
690	56	62.9	274	3	AAW23817	AAW23817 Plasmid p	763	55	61.8	306	9	ADW58064	Adw58064 A single
691	56	62.9	274	3	AAW67493	AAW67493 Amino aci	764	55	61.8	319	9	ABR30747	AbR30747 CD20 EC d
692	56	62.9	274	5	AAW47631	AAW47631 Murine MA	765	55	61.8	378	9	AEA36900	Aea36900 Anti-CD3x
693	56	62.9	274	5	ABG97808	ABG97808 Mouse MAB	766	55	61.8	451	8	ADW97545	Adw97545 Artificialia
694	56	62.9	274	5	ABG35311	ABG35311 Thrombopo	767	55	61.8	483	8	ADW97549	Adw97549 Artificialia
695	56	62.9	445	8	ADJ11308	ADJ11308 BHA10 VL#	768	55	61.8	494	9	ADW21531	Adw21531 Mature fo
696	56	62.9	464	8	ADJ11354	ADJ11354 BHA10 VL#	769	55	61.8	494	9	ADW21521	Adw21521 Mature fo
697	56	62.9	495	4	AAW72414	AAW72414 Double-ne	770	55	61.8	495	9	ADW21517	Adw21517 Mature fo
698	56	62.9	502	9	AEA06285	AEA06285 Anti-CD47	771	55	61.8	495	9	ADW21527	Adw21527 Mature fo
699	56	62.9	514	9	AEA41144	AEA41144 Human Ieu	772	55	61.8	496	9	ADW21523	Adw21523 Mature fo
700	56	62.9	532	2	AAW35565	AAW35565 HindIII-E	773	55	61.8	496	9	ADW21533	Adw21533 Mature fo
701	56	62.9	697	8	ADQ07403	ADQ07403 hCBEL1/hB	774	55	61.8	496	9	ADW283619	Adw283619 CD3 speci
702	56	62.9	697	8	ADQ12180	ADQ12180 Heavy cha	775	55	61.8	496	9	ADW283625	Adw283625 CD3 speci
703	56	62.9	731	8	ADQ07407	ADQ07407 hCBEL1/hB	776	55	61.8	496	9	ADW283641	Adw283641 CD3 speci
704	56	62.9	731	8	ADQ12184	ADQ12184 hCBEL1/h	777	55	61.8	496	9	ADW283615	Adw283615 CD3 speci
705	55	61.8	17	2	AAW93475	AAW93475 mak TTC8	778	55	61.8	496	9	ADW283653	Adw283653 CD3 speci
706	55	61.8	17	5	AAW81234	AAW81234 Murine tr	779	55	61.8	496	9	ADW283637	Adw283637 CD3 speci
707	55	61.8	17	5	AAW98850	AAW98850 Mouse AC1	780	55	61.8	496	9	ADW283629	Adw283629 CD3 speci
708	55	61.8	17	5	AAW23924	AAW23924 Mouse ant	781	55	61.8	496	9	ADW283645	Adw283645 CD3 speci
709	55	61.8	17	8	ADW87908	ADW87908 Mouse AC1	782	55	61.8	496	9	ADW283649	Adw283649 CD3 speci
710	55	61.8	103	9	ADW60816	ADW60816 Hybrid pr	783	55	61.8	496	9	ADW283653	Adw283653 CD3 speci
711	55	61.8	112	6	ABR54974	ABR54974 Mouse Igg	784	55	61.8	496	9	ADW283657	Adw283657 CD3 speci
712	55	61.8	112	6	ABR54972	ABR54972 Mouse Igg	785	55	61.8	497	9	ADW283621	Adw283621 CD3 speci
713	55	61.8	112	6	ABR54975	ABR54975 Mouse Igg	786	55	61.8	497	9	ADW283659	Adw283659 CD3 speci
714	55	61.8	112	6	ABR54973	ABR54973 Mouse Igg	787	55	61.8	497	9	ADW283415	Adw283415 C-termina
715	55	61.8	112	6	ABR19405	ABR19405 Igg heavy	788	55	61.8	497	9	ADW283417	Adw283417 C-termina
716	55	61.8	112	9	ABE19403	ABE19403 Igg heavy	789	55	61.8	497	9	ADW283635	Adw283635 CD3 speci
717	55	61.8	112	9	ABE19404	ABE19404 Igg heavy	790	55	61.8	497	9	ADW283627	Adw283627 CD3 speci
718	55	61.8	112	9	ABE19402	ABE19402 Igg heavy	791	55	61.8	497	9	ADW283639	Adw283639 CD3 speci
719	55	61.8	113	2	AAW89348	AAW89348 Mouse 23F	792	55	61.8	497	9	ADW283647	Adw283647 CD3 speci
720	55	61.8	113	2	AAW93480	AAW93480 mak TTC8	793	55	61.8	497	9	ADW283655	Adw283655 CD3 speci
721	55	61.8	116	8	ADQ32158	ADQ32158 Mouse ant	794	55	61.8	497	9	ADW283651	Adw283651 CD3 speci
722	55	61.8	117	1	AAW80149	AAW80149 Biosynthe	795	55	61.8	497	9	ADW283643	Adw283643 CD3 speci
723	55	61.8	117	1	AAW80148	AAW80148 Biosynthe	796	55	61.8	497	9	ADW283623	Adw283623 CD3 speci
724	55	61.8	117	1	AAW62295	AAW62295 Sequence	797	55	61.8	497	9	ADW283631	Adw283631 CD3 speci
725	55	61.8	117	1	AAW62296	AAW62296 Human mye	798	55	61.8	497	9	ADW283617	Adw283617 CD3 speci
726	55	61.8	117	5	AAW98848	AAW98848 Mouse AC1	799	55	61.8	500	9	ADW66095	Adw66095 Anti-CD3-
727	55	61.8	117	5	AAW23922	AAW23922 Mouse ant	800	55	61.8	500	9	ADW66097	Adw66097 Anti-CD3-
728	55	61.8	117	7	ADH17836	ADH17836 Murine an	801	55	61.8	501	9	ADW21519	Adw21519 Mature fo
729	55	61.8	117	8	ADJ87904	ADJ87904 Mouse AC1	802	55	61.8	501	9	ADW21529	Adw21529 Mature fo
730	55	61.8	117	9	ADW11467	ADW11467 Murine an	803	55	61.8	503	9	ADW66087	Adw66087 Anti-CD3-
731	55	61.8	117	9	ADW86134	ADW86134 Novel cyt	804	55	61.8	503	9	ADW66081	Adw66081 Anti-CD3-
732	55	61.8	117	9	ADW60815	ADW60815 Hybrid pr	805	55	61.8	504	9	ADW21525	Adw21525 Mature fo
733	55	61.8	117	9	ABE13686	ABE13686 Human ant	806	55	61.8	504	9	ADW21535	Adw21535 Mature fo
734	55	61.8	117	9	ABE13687	ABE13687 Human ant	807	55	61.8	515	9	ADW283441	Adw283441 Deimmuniz
735	55	61.8	117	9	ABE13685	ABE13685 Human ant	808	55	61.8	521	9	ADW66121	Adw66121 Anti-CD3-
736	55	61.8	117	9	ABE13679	ABE13679 Human hea	809	55	61.8	548	7	ADW25711	Adw25711 Binding d
737	55	61.8	117	9	ABE13690	ABE13690 Human ant	810	55	61.8	548	7	ADW21681	Adw21681 Antibody
738	55	61.8	118	1	AAW62293	AAW62293 Murine mo	811	54	60.7	10	8	ADQ32143	AdQ32143 Mouse ant
739	55	61.8	118	8	ADW25825	ADW25825 Anti-alph	812	54	60.7	17	2	AAW89159	AAW89159 Anti-p53
740	55	61.8	118	8	ADW50592	ADW50592 Protein o	813	54	60.7	17	8	ADW60472	Adw60472 Mouse ant
741	55	61.8	118	9	ADY60813	ADY60813 Mouse pro	814	54	60.7	17	9	ADW47112	Adw47112 Anti-CD20
742	55	61.8	120	2	AAW47934	AAW47934 Humanised	815	54	60.7	17	9	ADW97114	Adw97114 Murine MA
743	55	61.8	120	2	AAW89350	AAW89350 Humanised	816	54	60.7	17	9	ADW97117	Adw97117 Murine MA
744	55	61.8	120	2	ADW66173	ADW66173 Human Bpc	817	54	60.7	17	9	ADW245483	Adw245483 Murine fa
745	55	61.8	120	9	ADW21425	ADW21425 Human ant	818	54	60.7	17	9	ABE24624	AbE24624 Humanized
746	55	61.8	120	9	ADW28351	ADW28351 AntiEpcam	819	54	60.7	96	8	ADQ32145	AdQ32145 Mouse ant
747	55	61.8	121	2	AAW46484	AAW46484 S1C5 VH a	820	54	60.7	108	9	ADW97136	Adw97136 Murine MA
748	55	61.8	122	5	AAU81271	AAU81271 Murine tr	821	54	60.7	111	2	AAW89172	AAW89172 Anti-P53
749	55	61.8	122	5	AAU81270	AAU81270 Murine tr	822	54	60.7	112	6	ABR54969	AbR54969 Mouse Igg
750	55	61.8	124	2	AAW47931	AAW47931 Mutated h	823	54	60.7	112	6	ABR54971	AbR54971 Mouse Igg
751	55	61.8	130	9	ADY96925	ADY96925 Human imm	824	54	60.7	112	6	ABR54968	AbR54968 Mouse Igg
752	55	61.8	130	9	ADY96944	ADY96944 Human imm	825	54	60.7	112	6	ABR54967	AbR54967 Mouse Igg
753	55	61.8	130	9	ADY96932	ADY96932 Human imm	826	54	60.7	112	6	ABR54970	AbR54970 Mouse Igg
754	55	61.8	139	7	ADD25701	ADD25701 Binding d	827	54	60.7	112	6	ABR54989	AbR54989 Mouse Igg

828	54	60.7	112	9	AEb19401	IGF heavy	901	53	59.6	113	9	AEb19414	IGF heavy
829	54	60.7	112	9	AEb19398	IGF heavy	902	53	59.6	113	9	AEb19410	IGF heavy
830	54	60.7	112	9	AEb19397	IGF heavy	903	53	59.6	113	9	AEb19412	IGF heavy
831	54	60.7	112	9	AEb19400	IGF heavy	904	53	59.6	113	9	AEb19411	IGF heavy
832	54	60.7	112	9	AEb19399	IGF heavy	905	53	59.6	115	7	AEb13224	Humanised
833	54	60.7	113	8	ADb060449	Humanised	906	53	59.6	116	2	AAW00827	Variant v
834	54	60.7	113	8	ADb060448	Humanised	907	53	59.6	116	2	AAW03742	Murine mo
835	54	60.7	113	8	ADb060444	Humanised	908	53	59.6	116	2	AAW19014	Anti-huma
836	54	60.7	113	8	ADb060442	Mouse ant	909	53	59.6	117	2	AAW00837	Variable
837	54	60.7	113	8	ADb060450	Humanised	910	53	59.6	117	9	AEb13691	Human ant
838	54	60.7	113	8	ADb060447	Humanised	911	53	59.6	117	9	AEb13681	Human v
839	54	60.7	113	8	ADb060446	Humanised	912	53	59.6	118	6	AEb54983	Mouse IGF
840	54	60.7	113	8	AEb24594	Murine MA	913	53	59.6	118	8	ADb25823	Anti- α ph
841	54	60.7	113	9	AEb24596	Humanized	914	53	59.6	118	8	ADb25824	Anti- α ph
842	54	60.7	113	9	AEb24602	Humanized	915	53	59.6	118	9	ADb245473	Murine fa
843	54	60.7	113	9	AEb24600	Humanized	916	53	59.6	118	9	ADb258532	VEGF rece
844	54	60.7	113	9	AEb24598	Humanized	917	53	59.6	118	9	AEb44079	Anti-TPO
845	54	60.7	113	9	AEb24599	Humanized	918	53	59.6	118	9	AEb44063	Anti-TPO
846	54	60.7	113	9	AEb24601	Humanized	919	53	59.6	118	9	AEb44075	Anti-TPO
847	54	60.7	114	6	AEb54978	Mouse IGF	920	53	59.6	118	9	AEb44077	Anti-TPO
848	54	60.7	114	6	AEb54979	Mouse IGF	921	53	59.6	118	9	AEb19413	IGF heavy
849	54	60.7	114	6	AEb54977	Mouse IGF	922	53	59.6	119	8	ADb11890	CDR trans
850	54	60.7	114	6	AEb54986	Mouse IGF	923	53	59.6	119	8	ADb11886	Chimera a
851	54	60.7	114	9	ADb47056	Heavy cha	924	53	59.6	119	8	ADb25836	VEGF rece
852	54	60.7	115	9	ADb45481	Murine fa	925	53	59.6	120	8	ADb75107	Heavy cha
853	54	60.7	116	2	AAr79241	Heavy cha	926	53	59.6	120	8	ADb66947	Human 3B1
854	54	60.7	118	8	ADb032160	Mouse ant	927	53	59.6	121	8	AAW07437	Anti-DNA
855	54	60.7	119	8	ADbQ76091	Heterorec	928	53	59.6	121	8	ADb25649	Mouse act
856	54	60.7	119	9	ADbW86136	Novel cyt	929	53	59.6	122	2	AAJ21816	Anti-STX1
857	54	60.7	119	9	ADb251206	Amilo act	930	53	59.6	122	9	AEb44059	Anti-TPO
858	54	60.7	119	9	ADb242080	Human ant	931	53	59.6	124	2	AAb882973	FBS human
859	54	60.7	120	6	ABP59952	Monoclonal	932	53	59.6	124	2	AAb882974	FBS human
860	54	60.7	120	6	ABP59987	Antibody	933	53	59.6	124	2	AAb82972	FBS human
861	54	60.7	120	7	ADbF69657	Humanised	934	53	59.6	124	2	AAb82965	FBS antib
862	54	60.7	120	7	ADbF69652	Humanised	935	53	59.6	124	2	AAb82971	FBS human
863	54	60.7	120	9	AEb03871	B-CLL pha	936	53	59.6	125	3	AAW08504	C6 human
864	54	60.7	120	9	AEb03876	B-CLL pha	937	53	59.6	138	3	AAJ77591	Anti-huma
865	54	60.7	138	8	ADb26639	Mouse ant	938	53	59.6	138	4	AAJ77595	Anti-huma
866	54	60.7	139	6	ABG74245	Mouse ant	939	53	59.6	138	4	AAb78864	Anti-huma
867	54	60.7	140	4	AAb74791	Anti-CA12	940	53	59.6	138	4	AAb78860	Anti-huma
868	54	60.7	219	2	AAW53597	Amilo act	941	53	59.6	139	2	AAW55774	Anti-huma
869	54	60.7	239	6	ADbA91408	Anti-Abet	942	53	59.6	139	2	AAW55773	Anti-huma
870	54	60.7	239	7	ADbC79231	Anti-CA12	943	53	59.6	139	2	AAW62216	Humanised
871	54	60.7	239	7	ADbC79232	Control s	944	53	59.6	139	2	AAW62204	Humanised
872	54	60.7	251	4	AAb74793	Single ch	945	53	59.6	139	2	AAW62211	Humanised
873	54	60.7	258	4	AAb74794	Single ch	946	53	59.6	139	2	AAW62215	Humanised
874	54	60.7	269	8	ADb28054	NPB polyp	947	53	59.6	139	2	AAW62199	Humanised
875	54	60.7	459	9	ADbW97104	Murine ma	948	53	59.6	139	2	AAW62214	Humanised
876	54	60.7	460	9	ADbW97108	Murine ma	949	53	59.6	139	2	AAW62217	Humanised
877	54	60.7	460	9	ADbW97139	Murine ma	950	53	59.6	139	2	AAW62196	Humanised
878	54	60.7	546	9	AEb92076	Undefined	951	53	59.6	139	2	AAW62188	Mouse ant
879	53	59.6	16	7	ADbC03155	Colton spe	952	53	59.6	139	2	AAW62201	Humanised
880	53	59.6	17	3	AAJ77580	Anti-huma	953	53	59.6	139	2	AAW62210	Humanised
881	53	59.6	17	4	AAb78849	Anti-huma	954	53	59.6	139	2	AAW62205	Humanised
882	53	59.6	17	8	ADbL1875	CDR-1 hea	955	53	59.6	139	2	AAW62206	Humanised
883	53	59.6	17	8	ADbJ25664	Mouse aPC	956	53	59.6	139	2	AAW62209	Humanised
884	53	59.6	17	8	ADbM24790	Humanised	957	53	59.6	139	2	AAW62198	Humanised
885	53	59.6	17	8	ADbP84877	Complemen	958	53	59.6	139	2	AAW62218	Humanised
886	53	59.6	17	8	ADbI8680	Peptide s	959	53	59.6	139	2	AAW62197	Humanised
887	53	59.6	17	8	ADbT75122	Murine he	960	53	59.6	139	2	AAW62202	Humanised
888	53	59.6	17	8	ADbU66950	Human 3B1	961	53	59.6	139	2	AAW62212	Humanised
889	53	59.6	17	9	ADb245475	Murine fa	962	53	59.6	139	2	AAW62200	Humanised
890	53	59.6	17	9	ADb258523	VEGF rece	963	53	59.6	139	2	AAW62203	Humanised
891	53	59.6	17	9	AEb43966	Anti-TPO	964	53	59.6	139	2	AAW62213	Humanised
892	53	59.6	17	9	AEb43963	Anti-TPO	965	53	59.6	139	2	AAW77295	HML 24 an
893	53	59.6	17	9	AEb43945	Anti-TPO	966	53	59.6	139	2	AAJ02557	Humanised
894	53	59.6	17	9	AEb43969	Anti-TPO	967	53	59.6	139	2	AAJ02568	Humanised
895	53	59.6	17	9	AEb43969	Anti-TPO	968	53	59.6	139	2	AAJ02573	Humanised
896	53	59.6	96	6	ABG74915	Murine NM	969	53	59.6	139	2	AAJ02561	Humanised
897	53	59.6	113	6	ABR54982	Mouse IGF	970	53	59.6	139	2	AAJ02558	Humanised
898	53	59.6	113	6	ABR54981	Mouse IGF	971	53	59.6	139	2	AAJ02546	H chain v
899	53	59.6	113	6	ABR54984	Mouse IGF	972	53	59.6	139	2	AAJ02570	Humanised
900	53	59.6	113	6	ABR54980	Mouse IGF	973	53	59.6	139	2	AAJ02575	Humanised

974	53	59.6	139	2	AAV02564	AAV02564 Humanised
975	53	59.6	139	2	AAV02565	AAV02565 Humanised
976	53	59.6	139	2	AAV02572	AAV02572 Humanised
977	53	59.6	139	2	AAV02571	AAV02571 Humanised
978	53	59.6	139	2	AAV02555	AAV02555 Humanised
979	53	59.6	139	2	AAV02559	AAV02559 Humanised
980	53	59.6	139	2	AAV02560	AAV02560 Humanised
981	53	59.6	139	2	AAV02563	AAV02563 Humanised
982	53	59.6	139	2	AAV02567	AAV02567 Humanised
983	53	59.6	139	2	AAV02566	AAV02566 Humanised
984	53	59.6	139	2	AAV02574	AAV02574 Humanised
985	53	59.6	139	2	AAV02562	AAV02562 Humanised
986	53	59.6	139	2	AAV02556	AAV02556 Humanised
987	53	59.6	139	2	AAV02569	AAV02569 Humanised
988	53	59.6	139	2	AAV32771	AAV32771 Anti-HM1.
989	53	59.6	139	2	AAV32770	AAV32770 Anti-HM1.
990	53	59.6	139	2	AAV05487	AAV05487 H chain V
991	53	59.6	139	2	AAV05486	AAV05486 H chain V
992	53	59.6	139	5	AAV52354	AAV52354 H chain V
993	53	59.6	139	5	AAV52355	AAV52355 H chain V
994	53	59.6	139	6	ABG71946	ABG71946 Human res
995	53	59.6	139	8	ADO60011	ADO60011 H chain V
996	53	59.6	139	8	ADO60010	ADO60010 H chain V
997	53	59.6	140	2	AAW77294	AAW77294 HM1.24 an
998	53	59.6	195	7	ABR84724	ABR84724 Vector pg
999	53	59.6	195	7	ABR84722	ABR84722 Vector pg
1000	53	59.6	450	7	ABR83153	ABR83153 Hu007 ant

ALIGNMENTS

RESULT 1
ADO32141
ADO32141 standard; peptide; 17 AA.

AC ADO32141;
DT 12-AUG-2004 (first entry)

DE Mouse anti-CD3 antibody My9-6 heavy chain CDR2 SEQ ID NO:57.

XX anti-CD3 antibody; epitope-binding fragment;
KW complementarity-determining region; CDR; immunoglobulin; cytostatic;
KW antibody; myelodysplastic syndrome; acute myeloid leukaemia;
KW chronic myeloid leukaemia; pro-myelocytic leukaemia; mouse; My9-6;
heavy chain.
XX Mus musculus.
OS
XX WO2004043344-A2.
XX 27-MAY-2004.
XX 05-NOV-2003; 2003WO-US032737.
XX 07-NOV-2002; 2002US-0424332P.
XX (IMMU-) IMMUNOGEN INC.
XX Hoffee MG, Tavares D, Lutz RJ;
XX WPI; 2004-411619/38.
XX New antibodies that bind to CD33, useful for treating a disease
XX associated with CD33 expression, such as myelodysplastic syndrome, acute
XX or chronic myeloid leukemia.
XX Example 3; SEQ ID NO 57; 124pp; English.
XX The present invention describes an isolated anti-CD33 antibody or its
XX epitope-binding fragment comprising: (a) at least one complementarity-
XX determining region (CDR); or (b) at least heavy chain variable region

comprising 3 CDRs, and at least one light chain variable region, where
the CDR has the ability to bind CD33. Also described: (1) an
immunoglobulin comprising the antibody or its epitope-binding fragment
linked to a drug or prodrug; (2) a composition comprising the antibody or
epitope-binding fragment and a drug or prodrug; (3) a pharmaceutical
composition comprising the immunoglobulin, composition or the antibody
defined above, or its epitope-binding fragment, and a pharmaceutical
agent; (4) a diagnostic reagent comprising the antibody defined above,
where the antibody or antibody fragment is labelled; (5) inhibiting the
growth of a cell expressing CD33 by contacting the cell with the above
defined antibody or its epitope-binding fragment, immunoglobulin, or
(pharmaceutical) composition; (6) determining whether a biological sample
contains a myelogenous cancer cell; (7) an improved antibody or its
epitope-binding fragment that specifically binds to CD33; (8) an isolated
polynucleotide encoding the antibody or its epitope-binding fragment
defined above; (9) an isolated polynucleotide encoding a light or heavy
chain of the antibody defined above or its epitope-binding fragment; (10)
a recombinant vector comprising the polynucleotide; (11) a host cell
transformed with the recombinant vector; (12) producing an antibody or
its epitope-binding fragment having the ability to bind CD33; and (13)
obtaining CD33 from a biological material. The anti-CD33 antibody has
cytostatic activity. The antibody or its epitope-binding fragment,
immunoglobulin, composition can be used for treating a subject having a
disease where CD33 is expressed, such as myelodysplastic syndrome, acute
myeloid leukaemia, chronic myeloid leukaemia or pro-myelocytic leukaemia.
It can also be used for inhibiting the growth of cells expressing CD33,
and for in vivo imaging or as affinity purification agents. The present
sequence represents the mouse anti-CD33 antibody My9-6 heavy chain CDR2,
which is used in an example from the present invention.

Sequence 17 AA;

Query Match 98.9%; Score 88; DB 8; Length 17;
Best Local Similarity 94.1%; Pred. No. 2.1e-07;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 VIYPGNDISYNKFKG 17
Db 1 VIYPGNDISYNKFKG 17

RESULT 2
ADO32086
ID ADO32086 standard; peptide; 17 AA.
XX ADO32086;
XX 12-AUG-2004 (first entry)

DE Mouse anti-CD3 antibody My9-6 heavy chain CDR2 SEQ ID NO:2.

XX anti-CD3 antibody; epitope-binding fragment;
KW complementarity-determining region; CDR; immunoglobulin; cytostatic;
KW antibody; myelodysplastic syndrome; acute myeloid leukaemia;
KW chronic myeloid leukaemia; pro-myelocytic leukaemia; mouse; My9-6;
heavy chain.
XX Mus musculus.
OS
XX WO2004043344-A2.
XX 27-MAY-2004.
XX 05-NOV-2003; 2003WO-US032737.
XX 07-NOV-2002; 2002US-0424332P.
XX (IMMU-) IMMUNOGEN INC.
XX Key Location/Qualifiers
XX FT Misc-difference 16
XX FT /label= Lys, Gln
XX FT
XX EN WO2004043344-A2.
XX 27-MAY-2004.
XX 05-NOV-2003; 2003WO-US032737.
XX 07-NOV-2002; 2002US-0424332P.
XX (IMMU-) IMMUNOGEN INC.

Pt	Hoffee MG; Tavares D, Lutz RJ;
Dx	WPI; 2004-411619/38.
Xx	New antibodies that bind to CD33, useful for treating a disease
Pt	associated with CD33 expression, such as myelodysplastic syndrome, acute
Pt	or chronic myeloid leukemia.
Px	Claim 1; SEQ ID NO 2; 124pp; English.
Px	The present invention describes an isolated anti-CD33 antibody or its
Cc	epitope-binding fragment comprising: (a) at least one complementarity-
Cc	determining region (CDR); or (b) at least heavy chain variable region
Cc	comprising 3 CDRs, and at least one light chain variable region, where
Cc	the CDR has the ability to bind CD33. Also described: (1) an
Cc	immunocoujugate comprising the antibody or its epitope-binding fragment
Cc	linked to a drug or prodrug; (2) a composition comprising the antibody or
Cc	epitope-binding fragment and a drug or prodrug; (3) a pharmaceutical
Cc	composition comprising the immunocoujugate, composition or the antibody
Cc	defined above, or its epitope-binding fragment, and a pharmaceutical
Cc	agent; (4) a diagnostic reagent comprising the antibody defined above,
Cc	where the antibody or antibody fragment is labelled; (5) inhibiting the
Cc	growth of a cell expressing CD33 by contacting the cell with the above
Cc	defined antibody or its epitope-binding fragment, immunocoujugate, or
Cc	(pharmaceutical) composition; (6) determining whether a biological sample
Cc	contains a myelogenous cancer cell; (7) an improved antibody or its
Cc	epitope-binding fragment that specifically binds to CD33; (8) an isolated
Cc	polynucleotide encoding the antibody or its epitope-binding fragment
Cc	defined above; (9) an isolated polynucleotide encoding a light or heavy
Cc	chain of the antibody defined above or its epitope-binding fragment; (10)
Cc	a recombinant vector comprising the polynucleotide; (11) a host cell
Cc	transformed with the recombinant vector; (12) producing an antibody or
Cc	its epitope-binding fragment having the ability to bind CD33; and (13)
Cc	obtaining CD33 from a biological material. The anti-CD33 antibody has
Cc	cytostatic activity. The antibody or its epitope-binding fragment,
Cc	immunocoujugate, composition can be used for treating a subject having a
Cc	disease where CD33 is expressed, such as myelodysplastic syndrome, acute
Cc	myeloid leukemia, chronic myeloid leukemia or pro-myelocytic leukaemia.
Cc	It can also be used for inhibiting the growth of cells expressing CD33,
Cc	and for in vivo imaging or as affinity purification agents. The present
Cc	sequence represents the mouse anti-CD33 antibody MY9-6 heavy chain CDR2,
Cc	which is used in an example from the present invention.
Sq	Sequence 17 AA;
Sq	
Query Match	98.9%; Score 88; DB 8; Length 17;
Best Local Similarity	100.0%; Pred. No. 2.1e-07;
Matches 17; Conservative	Mismatches 0; Indels 0; Gaps 0;
Oy	1 VIYPGNDDISYNQKFXG 17
Dd	1 VIYPGNDDISYNQKFXG 17
RESULT 3	
ID ADO32157	ADO32157 standard; protein; 117 AA.
AC ADO32157;	
XX 12-AUG-2004 (first entry)	
DE Mouse anti-CD33 antibody heavy chain homologous protein SEQ ID NO:73.	
XX anti-CD33 antibody; epitope-binding fragment;	
Kw complementarity-determining region; CDR; immunocoujugate; cytostratic;	
Kw antibody; myelodysplastic syndrome; acute myeloid leukaemia;	
Kw chronic myeloid leukaemia; pro-myelocytic leukaemia; mouse; heavy chain.	
OS Mus musculus.	
XX WO2004043344-A2.	
XX	

PD 27-MAY-2004.
XX
PF 05-NOV-2003; 2003WO-US02737.
XX
PR 07-NOV-2002; 2002US-0424332P.
XX
PA (IMMUN) IMMUNOGEN INC.
XX
PI Hoffee MG, Tavares D, Lutz RJ;
XX
PT WPI, 2004-411619/38.
XX
DR New antibodies that bind to CD33, useful for treating a disease
PT associated with CD33 expression, such as myelodysplastic syndrome, acute
XX or chronic myeloid leukemia.
XX
PS Example 3; SEQ ID NO 73; 124bp; English.
XX
CC The present invention describes an isolated anti-CD33 antibody or its
CC epitope-binding fragment comprising: (a) at least one complementarity-
CC determining region (CDR); or (b) at least heavy chain variable region
CC comprising 3 CDRs, and at least one light chain variable region, where
CC the CDR has the ability to bind CD33. Also described: (1) an
CC immunoconguate comprising the antibody or its epitope-binding fragment
CC linked to a drug or prodrug; (2) a composition comprising the antibody or
CC epitope-binding fragment and a drug or prodrug; (3) a pharmaceutical
CC composition comprising the immunoconguate, composition or the antibody
CC defined above, or its epitope-binding fragment, and a pharmaceutical
CC agent; (4) a diagnostic reagent comprising the antibody defined above,
CC where the antibody or antibody fragment is labelled; (5) inhibiting the
CC growth of a cell expressing CD33 by contacting the cell with the above
CC defined antibody or its epitope-binding fragment, immunoconguate, or
CC (pharmaceutical) composition; (6) determining whether a biological sample
CC contains a myelogenous cancer cell; (7) an improved antibody or its
CC polynucleotide encoding the antibody or its epitope-binding fragment
CC polynucleotide encoding the antibody or its epitope-binding fragment
CC defined above; (9) an isolated polynucleotide encoding a light or heavy
CC chain of the antibody defined above or its epitope-binding fragment; (10)
CC a recombinant vector comprising the polynucleotide; (11) a host cell
CC transformed with the recombinant vector; (12) producing an antibody or
CC its epitope-binding fragment having the ability to bind CD33; and (13)
CC obtaining CD33 from a biological material. The anti-CD33 antibody has
CC cytostatic activity. The antibody or its epitope-binding fragment,
CC immunoconguate, composition can be used for treating a subject having a
CC disease where CD33 is expressed, such as myelodysplastic syndrome, acute
CC myeloid leukaemia, chronic myeloid leukaemia or pro-myelocytic leukaemia.
CC It can also be used for inhibiting the growth of cells expressing CD33,
CC and for in vivo imaging or as affinity purification agents. The present
CC sequence represents a mouse anti-CD33 antibody heavy chain homologous
CC amino acid sequence, which is used in an example from the present
XX invention.

SEQ Sequence 117 AA;

Query Match 98.9%; Score 88; DB 8; Length 117;
Best Local Similarity 94.1%; Pred. No. 1.8e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

QY 1 VYPPGNDISYNOKFXG 17
| | | | | | | | | | | | | | | | | | | | |
Db 50 VYPPGNDISYNOKFXG 66

RESULT 4
AD032091
ID AD032091 standard, protein, 118 AA.
XX
AC AD032091;
XX
DT 12-AUG-2004 (first entry)
XX
DE Mouse anti-CD33 antibody My9-6 heavy chain variable region SEQ ID NO:7.
XX

KW anti-CD33 antibody; epitope-binding fragment;
 KW complementarity-determining region; CDR; immunconjugate; cytostatic;
 KW antibody; myelodysplastic syndrome; acute myeloid leukaemia;
 KW chronic myeloid leukaemia; pro-myelocytic leukaemia; mouse; My9-6;
 KW heavy chain.

OS Mus musculus.

PN MO2004043344-A2.

PD 27-MAY-2004.

XX 05-NOV-2003; 2003WO-US032737.

PF 07-NOV-2002; 2002US-0424332P.

XX (IMMU-) IMMUNOGEN INC.

PI Hoffee MG, Tavares D, Lutz RJ;

DR WPI; 2004-411619/38.

XX N-PSDB; ADO32140.

PT New antibodies that bind to CD33, useful for treating a disease
 PT associated with CD33 expression, such as myelodysplastic syndrome, acute
 PT or chronic myeloid leukemia.

XX Claim 5; SEQ ID NO 7; 124dp; English.

XX The present invention describes an isolated anti-CD33 antibody or its
 CC epitope-binding fragment comprising: (a) at least one complementarity-
 CC determining region (CDR); or (b) at least heavy chain variable region
 CC comprising 3 CDRs, and at least one light chain variable region, where
 CC the CDR has the ability to bind CD33. Also described: (1) an
 CC immunconjugate comprising the antibody or its epitope-binding fragment
 CC linked to a drug or produg; (2) a composition comprising the antibody or
 CC epitope-binding fragment and a drug or produg; (3) a pharmaceutical
 CC composition comprising the immunconjugate, composition or the antibody
 CC defined above, or its epitope-binding fragment, and a pharmaceutical
 CC agent; (4) a diagnostic reagent comprising the antibody defined above,
 CC where the antibody or antibody fragment is labelled; (5) inhibiting the
 CC growth of a cell expressing CD33 by contacting the cell with the above
 CC defined antibody or its epitope-binding fragment, immunconjugate, or
 CC (pharmaceutical) composition; (6) determining whether a biological sample
 CC contains a myelogenous cancer cell; (7) an improved antibody or its
 CC epitope-binding fragment that specifically binds to CD33; (8) an isolated
 CC polynucleotide encoding the antibody or its epitope-binding fragment
 CC defined above; (9) an isolated polynucleotide encoding a light or heavy
 CC chain of the antibody defined above or its epitope-binding fragment; (10)
 CC a recombinant vector comprising the polynucleotide; (11) a host cell
 CC transformed with the recombinant vector; (12) producing an antibody or
 CC its epitope-binding fragment having the ability to bind CD33; and (13)
 CC obtaining CD33 from a biological material. The anti-CD33 antibody has
 CC cytostatic activity. The antibody or its epitope-binding fragment,
 CC immunconjugate, composition can be used for treating a subject having a
 CC disease where CD33 is expressed, such as myelodysplastic syndrome, acute
 CC myeloid leukaemia, chronic myeloid leukaemia or pro-myelocytic leukaemia.
 CC It can also be used for inhibiting the growth of cells expressing CD33,
 CC and for in vivo imaging or as affinity purification agents. The present
 CC sequence represents the mouse anti-CD33 antibody My9-6 heavy chain
 CC variable region, which is used in an example from the present invention.

XX Sequence 118 AA;

SO Query Match 98.9%; Score 88; DB 8; Length 118;

Beet Local Similarity 94.1%; Pred. No. 1.8e-06;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 VITYPNDISYNOKFXG 17

Db 50 VITYPNDISYNOKFXG 66

RESULT 5

AD032093 ID AD032093 standard; protein; 118 AA.

XX AD032093;

DT 12-AUG-2004 (first entry)

XX Humanised mouse anti-CD33 antibody My9-6 heavy chain SEQ ID NO:9.

KW anti-CD33 antibody; epitope-binding fragment;

KW complementarity-determining region; CDR; immunconjugate; cytostatic;

KW antibody; myelodysplastic syndrome; acute myeloid leukaemia;

KW chronic myeloid leukaemia; pro-myelocytic leukaemia; mouse; humanised;

KW My9-6; heavy chain.

XX Mus musculus.

OS Homo sapiens.

OS Synthetic.

PN MO2004043344-A2.

PD 27-MAY-2004.

XX 05-NOV-2003; 2003WO-US032737.

PF 07-NOV-2002; 2002US-0424332P.

XX (IMMU-) IMMUNOGEN INC.

PI Hoffee MG, Tavares D, Lutz RJ;

DR WPI; 2004-411619/38.

XX New antibodies that bind to CD33, useful for treating a disease

PT associated with CD33 expression, such as myelodysplastic syndrome, acute

PT or chronic myeloid leukemia.

XX Claim 11; SEQ ID NO 9; 124dp; English.

XX The present invention describes an isolated anti-CD33 antibody or its
 CC epitope-binding fragment comprising: (a) at least one complementarity-
 CC determining region (CDR); or (b) at least heavy chain variable region
 CC comprising 3 CDRs, and at least one light chain variable region, where
 CC the CDR has the ability to bind CD33. Also described: (1) an
 CC immunconjugate comprising the antibody or its epitope-binding fragment
 CC linked to a drug or produg; (2) a composition comprising the antibody or
 CC epitope-binding fragment and a drug or produg; (3) a pharmaceutical
 CC composition comprising the immunconjugate, composition or the antibody
 CC defined above, or its epitope-binding fragment, and a pharmaceutical
 CC agent; (4) a diagnostic reagent comprising the antibody defined above,
 CC where the antibody or antibody fragment is labelled; (5) inhibiting the
 CC growth of a cell expressing CD33 by contacting the cell with the above
 CC defined antibody or its epitope-binding fragment, immunconjugate, or
 CC (pharmaceutical) composition; (6) determining whether a biological sample
 CC contains a myelogenous cancer cell; (7) an improved antibody or its
 CC epitope-binding fragment that specifically binds to CD33; (8) an isolated
 CC polynucleotide encoding the antibody or its epitope-binding fragment
 CC defined above; (9) an isolated polynucleotide encoding a light or heavy
 CC chain of the antibody defined above or its epitope-binding fragment; (10)
 CC a recombinant vector comprising the polynucleotide; (11) a host cell
 CC transformed with the recombinant vector; (12) producing an antibody or
 CC its epitope-binding fragment having the ability to bind CD33; and (13)
 CC obtaining CD33 from a biological material. The anti-CD33 antibody has
 CC cytostatic activity. The antibody or its epitope-binding fragment,
 CC immunconjugate, composition can be used for treating a subject having a
 CC disease where CD33 is expressed, such as myelodysplastic syndrome, acute
 CC myeloid leukaemia, chronic myeloid leukaemia or pro-myelocytic leukaemia.
 CC It can also be used for inhibiting the growth of cells expressing CD33,
 CC and for in vivo imaging or as affinity purification agents. The present
 CC sequence represents a humanised mouse anti-CD33 antibody My9-6 heavy
 CC chain variable region, which is used in an example from the present
 CC invention.

XX SQ Sequence 118 AA;
 Query Match 98.9%; Score 88; DB 8; Length 118;
 Best Local Similarity 94.1%; Pred. No. 1.8e-06;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 1 VYPGNDISYNOKFXG 17
 |||||
 50 VYFGNDISYNOKFQG 66

Db

RESULT 6
 AAY80140
 ID AAY80140 standard; peptide; 17 AA.
 XX AAY80140;
 AC
 XX 19-MAY-2000 (first entry)
 DT
 XX Chimeric anti-CD25 antibody Ig heavy chain hypervariable region CDR2.
 DE Chimeric anti-CD25 antibody; CD25 binding molecule; immunoglobulin;
 XX Chimeric anti-CD25 antibody; CD25 binding molecule; immunoglobulin;
 KW hypervariable region; complementary determining region; CDR1; CDR2; CDR3;
 KM inflammation; rheumatoid arthritis; hyperproliferative skin disease.
 XX Homo sapiens.
 OS
 XX MO200006604-A2.
 PN
 XX 10-FEB-2000.
 PD
 XX 26-JUL-1999; 99WO-EP005316.
 PF
 XX 27-JUL-1998; 98GB-00016281.
 PR 27-MAY-1999; 99GB-00012460.
 XX
 PA (NOVS) NOVARTIS AG.
 PA (NOVS) NOVARTIS-ERRINDUNGEN VERW GES MBH.
 PA (UNLO) UNIV COLLEGE LONDON.
 PI Amlot PL, Schreier MH;
 XX WPI; 2000-183090/16.
 DR Use of CD25 binding molecules in the treatment of rheumatoid arthritis
 XX and inflammatory or hyperproliferative skin diseases.
 PT
 XX Claim 1; Page 11; 14pp; English.
 PS
 XX The present invention describes CD25 binding molecules, which are used to
 CC treat rheumatoid arthritis and inflammatory or hyperproliferative skin
 CC diseases. The CD25 binding molecule comprises at least one antigen
 CC binding site comprising at least one domain which comprises in sequence,
 CC the hypervariable regions CDR1 (having the sequence RYMMH), CDR2 (having
 CC the sequence AIRPGNSDTSYNOKFEG) and CDR3 (having the sequence DYGYDFP),
 CC or their direct equivalents. The CD25 binding molecules are used in the
 CC treatment of rheumatoid arthritis and inflammatory or hyperproliferative
 CC skin diseases, such as psoriasis, atopic dermatitis, contact dermatitis
 CC and further eczematous dermatitis, seborrheic dermatitis, lichen
 CC planus, Pemphigus, bullous Pemphigoid, Epidermolysis bullosa, urticaria,
 CC angiodemas, vasculitides, erythemas, cutaneous eosinophilias, lupus
 CC erythematosus and acne. A more preferred CD25 binding molecule for use in
 CC accordance with the present invention is selected from a chimeric anti-
 CC CD25 antibody which comprises at least: (1) one immunoglobulin heavy
 CC chain, or fragment, which comprises (i) a variable domain comprising in
 CC sequence the hypervariable regions CDR1, CDR2 and CDR3 (as above) and
 CC (ii) the constant part, or fragment, of a human heavy chain; and (2) one
 CC immunoglobulin light chain, or fragment, which comprises (i) a variable
 CC domain comprising in sequence the hypervariable regions CDR1', CDR2' and
 CC CDR3' (SASSISMQ, DTSKLAS and HORSSTY, respectively) and (ii) the
 CC constant part, or fragment, of a human light chain

SQ Sequence 17 AA;
 Query Match 82.0%; Score 73; DB 3; Length 17;
 Best Local Similarity 81.2%; Pred. No. 6.2e-05;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 2 IYPGNDISYNOKFXG 17
 |||||
 2 IYPGNSDTSYNOKFEG 17

Db

RESULT 7
 AAB12175
 ID AAB12175 standard; peptide; 17 AA.
 XX AAB12175;
 AC
 XX 10-NOV-2000 (first entry)
 DT
 XX Human CDR2 for IL-2R monoclonal antibody.
 DE Human CDR2 for IL-2R monoclonal antibody.
 XX Human, CDR; humanised antibody; complementarily determining region;
 KW IL-2Ralpha; interleukin-2 receptor; transplant rejection; CD25;
 KM immunosuppression.
 XX Homo sapiens.
 OS
 XX MO200030679-A1.
 PN
 XX 02-JUN-2000.
 PD
 XX 22-NOV-1999; 99WO-EP008988.
 PF
 XX 23-NOV-1998; 98GB-00025632.
 PR
 XX (NOVS) NOVARTIS AG.
 PA (NOVS) NOVARTIS-ERRINDUNGEN VERW GES MBH.
 PA Feutren G, Howell RK, Marbach P, Roberts A, Schreier MH;
 PI Schulz M;
 XX WPI; 2000-399934/34.
 DR
 XX Preventing or treating transplant rejection in a recipient comprises
 PT administering a monoclonal antibody specific for interleukin-2 receptor
 PT beyond the very early phase following transplantation.
 PT
 XX Disclosure; Page 2; 17pp; English.
 PS
 XX The present sequence is a human complementarily determining region (CDR).
 CC This sequence was used to generate a humanised antibody specific for the
 CC alpha subunit of interleukin-2 receptor (IL-2Ralpha). The humanised IL-
 CC 2Ralpha antibody would be useful for preventing or treating transplant
 CC rejection in a recipient of organ, tissue or modified or unmodified cell
 CC transplant. The use of a monoclonal antibody specific for IL-2R decreases
 CC recipient rejection in an immunosuppression-intolerant or non-compliant
 CC recipient compared with available therapies. Also, undesirable side
 CC effects associated with current treatments e.g. renal dysfunction,
 CC hirsutism, gingival hyperplasia and hypertension are avoided
 CC
 XX Sequence 17 AA;
 Query Match 82.0%; Score 73; DB 3; Length 17;
 Best Local Similarity 81.2%; Pred. No. 6.2e-05;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 2 IYPGNDISYNOKFXG 17
 |||||
 2 IYPGNSDTSYNOKFEG 17

Db

RESULT 8
 AA014423

ID AA014423 standard; peptide; 17 AA.
 XX
 AC AA014423;
 XX
 DT 03-MAY-2002 (first entry)
 XX
 DE CD25 binding protein domain 1 hypervariable region CDR2.
 XX
 KM CD25 binding protein; hypervariable region; CDR2; gastrointestinal tract;
 KM inflammatory disease; irritable bowel syndrome; IBS; Crohn's disease;
 KM ulcerative colitis; inflammatory intestinal disease; medicament.
 XX
 OS Unidentified.
 XX
 PN MO200172645-A1.
 XX
 PD 04-OCT-2001.
 XX
 PF 28-MAR-2001; 2001WO-EP003541.
 XX
 PR 30-MAR-2000; 2000GB-00007911.
 XX
 PA (NOVS) NOVARTIS AG.
 PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
 XX
 PI Adam H, Faerber L;
 XX
 DR WPI; 2001-626258/72.
 XX
 PT CD25 binding molecule which comprises antigen binding site comprising
 PT fully defined CDR1, CDR2, CDR3 hypervariable regions; for treating
 PT Crohn's disease, ulcerative colitis, irritable bowel syndrome.
 XX
 PS Claim 1; Page 12; 19pp; English.
 XX
 CC The invention comprises a CD25 binding protein comprising at least one
 CC CD25 binding domain containing the hypervariable regions CDR1, CDR2 and
 CC CDR3. The CD25 binding domain 1 hypervariable regions are shown in
 CC AA014422 - AA014424. CD25 binding domain 2 hypervariable regions are
 CC shown in AA014425 - AA014427. The CD25 binding protein is useful for
 CC treating an inflammatory disease of the gastrointestinal tract, such as:
 CC irritable bowel syndrome, IBS; Crohn's disease; ulcerative colitis; or
 CC other inflammatory intestinal disease. The CD25 binding protein is also
 CC useful in the manufacture of a medicament for the treatment of
 CC inflammatory disease of the intestinal tract. The present amino acid
 CC sequence represents the CD25 binding domain 1 hypervariable region CDR2
 XX
 SQ Sequence 17 AA;
 QY
 Query Match 82.0%; Score 73; DB 4; Length 17;
 Best Local Similarity 81.2%; Pred. No. 6.2e-05;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 DB 2 IYPGNDISYNQKFXG 17
 2 IYPGNSDTSYNQKFEFG 17
 RESULT 9
 ABB82655
 ID ABB82655 standard; peptide; 17 AA.
 XX
 AC ABB82655;
 XX
 DT 19-FEB-2003 (first entry)
 XX
 DE CDR2 fragment of a chimeric anti-CD25 antibody.
 XX
 KM CD25; immunosuppressive; hepatotropic; antiasthmatic; dermatological;
 KM antiarthritic; cytostatic; nephrotropic; neuroprotective; antitumor;
 KM antiinflammatory; vasotropic; complementarily determining region;
 KM steroid; CDR; anti-CD25 antibody.
 XX

OS Unidentified.
 XX
 PN MO200281508-A2.
 XX
 PD 17-OCT-2002.
 XX
 PF 05-APR-2002; 2002WO-EP003808.
 XX
 PR 06-APR-2001; 2001GB-00008816.
 PR 06-APR-2001; 2001GB-00008817.
 PR 06-APR-2001; 2001GB-00008821.
 XX
 PA (UYBR-) UNIV BRISTOL.
 XX
 PI Hearing SD, Dayan CM, Norman MR;
 XX
 DR WPI; 2003-067514/06.
 XX
 PT CD25 binding molecules useful for prevention and treatment of autoimmune
 PT hepatitis, asthma, eczema, vasculitis, temporal arthritis, leukemia,
 PT multiple sclerosis and Crohn's disease in steroid-resistant patients.
 XX
 PS Claim 1; Page 20; 22pp; English.
 XX
 CC The invention relates to a CD25 binding molecule (I) comprising at least
 CC one antigen binding site having at least one domain which comprises in
 CC sequence, the hypervariable regions CDR1, CDR2 and CDR3 (complementarily
 CC determining region), for use in prevention or treatment of diseases such
 CC as autoimmune hepatitis, asthma, eczema, vasculitis, temporal arthritis,
 CC leukemia, glomerulonephritis, multiple sclerosis and Crohn's disease in a
 CC steroid-resistant patient. (I) is useful in the manufacture of a
 CC medicament for use in the prevention and treatment of autoimmune
 CC hepatitis, asthma, eczema, vasculitis, temporal arthritis, systemic lupus
 CC erythematosus, leukemia, glomerulonephritis, multiple sclerosis,
 CC ulcerative colitis, sarcoid and Crohn's disease in a steroid-sensitive or
 CC steroid-resistant patient. (I) is coadministered with a further drug
 CC substance. The use of CD25 binding molecules make the steroid-sensitive
 CC patients respond quicker and allow a lower dose of steroids to be used,
 CC thus significantly reducing the side effects of steroid treatments. The
 CC present sequence represents a hypervariable CDR2 fragment of a chimeric
 CC anti-CD25 antibody, a CD25 binding molecule
 XX
 SQ Sequence 17 AA;
 QY
 Query Match 82.0%; Score 73; DB 6; Length 17;
 Best Local Similarity 81.2%; Pred. No. 6.2e-05;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 DB 2 IYPGNDISYNQKFXG 17
 2 IYPGNSDTSYNQKFEFG 17
 RESULT 10
 AAR91365
 ID AAR91365 standard; protein; 106 AA.
 XX
 AC AAR91365;
 XX
 DT 09-OCT-1996 (first entry)
 XX
 DE Anti-proenkephalin antibody PE-1.
 XX
 KM Proenkephalin; antibody; PE; apoptosis inducer; opioid receptor; cancer;
 KM monoclonal; cytoplasmic anchor; nuclear localisation signal; cataract;
 KM opioid peptide precursor; Opi; lens cell; cell cycle arrest agent;
 KM chemotherapeutic; genotoxic; cell cycle synchronisation; therapy.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FH Region 30..34
 FT /note="CDR1"

```

FT Region 49. .65
FT /note= "CDR2"
FT Region 98. .106
FT /note= "CDR3"
XX
XX WO9606863-A1.
XX
XX 07-MAR-1996.
XX
XX 30-AUG-1995; 95WO-GB002037.
XX
XX 30-AUG-1994; 94GB-00017444.
XX
XX 23-SEP-1994; 94GB-00019285.
XX
XX (UYDU-) UNIV DUNDEE.
XX
XX Spruce BA, Prescott A, Boettger A, Dewar DA;
XX
XX WPI; 1996-160311/16.
XX
XX New agents for inducing apoptosis in cells - which are able to modulate a
XX biochemical pathway in which prode. of opioid peptide precursor genes
XX participate.
XX
XX Claim 6; Fig 5; 64pp; English.
XX
XX AAR91363-R91366, AAR91368-R19373 and AAR95283-R95286 represent partial
XX sequences of anti-proenkephalin (anti-PE) antibodies, which are used in
XX an agent for inducing apoptosis in cells. This sequence represents the
XX anti-PE antibody PE-1, and recognises residues 187-192 of the PE sequence
XX (see AAR91362). The agents preferably neutralise PE or its proteolytic
XX derivatives, increase the level of, activate or mimic nuclear PE, and act
XX as an antagonist to receptors related or identical to the delta and kappa
XX opioid receptors. The agent is preferably a neutralising monoclonal
XX antibody (such as this sequence), or a fragment or allelic form of one of
XX these antibodies. A cytoplasmic anchor, or a nuclear localisation signal
XX may also be included in the agent. The agent is able to modulate a
XX biochemical pathway in a cell in which products of opioid peptide
XX precursor (OPP) genes participate in order to induce the cell to
XX apoptose. The agents can be used for the treatment of cancer or for
XX inducing apoptosis in lens cells following a cataract operation. These
XX agents promote apoptosis of proliferating cells with less, or no, effect
XX on normal mature cell types. The agents may be administered in
XX combination with a genotoxic or cell cycle arrest agent. Alternatively,
XX the agent may be complexed with a chemotherapeutic, irradiation or cell
XX cycle arrest (synchronisation) agent
XX
XX Sequence 106 AA;
SQ
XX
XX Query Match 82.0%; Score 73; DB 2; Length 106;
XX Best Local Similarity 81.2%; Pred. No. 0.00047;
XX Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 2 IYPGNDISYNQKFXG 17
XX ||||| |||||
XX 50 IYPGNSDTSYNQKFXG 65
XX
XX
XX RESULT 11
XX ADO32164
XX ID ADO32164 standard; protein; 114 AA.
XX
XX AC ADO32164;
XX
XX 12-AUG-2004 (first entry)
XX
XX Mouse anti-CD3 antibody heavy chain homologous protein SEQ ID NO:80.
XX
XX anti-CD3 antibody; epitope-binding fragment;
XX complementarity-determining region; CDR; immunoglobulin; cytostatic;
XX antibody; myelodysplastic syndrome; acute myeloid leukaemia;
XX chronic myeloid leukaemia; pro-myelocytic leukaemia; mouse; heavy chain.
XX

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OS Mus musculus.
XX
XX WO2004043344-A2.
XX
XX 27-MAY-2004.
XX
XX 05-NOV-2003; 2003WO-US032737.
XX
XX 07-NOV-2002; 2002US-0424332P.
XX
XX (IMMU-) IMMUNOGEN INC.
XX
XX Hoffee MG, Tavares D, Lutz RJ;
XX
XX WPI; 2004-411619/38.
XX
XX New antibodies that bind to CD33, useful for treating a disease
XX associated with CD33 expression, such as myelodysplastic syndrome, acute
XX or chronic myeloid leukemia.
XX
XX Example 3; SEQ ID NO 80; 124pp; English.
XX
XX The present invention describes an isolated anti-CD33 antibody or its
XX epitope-binding fragment comprising: (a) at least one complementarity-
XX determining region (CDR); or (b) at least heavy chain variable region
XX comprising 3 CDRs, and at least one light chain variable region, where
XX the CDR has the ability to bind CD33. Also described: (1) an
XX immunoglobulin comprising the antibody or its epitope-binding fragment
XX linked to a drug or prodrug; (2) a composition comprising the antibody or
XX epitope-binding fragment and a drug or prodrug; (3) a pharmaceutical
XX composition comprising the immunoglobulin, composition or the antibody
XX defined above, or its epitope-binding fragment, and a pharmaceutical
XX agent; (4) a diagnostic reagent comprising the antibody defined above,
XX where the antibody or antibody fragment is labelled; (5) inhibiting the
XX growth of a cell expressing CD33 by contacting the cell with the above
XX defined antibody or its epitope-binding fragment, immunoglobulin, or
XX (pharmaceutical) composition; (6) determining whether a biological sample
XX contains a myelogenous cancer cell; (7) an improved antibody or its
XX epitope-binding fragment that specifically binds to CD33; (8) an isolated
XX polynucleotide encoding the antibody or its epitope-binding fragment
XX defined above; (9) an isolated polynucleotide encoding a light or heavy
XX chain of the antibody defined above or its epitope-binding fragment; (10)
XX a recombinant vector comprising the polynucleotide; (11) a host cell
XX transformed with the recombinant vector; (12) producing an antibody or
XX its epitope-binding fragment having the ability to bind CD33; and (13)
XX obtaining CD33 from a biological material. The anti-CD33 antibody has
XX cytostatic activity. The antibody or its epitope-binding fragment,
XX immunoglobulin, composition can be used for treating a subject having a
XX disease where CD33 is expressed, such as myelodysplastic syndrome, acute
XX myeloid leukaemia, chronic myeloid leukaemia or pro-myelocytic leukaemia.
XX It can also be used for inhibiting the growth of cells expressing CD33,
XX and for in vivo imaging or as affinity purification agents. The present
XX sequence represents a mouse anti-CD33 antibody heavy chain homologous
XX amino acid sequence, which is used in an example from the present
XX invention.
XX
XX Sequence 114 AA;
SQ
XX
XX Query Match 82.0%; Score 73; DB 8; Length 114;
XX Best Local Similarity 81.2%; Pred. No. 0.00051;
XX Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 2 IYPGNDISYNQKFXG 17
XX ||||| |||||
XX 49 IYPGNSDTSYNQKFXG 64
XX
XX
XX RESULT 12
XX AAR64224
XX ID AAR64224 standard; protein; 116 AA.
XX
XX AC AAR64224;
XX

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DT 21-SEP-1995 (first entry)
XX Anti-(6-4) photoproduct 64M-2 antibody variable heavy chain.
DE Anti-(6-4) photoproduct 64M-2 antibody; variable heavy chain;
XX recombinant production.
KM Mus musculus.
XX
OS Mus musculus.
FH Key Location/Qualifiers
FT Misc-difference 29 /note= "STOP codon or Trp"
FT Misc-difference 79 /label= Ala, Val
FT
XX JP06335391-A.
XX
XX 06-DEC-1994.
XX
XX 27-MAY-1993; 93JP-00146798.
XX
XX 27-MAY-1993; 93JP-00146798.
XX
XX (DAII-) DAII CHI KAKAGU YAKUHIN KK.
XX
XX WPI: 1995-056903/08.
XX N-PSDB; AAQ80317.
XX
XX Dna sequence of the heavy and light chain variable regions of an anti(6-
PT 4) photoproduct 64M-2 antibody - used in the production of a recombinant
PT antibody for the recognition of (6-4) photoproduct.
XX
XX
PS Claim 7; Page 2-3; 12pp; Japanese.
XX
XX AAQ80317 and AAQ80318 encode AAR64224 and AAR64225 the variable heavy and
CC light chains of the anti-(6-4) photoproduct 64M-2 antibody. The DNA
CC sequences can be used to transform host cells for the recombinant
CC production of the antibody, which can be used in assays for the
CC photoproduct
XX
XX Sequence 116 AA;
SQ
Query Match 82.0%; Score 73; DB 2; Length 116;
Best Local Similarity 81.2%; Pred. No. 0.00052;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 IYPGNDISYNQKFXG 17
Db 47 IYPGNSDTSYNQKFXG 62
RESULT 13
AEA88769
ID AEA88769 standard; protein; 127 AA.
XX
XX AEA88769;
AC
XX 25-AUG-2005 (first entry)
XX
XX Murine SARS-specific monoclonal antibody VH chain, F26G9-VH SEQ ID: 3.
XX
XX Monoclonal antibody; development; antibody therapy; diagnostic;
KM microorganism detection; vaccine; severe acute respiratory syndrome;
KM respiratory-gen.; virucide; infection; respiratory disease;
KM antimicrobial; heavy chain variable region; F26G9.
XX
XX Mus musculus.
XX
XX WO2005054469-A1.
XX
XX 16-JUN-2005.
XX
XX 06-DEC-2004; 2004WO-CA002084.
```

```
XX
XX 05-DEC-2003; 2003US-0526971P.
PR 06-MAY-2004; 2004US-0568225P.
XX
XX (CNDD ) CANADA MIN HEALTH.
XX
XX Berry J, Jones S, Yuan XY, Gubbins M, Andonov A, Weingarti H;
PI Drebot M, Plummer F;
XX
XX WPI: 2005-425414/43.
XX N-PSDB; AEA88787.
XX
XX Novel severe acute respiratory syndrome neutralizing monoclonal antibody
PT chosen from F26G3, F26G7, F26G9, F26G10, F26G18 and F26G19, useful for
PT treating severe acute respiratory syndrome infection.
XX
XX Disclosure; SEQ ID NO 3; 75pp; English.
XX
XX The present invention relates to a severe acute respiratory syndrome
CC (SARS) neutralizing monoclonal antibody. The invention is useful for
CC treating, preventing or ameliorating symptoms associated with SARS
CC infection in patients and for detecting SARS virus within biological
CC samples, and for the development of diagnostic tests, pathogenicity and
CC vaccine studies. The present sequence is the murine SARS-specific
CC monoclonal antibody variable heavy chain (VH) protein.
XX
XX Sequence 127 AA;
SQ
Query Match 82.0%; Score 73; DB 9; Length 127;
Best Local Similarity 81.2%; Pred. No. 0.00058;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 IYPGNDISYNQKFXG 17
Db 50 IYPGNSDTSYNQKFXG 65
RESULT 14
AAR14153
ID AAR14153 standard; protein; 136 AA.
XX
XX AAR14153;
AC
XX 25-MAR-2003 (revised)
XX 06-DEC-1991 (first entry)
XX
XX Ig heavy chain V region of RFT5 anti-CD25 antibody.
DE
XX
XX T-cell proliferation inhibitor; immunomodulation; T-cell leukaemia;
XX humanised antibody; human-mouse chimeric antibody; ss.
XX
XX Mus musculus.
XX
XX Key Location/Qualifiers
FH Peptide 1..19
FT /label= leader
FT Region 20..49
FT /label= FR1
FT Domain 50..54
FT /label= CDR1
FT Region 55..68
FT /label= FR2
FT Domain 69..85
FT /label= CDR2
FT Region 86..117
FT /label= FR3
FT Domain 118..125
FT /label= CDR3
FT Region 126..136
FT /label= FR4
XX
XX EP449769-A.
```

PD 02-OCT-1991.
 XX
 PF 13-MAR-1991; 91EP-00810166.
 XX
 PR 16-MAR-1990; 90GB-00005962.
 PR 05-SEP-1990; 90GB-00019333.
 XX
 PA (SANO) SANDOZ LTD.
 PA (UNIO) ROYAL FREE HOSPITAL SCHOOL MED.
 PA (AMLO/) AMLOT P L.
 XX
 PI Amiot P, Akbar AN, Heinrich G, Cammisuli S;
 XX
 DR WPI; 1991-290161/40.
 DR N-PSDB; AAQ13833.
 XX
 PT New CD25 binding molecules hyper-variable regions CDR2 and CDR3 - used in
 PT immuno-suppression e.g. graft rejection, malignancies of CD25 cells and
 PT for treating HIV infections.
 XX
 PS Claim 1; Page 13-14; 32pp; English.
 XX
 CC This sequence is the heavy chain variable region of the murine CD25-
 CC binding antibody, RFT5-1gG2a. The three CDR regions (see Features Table)
 CC are characteristic of the CD25-binding mol. covered by the invention. A
 CC mouse/human chimeric antibody is expressed using the V(H) domain-encoding
 CC sequence (along with the promoter and enhancer) fused into the EcoRI
 CC restriction site of pSV2 neo- human gamma, constant part. The chimeric
 CC antibody heavy chain thus comprises the human gamma-1-type heavy chain
 CC and RFT5-1gG2a variable region. A similarly humanised murine CD25-Ab
 CC light chain can be prepared (see AAQ13834) to give a chimeric antibody.
 CC CD25-binding molecules inhibit T-cell proliferation and show good
 CC immunomodulatory activity. They are pref. used with CD7 Ab. (Updated on
 CC 25-MAR-2003 to correct PA field.)
 CC
 XX
 SQ Sequence 136 AA;
 Query Match 82.0%; Score 73; DB 2; Length 136;
 Best Local Similarity 81.2%; Pred. No. 0.00063;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 IYPGNDISYNOKFXG 17
 Db 70 IYPGNSDTSYNOKFEG 85
 RESULT 15
 ADCT9230 standard; protein; 219 AA.
 XX
 AC ADC79230;
 XX
 DT 01-JAN-2004 (first entry)
 XX
 DE OC125-3.11 amino acid sequence.
 XX
 KM CA 125 tumour antigen; CA 125 tumour antigen modulator;
 KM CA 125 tumour antigen-associated disease; cytostatic; gene therapy.
 XX
 OS Synthetic.
 XX
 PN WO2003076465-A2.
 XX
 PD 18-SEP-2003.
 XX
 PF 11-MAR-2003; 2003WO-CA000341.
 XX
 PR 11-MAR-2002; 2002US-0363306P.
 PR 28-FEB-2003; 2003CA-02420494.
 XX
 PA (UYSH) UNIV SHERBROOKE.
 XX
 PI Rancourt C, Piche A, Beaudin J;

XX
 DR WPI; 2003-722323/68.
 XX
 PT New modulator capable of negatively modulating a CA 125 tumor antigen in
 PT a mammalian cell, useful for preparing a composition for preventing or
 PT treating CA 125 tumor antigen-associated disease in a mammal.
 XX
 PS Disclosure; Fig 29C; 90pp; English.
 XX
 CC The present invention describes a modulator capable of negatively
 CC modulating a CA 125 tumour antigen in a mammalian cell. Also described:
 CC (1) a recombinant nucleic acid comprising at least one sequence selected
 CC from the group consisting of ADC79233, ADC79234, ADC79235, ADC79236,
 CC ADC79237 and ADC79238; (2) a vector comprising the recombinant nucleic
 CC acid; (3) a host cell; (4) a pharmaceutical composition; (5) preventing
 CC or treating CA 125 tumour antigen-associated disease in a mammal; and (6)
 CC negatively modulating a CA 125 tumour antigen in a mammalian cell. A
 CC modulator capable of negatively modulating a CA 125 tumour antigen has
 CC cytostatic activity, and can be used in gene therapy. The modulator,
 CC recombinant nucleic acid, vector or host cell can be used for preparing a
 CC composition for preventing or treating CA 125 tumour antigen-associated
 CC disease in a mammal. The present sequence is used in the exemplification
 CC of the present invention.
 CC
 XX
 SQ Sequence 219 AA;
 Query Match 82.0%; Score 73; DB 7; Length 219;
 Best Local Similarity 81.2%; Pred. No. 0.0011;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 IYPGNDISYNOKFXG 17
 Db 51 IYPGNSDTSYNOKFXG 66
 RESULT 16
 ADG32327 standard; protein; 248 AA.
 ID ADG32327
 XX
 AC ADG32327;
 XX
 DT 26-FEB-2004 (first entry)
 XX
 DE Mouse scFV SS2 antibody targeted against s_sclerostorium SegID 36.
 XX
 KM mouse; murine; scFV; anti-fungal peptide; AFP; scFV; disease resistant;
 KM transgenic; plant; fungal infection; antibody;
 KM pathogen-specific antibody; fungicidal; agriculture.
 XX
 OS Mus sp.
 XX
 PN WO2003089475-A2.
 XX
 PD 30-OCT-2003.
 XX
 PF 14-APR-2003; 2003WO-EP003852.
 XX
 PR 22-APR-2002; 2002EP-00008929.
 PR 28-MAY-2002; 2002EP-00011807.
 XX
 PA (FRAU) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.
 XX
 PI Peschen D, Fischer R, Schillberg S, Liao Y, Dorfmueller S;
 XX
 DR WPI; 2003-854088/79.
 DR N-PSDB; ADG32302.
 XX
 PT New fusion protein comprising an anti-fungal protein or peptide and an
 PT antibody fragment, useful in agriculture and horticulture for producing
 PT Ascomyceta-resistant transgenic plants, plant cells or plant tissues.
 XX
 XX Example 13; SEQ ID NO 36; 47pp; English.
 XX

CC This invention relates to a novel fusion protein comprising an anti-fungal protein or peptide (AFP) and an antibody fragment (scFv).
CC Specifically, it refers to AFPs recognizing an epitope of an Ascomyceta and a cellular targeting sequence, which can be used to generate disease resistant transgenic plants that are protected against fungal infection.
CC Accordingly, a method is described for antibody based resistance in plants such that the undesirable and expensive chemical controls often used in agriculture are not required. The present invention provides antibodies, recombinant antibodies and fragments thereof, as well as fusion proteins that can be used as pathogen-specific antibodies targeted to different plant cell compartments. As such, these fungicidal agents confer a broad spectrum of disease resistance in both economically important crops and ornamental plants. This polypeptide is an antibody used in an exemplification of the invention.

CC Sequence 248 AA;
SQ

Query Match 82.0%; Score 73; DB 7; Length 248;
Best Local Similarity 81.2%; Pred. No. 0.0012;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGNDISYNQKFXG 17
Db 53 IYPGNSDTSYNQKFXG 68
|||||
|

RESULT 17
ADG32341
ID ADG32341 standard; protein; 615 AA.
XX
AC ADG32341;
XX
DT 26-FEB-2004 (first entry)
XX
DE Fusion protein of AFP chitinase-scfv SS2 SegID 50.
XX
KW wheat; scFv; anti-fungal peptide; AFP; scFv; disease resistant;
transgenic; plant; fungal infection; antibody;
KW pathogen-specific antibody; fungicidal; agriculture; mouse; chimeric;
murine.
XX
OS Chimeric.
OS Synthetic.
OS Triticum sp.
OS Mus musculus.
XX
PN WO2003089475-A2.
XX
PD 30-OCT-2003.
XX
PF 14-APR-2003; 2003WO-EP003852.
XX
PR 22-APR-2002; 2002EP-00008929.
PR 28-MAY-2002; 2002EP-00011807.
XX
PA (FRAU) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.
XX
PI Peschen D, Fischer R, Schillberg S, Liao Y, Dorfmueller S;
XX
DR WPI; 2003-854088/79.
DR N-PSDB; ADG32316.
XX
XX New fusion protein comprising an anti-fungal protein or peptide and an antibody fragment, useful in agriculture and horticulture for producing Ascomyceta-resistant transgenic plants, plant cells or plant tissues.
XX
PS Claim 21; SEQ ID NO 50; 47pp; English.
XX
CC This invention relates to a novel fusion protein comprising an anti-fungal protein or peptide (AFP) and an antibody fragment (scFv).
CC Specifically, it refers to AFPs recognizing an epitope of an Ascomyceta and a cellular targeting sequence, which can be used to generate disease resistant transgenic plants that are protected against fungal infection.

CC Accordingly, a method is described for antibody based resistance in plants such that the undesirable and expensive chemical controls often used in agriculture are not required. The present invention provides antibodies, recombinant antibodies and fragments thereof, as well as fusion proteins that can be used as pathogen-specific antibodies targeted to different plant cell compartments. As such, these fungicidal agents confer a broad spectrum of disease resistance in both economically important crops and ornamental plants. This polypeptide is a fusion protein of the order [targeting sequence - AFP - linker - antibody fragment - tag] of the invention.

CC Sequence 615 AA;
SQ

Query Match 82.0%; Score 73; DB 7; Length 615;
Best Local Similarity 81.2%; Pred. No. 0.0033;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGNDISYNQKFXG 17
Db 394 IYPGNSDTSYNQKFXG 409
|||||
|

RESULT 18
ADC66265
ID ADC66265 standard; protein; 17 AA.
XX
AC ADC66265;
XX
DT 18-DEC-2003 (first entry)
XX
DE Mouse protein sequence for generating anti-CD20 antibody.
XX
KW immunosuppressant; cytostatic; antibody; CD20;
KW N-glycoside bond complex sugar chain; fucose; N-acetylglucosamine;
KW sugar chain; cancer; immune disorder.
XX
OS Mus musculus.
XX
PN WO2003055993-A1.
XX
PD 10-JUL-2003.
XX
PF 25-DEC-2002; 2002WO-JP013534.
XX
PR 25-DEC-2001; 2001JP-00392753.
PR 09-APR-2002; 2002JP-00106948.
PR 01-NOV-2002; 2002JP-00319975.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Shitara K, Sakurada M, Uchida K, Shinkawa T, Satoh M, Nakano R;
XX
DR WPI; 2003-559274/52.
XX
PT Antibody binding to CD20 and having Fc-bound sugar chains of low fucose content for treatment of cancer and immune disorders.
XX
PS Claim 30; SEQ ID NO 9; 200pp; Japanese.
XX
CC The invention relates to cells producing an antibody molecule specifically binding to CD20 are new, in which the antibody contains N-glycoside bond complex sugar chains bonded to the Fc region of the antibody peptide chains, of which less than 20% have a fucose residue bonded to the N-acetylglucosamine residue at the reducing end of the sugar chain. The cells are used in the treatment and prevention of cancer and immune disorders. This sequence corresponds to a protein used in the method of the invention.

CC Sequence 17 AA;
SQ

Query Match 80.9%; Score 72; DB 7; Length 17;
Best Local Similarity 81.2%; Pred. No. 9.1e-05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGNDISYNQKFXG 17
 |||||
 DB 2 IYPGNGDTSYNQKFXG 17
 |||||

RESULT 19
 ADJ94575
 ID ADJ94575 standard; peptide; 17 AA.
 XX

AC ADJ94575;
 XX

XX 06-MAY-2004 (first entry)
 XX

DE Humanised anti-CD20 monoclonal antibody heavy chain variable region #2.
 XX

KM humanised anti-CD20 monoclonal antibody; hCD20 monoclonal antibody; Mab;
 KM IV1AB variable region; B-cell lymphoma; leukaemia; autoimmune disease;
 KM thrombocytopenia; lupus; rheumatoid arthritis;
 KM heavy chain variable region.
 XX

OS Unidentified.
 XX

PN WO2003068821-A2.
 XX

PD 21-AUG-2003.
 XX

PF 14-FEB-2003; 2003WO-GB000665.
 XX

PR 14-FEB-2002; 2002US-0356132P.
 PR 07-OCT-2002; 2002US-0416232P.
 XX

PA (IMMU-) IMMUNOMEDICS INC.
 PA (MCCA/) MCCALL J D.
 XX

PI Hansen H, Qu Z, Goldenberg DM;
 XX

DR WPI; 2003-697522/66.
 XX

PT New humanized anti-CD20 monoclonal antibody (Mab) that retains
 PT substantially the B-cell and B-cell lymphoma and leukemia cell targeting
 PT of the murine anti-CD20 Mab, useful for treating B-cell lymphoma,
 PT leukemia or an autoimmune diseases.
 XX

PS Claim 7; Page 68; 106pp; English.
 XX

CC The invention comprises a humanised anti-CD20 (hCD20) monoclonal antibody
 CC (Mab) or its antigen-binding fragment containing the complementarity
 CC determining regions (CDRs) of at least one murine anti-CD20 Mab variable
 CC region and the framework regions (FR) of at least one human IV1AB
 CC variable region. The antibodies of the invention are useful for
 CC diagnosing or preventing B-cell lymphoma, leukaemia or an autoimmune
 CC disease (e.g. thrombocytopenia, lupus or rheumatoid arthritis). The
 CC present amino acid sequence represents a humanised antibody heavy chain
 CC variable region of the invention.
 XX

SO Sequence 17 AA;
 XX

Query Match 80.9%; Score 72; DB 7; Length 17;
 Best Local Similarity 81.2%; Pred. No. 9.1e-05;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGNDISYNQKFXG 17
 |||||
 DB 2 IYPGNGDTSYNQKFXG 17
 |||||

RESULT 20
 ADP79604
 ID ADP79604 standard; peptide; 17 AA.
 XX

AC ADP79604;
 XX

DT 04-NOV-2004 (first entry)
 XX

DE Murine 2H7 and humanised 2H7.v16 variant VH domain CDR2 SEQ ID NO:11.
 XX

KM humanised antibody; anti-human CD20 antibody; cytostatic; antineoplastic;
 KM antiarthritic; immunosuppressive; antiinflammatory; haemostatic;
 KM neuroprotective; antipsoriatic; muscular; antidiabetic; antianemic;
 KM nephrotropic; hepatotropic; CNS; CD20 inhibitor;
 KM humanised CD20 binding antibody; CD20 positive cancer; leukaemia;
 KM autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
 KM inflammatory bowel disease; thrombocytopenic purpura;
 KM autoimmune thrombocytopenia; multiple sclerosis; psoriasis;
 KM myasthenia gravis; vasculitis; diabetes mellitus; glomerulonephritis;
 KM autoimmune haemolytic anaemia.
 XX

OS Mus sp.
 OS Homo sapiens.
 OS Synthetic.
 XX

PN WO2004056312-A2.
 XX

PD 08-JUL-2004.
 XX

PF 16-DEC-2003; 2003WO-US040426.
 XX

PR 16-DEC-2002; 2002US-0434115P.
 PR 01-DEC-2003; 2003US-0526163P.
 XX

PA (GERTH) GENENTECH INC.
 XX

PI Adams CW, Chan AC, Crowley CW, Lowman HB, Nakamura GR, Presta LG;
 XX

DR WPI; 2004-500261/47.
 XX

PT New humanized anti-CD20 antibodies, useful for treating a CD20 positive
 PT cancer (e.g. B cell lymphoma, leukemia, or non-Hodgkin's lymphoma) or
 PT autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis or
 PT psoriasis).
 XX

PS Claim 2; SEQ ID NO 11; 108pp; English.
 XX

CC The present invention describes a humanised antibody (I) that binds human
 CC CD20 or its antigen-binding fragment, which depletes primate B cells in
 CC vivo, and comprises in the H chain Variable region (VH) at least a CDR3
 CC sequence consisting of 9 amino acids (SEQ ID NO:12, ADP79605) from an
 CC anti-human CD20 antibody and substantially the human consensus framework
 CC (FR) residues of human heavy chain subgroup III (VHIII). (I) has
 CC cyostatic, antirheumatic, antiarthritic, immunosuppressive,
 CC antiinflammatory, haemostatic, neuroprotective, antipsoriatic, muscular,
 CC antidiabetic, antianemic, nephrotropic, hepatotropic and CNS
 CC activities, and can be used as a CD20 inhibitor. The humanised CD20
 CC binding antibody (I) can be used for treating a CD20 positive cancer
 CC (e.g. B cell lymphoma, leukaemia, non-Hodgkin's lymphoma, lymphocyte
 CC predominant Hodgkin's disease, chronic lymphocytic leukaemia or SLL), and
 CC autoimmune disease (e.g. rheumatoid arthritis, juvenile rheumatoid
 CC arthritis, systemic lupus erythematosus, Wegener's disease, inflammatory
 CC bowel disease, idiopathic thrombocytopenic purpura, thrombotic
 CC thrombocytopenic purpura, autoimmune thrombocytopenia, multiple
 CC sclerosis, psoriasis, Iga nephropathy, Igm polyneuropathies, myasthenia
 CC gravis, vasculitis, diabetes mellitus, Reynaud's syndrome, Sjogren's
 CC syndrome, glomerulonephritis, Dermatomyositis, Wegner's granulomatosis,
 CC ANCA (included under vasculitis), Aplastic anaemia, Autoimmune haemolytic
 CC anaemia, factor VIII deficiency, haemophilia A, autoimmune neutropenia,
 CC Castleman's syndrome, Goodpasture's syndrome, solid organ transplant
 CC rejection, graft versus host disease, Igm mediated, Hashimoto's
 CC thyroiditis, autoimmune hepatitis, lymphoid interstitial pneumonitis,
 CC bronchiolitis obliterans (non-transplant) vs NSIP, Guillain-Barre
 CC Syndrome, large vessel vasculitis, giant cell (Takayasu's) arteritis,
 CC medium vessel vasculitis, Kawasaki's Disease, or polyarteritis nodosa).
 CC The present sequence represents the 2H7 anti-CD20 murine monoclonal
 CC antibody and humanised 2H7.v16 variant heavy chain variable (VH) domain
 CC CDR2 amino acid sequence, which is used in an example from the present
 CC invention.

```

XX      SQ      Sequence 17 AA;
SQ      Query Match      80.9%; Score 72; DB 8; Length 17;
      Best Local Similarity 81.2%; Pred. No. 9.1e-05;
      Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY      2 IYPGNDISYNOKFXG 17
      ||||| |||||
      2 IYPGNGDTSYNOKFKG 17
      Db
      2 IYPGNGDTSYNOKFKG 17

RESULT 21
ADU80237
ID      ADU80237 standard; peptide; 17 AA.
XX      AC      ADU80237;
XX      DT      24-FEB-2005 (first entry)
XX      DE      CD20 binding molecule heavy chain CDR2 seqid 27.
XX      KM      cytostatic; gene therapy; antibody production; hematological disease;
XX      KM      immune disorder; neoplasm; b-cell lymphoma; CD20;
XX      KM      complementarity determining region 2; CDR2.
XX      OS      unidentified.
XX      PN      WO2004103404-A1.
XX      PD      02-DEC-2004.
XX      PF      20-MAY-2004; 2004WO-US015786.
XX      PR      20-MAY-2003; 2003US-0471958P.
XX      PR      20-MAY-2004; 52US-00471958.
XX      PA      (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX      PI      Watkins JD, Davies J, Marquis DM, Allan BW, Ondek B;
XX      DR      WPI; 2004-834173/82.
XX      DR      N-PSDB; ADU80238.
XX      PT      New composition comprising a CD20 binding molecule having a binding
XX      PT      affinity (Kd) for human CD20 and a dissociation rate (koff) for human,
XX      PS      useful for preparing a composition for treating B cell lymphoma.
XX      PS      Claim 11; SEQ ID NO 27; 84pp; English.
XX      CC      The invention describes a new composition comprising a CD20 binding
XX      CC      molecule having a binding affinity (Kd) for human CD20 of 5.0 x 10-10 M
XX      CC      or less, and a dissociation rate (koff) for human CD20 of 5.0 x 10-4 s-1
XX      CC      or less. Also described is a method of treating B cell lymphoma. The CD20
XX      CC      binding molecules are useful for preparing a composition for treating B
XX      CC      cell lymphoma. This is the amino acid sequence of a CD20 binding molecule
XX      CC      heavy chain complementarity determining region 2 (CDR2).
XX      SQ      Sequence 17 AA;
SQ      Query Match      80.9%; Score 72; DB 8; Length 17;
      Best Local Similarity 81.2%; Pred. No. 9.1e-05;
      Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY      2 IYPGNDISYNOKFXG 17
      ||||| |||||
      2 IYPGNGDTSYNOKFKG 17
      Db
      2 IYPGNGDTSYNOKFKG 17

RESULT 22
ADW47106
ID      ADW47106 standard; peptide; 17 AA.
XX

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AC      ADW47106;
XX      DT      24-MAR-2005 (first entry)
XX      DE      Anti-CD20 monoclonal antibody heavy chain HB20-1,2,6 CDR 2.
XX      KM      CD20; monoclonal antibody; rheumatoid arthritis; antiarthritic;
XX      KM      antineuritic; immune disorder; inflammation; musculoskeletal disease;
XX      KM      idiopathic thrombocytopenic purpura; hemostatic; hemolytic anemia.
XX      OS      Mus musculus.
XX      PN      WO2005000901-A2.
XX      PD      06-JAN-2005.
XX      PF      07-MAY-2004; 2004WO-US014326.
XX      PR      09-MAY-2003; 2003US-0469451P.
XX      PA      (UYDU-) UNIV DUKE.
XX      PI      Tedder TF, Uchida J, Hamaguchi Y, Poe JC;
XX      DR      WPI; 2005-066556/07.
XX      PT      Novel monoclonal antibody (mAb) binding to CD20 or mouse CD20, in which
XX      PT      density of binding of mAb to B cells is two-fold higher than density of
XX      PT      binding of mAb to B cells, useful for depleting B cells, and treating
XX      PS      B cell disorder.
XX      PS      Example 1; SEQ ID NO 65; 205pp; English.
XX      CC      The invention relates to a monoclonal antibody (mAb) or its antigen-
XX      CC      binding fragment that specifically binds to human CD20 or mouse CD20,
XX      CC      where the density of binding of mAb or antigen-binding fragment to B
XX      CC      cells is at least two-fold higher than the density of binding of mAb 1F5
XX      CC      to B cells. Also included are a pharmaceutical composition comprising mAb
XX      CC      in a carrier, a pharmaceutical composition (comprising mAb or its antigen
XX      CC      binding fragment which specifically binds to the same antigenic
XX      CC      determinant as a monoclonal antibody chosen from HB20-1, HB20-3, HB20-4
XX      CC      and HB20-25 in a carrier), a cell line producing the mAb, producing the
XX      CC      mAb, an antigen binding fragment of the mAb, an isolated nucleic acid
XX      CC      encoding a heavy chain or light chain comprising a variable region
XX      CC      (comprising CDR3, or CDR1, CDR2 and CDR3 regions from mAb chosen from
XX      CC      HB20-1, HB20-3, HB20-4, HB20-5, HB20-25, HB20-11, HB20-1, HB20-2, HB20-7,
XX      CC      HB20-8, HB20-10, HB20-14, HB20-16 and HB20-18), a vector
XX      CC      comprising the nucleic acid, a cell comprising the nucleic acid or
XX      CC      vector, and depleting B cells in a mammalian subject (involving
XX      CC      administering the mAb and anti-CD22 or anti-CD19 antibody). The anti-CD20
XX      CC      mAb, compositions and cells are useful for depleting B cells in a
XX      CC      mammalian subject and for treating a B cell disorder. The B cell disorder
XX      CC      is B cell malignancy or autoimmune disease e.g. rheumatoid arthritis,
XX      CC      idiopathic thrombocytopenic purpura or hemolytic anemia. The mammalian
XX      CC      subject is resistant to anti-CD20 mAb therapy or resistant to therapy
XX      CC      with mAb C288. The mammalian subject has been or is currently treated
XX      CC      with chemotherapy. The mammalian subject had a relapse in a B cell
XX      CC      disorder. The mammalian subject is immunocompromised. The present
XX      CC      sequence represents a CDR (complementarity determining region) from anti-
XX      CC      CD20 monoclonal antibody.
XX      SQ      Sequence 17 AA;
SQ      Query Match      80.9%; Score 72; DB 9; Length 17;
      Best Local Similarity 81.2%; Pred. No. 9.1e-05;
      Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY      2 IYPGNDISYNOKFXG 17
      ||||| |||||
      2 IYPGNGDTSYNOKFKG 17
      Db
      2 IYPGNGDTSYNOKFKG 17

RESULT 23

```


ADW21313
 ID ADW21313 standard; peptide; 17 AA.
 XX AC ADW21313;
 XX DT 07-APR-2005 (first entry)
 XX DE Mouse anti-CD20 antibody 2H7 VH CDR2.
 XX KW Antibody; immune disorder; cancer; cytostatic; neoplasm;
 KW rheumatoid arthritis; multiple sclerosis; systemic lupus erythematosus;
 KW phase display; Antineumatic; Antiarthritic; Neuroprotective;
 KW Antiinflammatory; Dermatological; Immunosuppressive; leukemia; lymphoma;
 KW myeloma; heavy chain variable region; CD20.
 XX OS Mus musculus.
 XX PN WO2005005462-A2.
 XX PD 20-JAN-2005.
 XX PF 04-JUN-2004; 2004WO-US017682.
 XX PR 05-JUN-2003; 2003US-0476414P.
 XX PR 05-JUN-2003; 2003US-0476481P.
 XX PR 06-JUN-2003; 2003US-0476531P.
 XX PA (GETH) GENENTECH INC.
 XX PI Chan AC, Gordon NC, Kelley RF, Koehler MFT, Starovasnik MA;
 XX WPI; 2005-092059/10.
 XX PT New polypeptide or Blyss antagonist, for treating an immune-related
 PT condition (e.g. rheumatoid arthritis, multiple sclerosis or systemic
 PT lupus erythematosus) or cancer (e.g. leukemia or lymphoma).
 XX PS Disclosure; SEQ ID NO 51; 226pp; English.
 XX CC The invention relates to a polypeptide comprising sequences of formula I,
 CC II or III, (detailed in the claims) which are antagonists of Blyss (B cell
 CC stimulator). Also included are a nucleic acid molecule encoding the
 CC polypeptide, a vector comprising the nucleic acid molecule, a host cell
 CC comprising the nucleic acid molecule, a method for producing a
 CC polypeptide, a composition comprising the polypeptide optionally further
 CC comprising a physiological carrier, a method for detecting an inhibitor
 CC of Blyss binding to BR3 (Blyss receptor 3) in vitro, a method for
 CC inhibiting Blyss binding to BR3 in a mammal, a method for inhibiting Blyss
 CC signaling in a mammal and a method for treating an immune-related
 CC condition or cancer in a mammal. The sequence of Formula I, II or III is
 CC a sequence fused or conjugated to an immunoadhesion protein or to an
 CC antibody, where the antibody is a F(ab) antibody, F(ab')₂ antibody, a
 CC scv antibody, a humanized antibody or multispecific antibody, e.g.
 CC antibodies directed against CD20. The polypeptide is conjugated to an
 CC agent, e.g. a growth inhibitory agent, a cytotoxic agent, a detection
 CC agent, an agent that improves the bioavailability of the polypeptide and
 CC an agent that improves the half-life of the polypeptide, where the
 CC cytotoxic agent is a toxin, an antibiotic or a radioactive isotope. The
 CC polypeptide, composition and methods are useful for treating an immune-
 CC related condition (many examples given in the specification), e.g.
 CC rheumatoid arthritis, multiple sclerosis or systemic lupus erythematosus
 CC or for treating cancer (many examples given in the specification), e.g.
 CC leukemia, lymphoma or myeloma. The present sequence represents the CDR
 CC (complementarity determining region) of the light or heavy chain variable
 CC region of a mouse antibody directed against human CD20.
 XX SQ Sequence 17 AA;
 XX
 Query Match 80.9%; Score 72; DB 9; Length 17;
 Best Local Similarity 81.2%; Pred. No. 9.1e-05;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 IYPGNDISYNQKFXG 17

Db |||||
 2 IYPGNDISYNQKFXG 17
 RESULT 24
 ADJ94601
 ID ADJ94601 standard; protein; 120 AA.
 XX AC ADJ94601;
 XX DT 06-MAY-2004 (first entry)
 XX DE Mouse anti-CD20 antibody variable heavy chain.
 XX KW humanised anti-CD20 monoclonal antibody; hCD20 monoclonal antibody; Mab;
 KW IVIAB variable region; B-cell lymphoma; leukaemia; autoimmune disease;
 KW thrombocytopenia; lupus; rheumatoid arthritis;
 KW heavy chain variable region; mouse; murine.
 XX OS Mus sp.
 XX PN WO2003068821-A2.
 XX PD 21-AUG-2003.
 XX PF 14-FEB-2003; 2003WO-GB000665.
 XX PR 14-FEB-2002; 2002US-0356132P.
 XX PR 07-OCT-2002; 2002US-0416232P.
 XX PA (IMMU-) IMMUNOMEDICS INC.
 XX PA (MCCA/) MCCALL J D.
 XX PI Hansen H, Qu Z, Goldenberg DM;
 XX WPI; 2003-697522/66.
 XX DR N-PSDB; ADJ94600.
 XX PT New humanized anti-CD20 monoclonal antibody (Mab) that retains
 PT substantially the B-cell and B-cell lymphoma and leukemia cell targeting
 PT of the murine anti-CD20 Mab, useful for treating B-cell lymphoma,
 PT leukemia or an autoimmune diseases.
 XX PS Example 1; Fig 1B; 106pp; English.
 XX CC The invention comprises a humanised anti-CD20 (hCD20) monoclonal antibody
 CC (Mab) or its antigen-binding fragment containing the complementarity
 CC determining regions (CDRs) of at least one murine anti-CD20 Mab variable
 CC region and the framework regions (FRs) of at least one human IVIAB
 CC variable region. The antibodies of the invention are useful for
 CC diagnosing or preventing B-cell lymphoma, leukaemia or an autoimmune
 CC disease (e.g. thrombocytopenia, lupus or rheumatoid arthritis). The
 CC present amino acid sequence represents a mouse anti-CD20 antibody
 CC variable heavy chain.
 XX SQ Sequence 120 AA;
 XX
 Query Match 80.9%; Score 72; DB 7; Length 120;
 Best Local Similarity 81.2%; Pred. No. 0.0008;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 IYPGNDISYNQKFXG 17
 Db 50 IYPGNDISYNQKFXG 65
 RESULT 25
 ADJ94605
 ID ADJ94605 standard; protein; 121 AA.
 XX AC ADJ94605;
 XX DT 06-MAY-2004 (first entry)

XX Chimeric anti-CD20 antibody variable heavy chain.
DE
XX
XX humanised anti-CD20 monoclonal antibody; hCD20 monoclonal antibody; Mab;
KW IY1AB variable region; B-cell lymphoma; leukaemia; autoimmune disease;
KW thrombocytopenia; lupus; rheumatoid arthritis;
KW heavy chain variable region.
XX
OS Chimeric.
OS Unidentified.
XX
XX WO2003068821-A2.
XX
XX 21-AUG-2003.
XX
XX 14-FEB-2003; 2003WO-GB000665.
XX
XX 14-FEB-2002; 2002US-0356132P.
PR 07-OCT-2002; 2002US-0416232P.
XX
XX (IMMU-) IMMUNOMEDICS INC.
XX (MCCA/) MCCA J D.
XX
XX Hansen H, Qu Z, Goldenberg DM;
PI WPI; 2003-697522/66.
XX N-PSDB; ADJ94604.
XX
XX New humanized anti-CD20 monoclonal antibody (Mab) that retains
PT substantially the B-cell and B-cell lymphoma and leukemia cell targeting
PT of the murine anti-CD20 Mab, useful for treating B-cell lymphoma,
PT leukemia or an autoimmune disease.
XX
XX Disclosure; Fig 2B; 106pp; English.
XX
XX The invention comprises a humanised anti-CD20 (hCD20) monoclonal antibody
CC (Mab) or its antigen-binding fragment containing the complementarity
CC determining regions (CDRs) of at least one murine anti-CD20 Mab variable
CC region and the framework regions (FRs) of at least one human IY1AB
CC variable region. The antibodies of the invention are useful for
CC diagnosing or preventing B-cell lymphoma, leukaemia or an autoimmune
CC disease (e.g. thrombocytopenia, lupus or rheumatoid arthritis). The
CC present amino acid sequence represents a chimeric anti-CD20 antibody
CC variable heavy chain.
XX
XX Sequence 121 AA;
SQ
Query Match 80.9%; Score 72; DB 7; Length 121;
Best Local Similarity 81.2%; Pred. No. 0.0008;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 IYPGNDISTYNOKEFG 17
DB 51 IYPGNDISTYNOKEFG 66
RESULT 26
ADJ94609
ID ADJ94609 standard; protein; 121 AA.
XX
XX ADJ94609;
XX
XX 06-MAY-2004 (first entry)
XX
XX Humanised anti-CD20 antibody variable heavy chain amino acid sequence #2.
DE
XX humanised anti-CD20 monoclonal antibody; hCD20 monoclonal antibody; Mab;
KW IY1AB variable region; B-cell lymphoma; leukaemia; autoimmune disease;
KW thrombocytopenia; lupus; rheumatoid arthritis;
KW heavy chain variable region.
XX
OS Synthetic.
OS Unidentified.

XX
XX WO2003068821-A2.
XX
XX 21-AUG-2003.
XX
XX 14-FEB-2003; 2003WO-GB000665.
XX
XX 14-FEB-2002; 2002US-0356132P.
PR 07-OCT-2002; 2002US-0416232P.
XX
XX (IMMU-) IMMUNOMEDICS INC.
XX (MCCA/) MCCA J D.
XX
XX Hansen H, Qu Z, Goldenberg DM;
PI WPI; 2003-697522/66.
XX
XX New humanized anti-CD20 monoclonal antibody (Mab) that retains
PT substantially the B-cell and B-cell lymphoma and leukemia cell targeting
PT of the murine anti-CD20 Mab, useful for treating B-cell lymphoma,
PT leukemia or an autoimmune disease.
XX
XX Claim 22; Fig 4A; 106pp; English.
XX
XX The invention comprises a humanised anti-CD20 (hCD20) monoclonal antibody
CC (Mab) or its antigen-binding fragment containing the complementarity
CC determining regions (CDRs) of at least one murine anti-CD20 Mab variable
CC region and the framework regions (FRs) of at least one human IY1AB
CC variable region. The antibodies of the invention are useful for
CC diagnosing or preventing B-cell lymphoma, leukaemia or an autoimmune
CC disease (e.g. thrombocytopenia, lupus or rheumatoid arthritis). The
CC present amino acid sequence represents a humanised anti-CD20 antibody
CC variable heavy chain.
XX
XX Sequence 121 AA;
SQ
Query Match 80.9%; Score 72; DB 7; Length 121;
Best Local Similarity 81.2%; Pred. No. 0.0008;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 IYPGNDISTYNOKEFG 17
DB 51 IYPGNDISTYNOKEFG 66
RESULT 27
ADJ94608
ID ADJ94608 standard; protein; 121 AA.
XX
XX ADJ94608;
XX
XX 06-MAY-2004 (first entry)
XX
XX Humanised anti-CD20 antibody variable heavy chain amino acid sequence #1.
DE
XX humanised anti-CD20 monoclonal antibody; hCD20 monoclonal antibody; Mab;
KW IY1AB variable region; B-cell lymphoma; leukaemia; autoimmune disease;
KW thrombocytopenia; lupus; rheumatoid arthritis;
KW heavy chain variable region.
XX
OS Synthetic.
OS Unidentified.
XX
XX WO2003068821-A2.
XX
XX 21-AUG-2003.
XX
XX 14-FEB-2003; 2003WO-GB000665.
XX
XX 14-FEB-2002; 2002US-0356132P.
PR 07-OCT-2002; 2002US-0416232P.
XX
XX (IMMU-) IMMUNOMEDICS INC.

PA (MCCA/) MCCAALL J D.
 XX Hansen H, Qu Z, Goldenberg DM;
 XX WPI; 2003-697522/66.
 XX
 PT New humanized anti-CD20 monoclonal antibody (Mab) that retains
 PT substantially the B-cell and B-cell lymphoma and leukemia cell targeting
 PT of the murine anti-CD20 Mab, useful for treating B-cell lymphoma,
 PT leukemia or an autoimmune diseases.
 XX
 PS Claim 22; Fig 4A; 106pp; English.
 XX
 CC The invention comprises a humanised anti-CD20 (hCD20) monoclonal antibody
 CC (Mab) or its antigen-binding fragment containing the complementarity
 CC determining regions (CDRs) of at least one murine anti-CD20 Mab variable
 CC region and the framework regions (FRs) of at least one human IV1AB
 CC variable region. The antibodies of the invention are useful for
 CC diagnosing or preventing B-cell lymphoma, leukemia or an autoimmune
 CC disease (e.g. thrombocytopenia, lupus or rheumatoid arthritis). The
 CC present amino acid sequence represents a humanised anti-CD20 antibody
 CC variable heavy chain.
 XX
 SQ Sequence 121 AA;
 XX
 QY Query Match 80.9%; Score 72; DB 7; Length 121;
 DB Best Local Similarity 81.2%; Pred. No. 0.0008;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 IYPGNDISYNQKFXG 17
 ||||| |||||
 51 IYPGNGDTSYNQKFKG 66
 XX
 RESULT 28
 ADJ94607
 ID ADJ94607 standard; protein; 121 AA.
 AC ADJ94607;
 AC
 XX 06-MAY-2004 (first entry)
 DT
 XX Chimeric anti-CD20 antibody variable heavy chain amino acid sequence.
 DE
 XX humanised anti-CD20 monoclonal antibody; hCD20 monoclonal antibody; Mab;
 KM IV1AB variable region; B-cell lymphoma; leukaemia; autoimmune disease;
 KM thrombocytopenia; lupus; rheumatoid arthritis;
 KM heavy chain variable region.
 XX
 OS Chimeric.
 OS Unidentified.
 OS
 XX WO2003068821-A2.
 PN
 XX 21-AUG-2003.
 PD
 XX 14-FEB-2003; 2003WO-GB000665.
 PF
 XX 14-FEB-2002; 2002US-0356132P.
 PR 07-OCT-2002; 2002US-0416232P.
 XX
 PA (IMMU-) IMMUNOMEDICS INC.
 PA (MCCA/) MCCAALL J D.
 XX Hansen H, Qu Z, Goldenberg DM;
 XX WPI; 2003-697522/66.
 XX
 PT New humanized anti-CD20 monoclonal antibody (Mab) that retains
 PT substantially the B-cell and B-cell lymphoma and leukemia cell targeting
 PT of the murine anti-CD20 Mab, useful for treating B-cell lymphoma,
 PT leukemia or an autoimmune diseases.
 XX

PS Claim 22; Fig 4A; 106pp; English.
 XX
 CC The invention comprises a humanised anti-CD20 (hCD20) monoclonal antibody
 CC (Mab) or its antigen-binding fragment containing the complementarity
 CC determining regions (CDRs) of at least one murine anti-CD20 Mab variable
 CC region and the framework regions (FRs) of at least one human IV1AB
 CC variable region. The antibodies of the invention are useful for
 CC diagnosing or preventing B-cell lymphoma, leukaemia or an autoimmune
 CC disease (e.g. thrombocytopenia, lupus or rheumatoid arthritis). The
 CC present amino acid sequence represents a chimeric anti-CD20 antibody
 CC variable heavy chain.
 XX
 SQ Sequence 121 AA;
 XX
 QY Query Match 80.9%; Score 72; DB 7; Length 121;
 DB Best Local Similarity 81.2%; Pred. No. 0.0008;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 IYPGNDISYNQKFXG 17
 ||||| |||||
 51 IYPGNGDTSYNQKFKG 66
 XX
 RESULT 29
 ADW03412
 ID ADW03412 standard; protein; 121 AA.
 AC ADW03412;
 AC
 XX 24-MAR-2005 (first entry)
 DT
 XX Murine anti-human CD20 antibody heavy chain variable region - SEQ ID 23.
 DE
 XX B-lymphocyte; b-cell lymphoma; autoimmune disease; immunosuppressive;
 KM non-hodgkin lymphoma; hodgkins disease; cytostatic;
 KM chronic lymphocytic leukemia; hairy cell leukemia; rheumatoid arthritis;
 KM antirheumatic; antirheumatic; systemic lupus erythematosus;
 KM wegener granulomatosis; antiallergic; antiinflammatory; vasotropic;
 KM inflammatory bowel disease; gastrointestinal-gen.;
 KM idiopathic thrombocytopenic purpura; hemostatic; multiple sclerosis;
 KM asthma; antiasthmatic; psoriasis; antipsoriatic; myasthenia gravis;
 KM muscular-gen.; neuroprotective; vasculitis; diabetes; antidiabetic;
 KM glomerulonephritis; nephrotropic; antibody; heavy chain variable region;
 KM anti-CD20.
 XX
 OS Mus sp.
 OS
 XX WO2005000351-A2.
 PN
 XX 06-JAN-2005.
 PD
 XX 04-JUN-2004; 2004WO-US017693.
 PF
 XX 05-JUN-2003; 2003US-0476414P.
 PR 05-JUN-2003; 2003US-0476481P.
 PR 06-JUN-2003; 2003US-0476531P.
 XX
 PA (GERTH) GENENTECH INC.
 PA Chan A, Gong Q, Martin F;
 XX WPI; 2005-058069/06.
 XX
 PT Depleting B cells from a mixed population of cells by contacting the
 PT cells with a BlyS antagonist and a CD20 binding antibody, useful for
 PT treating B cell malignancies and autoimmune disorders.
 XX
 PS Disclosure; SEQ ID NO 23; 114pp; English.
 XX
 CC The invention comprises a method of depleting B cells from a mixed
 CC population of cells, the method involves contacting the mixed population
 CC of cells with BlyS antagonist (e.g. an immunoadhesin) and a CD20 binding
 CC antibody (e.g. hu2H7.v16). The method of the invention is useful for

treating B cell malignancies and autoimmune disorders, such as: non-Hodgkin's lymphoma, Hodgkin's disease, follicular center cell lymphomas, lymphocytic leukemia, hairy cell leukemia, rheumatoid arthritis, systemic lupus erythematosus, Wegener's disease, inflammatory bowel disease, idiopathic thrombocytopenic purpura, multiple sclerosis, asthma, psoriasis, IGA nephropathy, myasthenia gravis, vasculitis, diabetes and glomerulonephritis. The present amino acid sequence represents a murine anti-human CD20 antibody (m2H7) heavy chain variable region.

Sequence 121 AA;

Query Match 80.9%; Score 72; DB 9; Length 121;
Best Local Similarity 81.2%; Pred. No. 0.0008;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IYPGNDISYNQKFXG 17
Db 51 IYPGNDISYNQKFG 66

RESULT 30
ADX16286
ID ADX16286 standard; protein; 121 AA.

AC ADX16286;

05-MAY-2005 (first entry)

VHD antibody heavy chain variable region.

immunosuppressive; Cytostatic; Antirheumatic; Antiarthritic;
CD20 modulator; antibody; pharmaceutical; autoimmune disease;
proliferative disorder; leukemia; lymphoma; rheumatoid arthritis;
immune disorder; hematological disease; neoplasm; inflammation;
musculoskeletal disease; hyperproliferation; antibody engineering;
heavy chain variable region; Vhd.

Homo sapiens.

WO2005016969-A2.

24-FEB-2005.

16-AUG-2004; 2004WO-EP009033.

14-AUG-2003; 2003EP-00018480.

14-NOV-2003; 2003US-0520171P.

(MERCK) MERCK PATENT GMBH.

Carr FJ, Williams S, Gillies SD;

WPI; 2005-196054/20.

New CD20-binding polypeptide (chimeric antibody), useful for treating autoimmune diseases and proliferative disorders such as leukemia, lymphomas and rheumatoid arthritis.

Claim 2; Fig 1; 64pp; English.

The invention relates to a polypeptide composition having the ability to bind to CD20 antigen. The CD20-binding polypeptide composition is in the form of a chimeric antibody and further including a human heavy chain constant region and a human light chain constant region, where the human heavy chain constant region is an Igg constant region, specifically an Igg1 constant region, and where the human light chain constant region is a human kappa light chain constant region. The polypeptide is fused to a cytokine, i.e. interleukin-2 (IL2). The C-terminus of the polypeptide is fused to the N-terminus of the cytokine. The polypeptides are in the form of a whole antibody, a Fab antibody fragment, a single-chain Fv antibody fragment, or a minibody. The polypeptide composition or a pharmaceutical composition is useful for manufacturing a medicament for the treatment of an autoimmune disease. The composition and method are useful for treating

proliferative disorders such as leukemia, lymphomas, rheumatoid arthritis, and other autoimmune diseases. The present sequence represents the VHD antibody heavy chain variable region used in the CD20-binding polypeptide composition of the invention.

Sequence 121 AA;

Query Match 80.9%; Score 72; DB 9; Length 121;
Best Local Similarity 81.2%; Pred. No. 0.0008;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IYPGNDISYNQKFXG 17
Db 51 IYPGNDISYNQKFG 66

RESULT 31
ADX16286
ID ADX16286 standard; protein; 121 AA.

AC ADX16286;

05-MAY-2005 (first entry)

2B8 antibody heavy chain variable region.

immunosuppressive; Cytostatic; Antirheumatic; Antiarthritic;
CD20 modulator; antibody; pharmaceutical; autoimmune disease;
proliferative disorder; leukemia; lymphoma; rheumatoid arthritis;
immune disorder; hematological disease; neoplasm; inflammation;
musculoskeletal disease; hyperproliferation; antibody engineering;
heavy chain variable region; 2B8.

Homo sapiens.

WO2005016969-A2.

24-FEB-2005.

16-AUG-2004; 2004WO-EP009033.

14-AUG-2003; 2003EP-00018480.

14-NOV-2003; 2003US-0520171P.

(MERCK) MERCK PATENT GMBH.

Carr FJ, Williams S, Gillies SD;

WPI; 2005-196054/20.

New CD20-binding polypeptide (chimeric antibody), useful for treating autoimmune diseases and proliferative disorders such as leukemia, lymphomas and rheumatoid arthritis.

Claim 1; Fig 1; 64pp; English.

The invention relates to a polypeptide composition having the ability to bind to CD20 antigen. The CD20-binding polypeptide composition is in the form of a chimeric antibody and further including a human heavy chain constant region and a human light chain constant region, where the human heavy chain constant region is an Igg constant region, specifically an Igg1 constant region, and where the human light chain constant region is a human kappa light chain constant region. The polypeptide is fused to a cytokine, i.e. interleukin-2 (IL2). The C-terminus of the polypeptide is fused to the N-terminus of the cytokine. The polypeptides are in the form of a whole antibody, a Fab antibody fragment, a single-chain Fv antibody fragment, or a minibody. The polypeptide composition or a pharmaceutical composition is useful for manufacturing a medicament for the treatment of an autoimmune disease. The composition and method are useful for treating proliferative disorders such as leukemia, lymphomas, rheumatoid arthritis, and other autoimmune diseases. The present sequence represents the 2B8 antibody heavy chain variable region used in the CD20-binding polypeptide composition of the invention.

CC bind to CD20 antigen. The CD20-binding polypeptide composition is in the
CC form of a chimeric antibody and further including a human heavy chain
CC constant region and a human light chain constant region, where the human
CC heavy chain constant region is an Igg constant region, specifically an
CC 1Gg1 constant region, and where the human light chain constant region is
CC a human kappa light chain constant region. The polypeptide is fused to a
CC cytokine, i.e. interleukin-2 (IL2). The C-terminus of the polypeptide is
CC fused to the N-terminus of the cytokine. The polypeptides are in the form
CC of a whole antibody, a Fab antibody fragment, a single-chain Fv antibody
CC fragment, or a minibody. The polypeptide composition or a pharmaceutical
CC composition is useful for manufacturing a medicament for the treatment of
CC an autoimmune disease. The composition and method are useful for treating
CC proliferative disorders such as leukemia, lymphomas, rheumatoid
CC arthritis, and other autoimmune diseases. The present sequence represents
CC the VNC antibody heavy chain variable region used in the CD20-binding
CC polypeptide composition of the invention.
XX
SQ Sequence 121 AA;
Query Match 80.9%; Score 72; DB 9; Length 121;
Best Local Similarity 81.2%; Pred. No. 0.0008;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 IYGNDDISYNOKFXG 17
Db 51 IYGNDDISYNOKFXG 66
RESULT 34
AAO27203
ID AAO27203 standard; protein; 122 AA.
XX
AC AAO27203;
XX
DT 17-SEP-2003 (first entry)
XX
DE Chimeric framework-patched hplf5 VH protein - alternative design.
XX
XX Framework-patching; complementarity determining region; CDR; human;
KW mouse; murine; cytostatic activity; cancer; Non-Hodgkin's lymphoma;
KW chimeric; gene therapy; rheumatoid arthritis; FR-patching; hplf5 VH;
KW alternative design.
XX
OS Homo sapiens.
OS Mus sp.
OS Synthetic.
OS Chimeric.
XX
XX Key Location/Qualifiers
FH Domain 31..35
FT /note= "Complementarity determining region (CDR) 1"
FT Domain 50..66
FT /note= "Complementarity determining region (CDR) 2"
FT Domain 99..111
FT /note= "Complementarity determining region (CDR) 3"
XX
XX WO2003002607-A1.
XX
XX 09-JAN-2003.
XX
XX 10-JUN-2002; 2002WO-US018512.
XX
XX 27-JUN-2001; 2001US-00892613.
XX
XX (LEUNG/) LEUNG S S.
XX
XX Leung SS;
XX
XX WPI; 2003-210245/20.
XX
XX New re-engineered or framework-patched immunoglobulin, useful for
FT preparing a composition for treating cancer, preferably Non-Hodgkin's
FT lymphoma or rheumatoid arthritis.
FT

XX
XX Example 2; Fig 10a; 66pp; English.
XX
XX The invention relates to a novel re-engineered or framework (FR)-patched
CC immunoglobulin, containing the heavy and/or light chain variable region
CC (VH/VL) sequences from a parent antibody. Within these chains, at least
CC one of the complementalised framework sequences, defined as FR1, FR2,
CC FR3 and FR4 are replaced, or patched, by the corresponding framework
CC sequences from the heavy and light chain immunoglobulin region of a
CC different species. The FR-patched immunoglobulin binds specifically to an
CC antigen with affinity comparable to, or within 3-fold of, that of the
CC parent immunoglobulin. The invention discloses the process of FR-patching
CC which is used to generate re-engineered immunoglobulin chains having one
CC or more complementarity determining regions (CDR's) from a donor
CC immunoglobulin and portions of framework sequences from one or more human
CC or primate immunoglobulins. The molecules obtained demonstrate cytostatic
CC activity as well as reduced or eliminated immunogenicity, whilst
CC maintaining the specificity and affinity of the parent antibody. The FR-
CC patched immunoglobulin is useful during the preparation of a composition
CC for treating cancer, preferably Non-Hodgkin's lymphoma and also during
CC the treatment of rheumatoid arthritis. Furthermore, the molecules of the
CC invention may also prove useful in gene therapy. The current sequence is
CC that of the chimeric FR-patched hplf5 alternatively designed VH protein
CC of the invention
XX
SQ Sequence 122 AA;
Query Match 80.9%; Score 72; DB 6; Length 122;
Best Local Similarity 81.2%; Pred. No. 0.0008;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 IYGNDDISYNOKFXG 17
Db 51 IYGNDDISYNOKFXG 66
RESULT 35
ADP79573
ID ADP79573 standard; protein; 122 AA.
XX
XX ADP79573;
XX
XX 04-NOV-2004 (first entry)
XX
XX Murine 2H7 heavy chain variable domain SEQ ID NO:7.
XX
XX humanised antibody; anti-human CD20 antibody; cytostatic; antirheumatic;
KW antiarthritic; immunosuppressive; antiinflammatory; haemostatic;
KW neuroprotective; antipsoriatic; muscular; antidiabetic; antianaemic;
KW nephrotropic; hepatotrophic; CNS; CD20 inhibitor;
KW humanised CD20 binding antibody; CD20 positive cancer; leukaemia;
KW inflammatory disease; rheumatoid arthritis; systemic lupus erythematosus;
KW inflammatory bowel disease; thrombocytopenic purpura;
KW autoimmune thrombocytopenia; multiple sclerosis; psoriasis;
KW myasthenia gravis; vasculitis; diabetes mellitus; glomerulonephritis;
KW autoimmune haemolytic anaemia.
XX
XX Mus sp.
XX
XX
XX Key Location/Qualifiers
FH Region 1..25
FT /label= FR1
FT Region 26..35
FT /label= CDR1
FT Region 36..49
FT /label= FR2
FT Region 50..66
FT /label= CDR2
FT Region 67..98
FT /label= FR3
FT Region 99..111
FT /label= CDR3
FT Region 112..122
FT

FT /label= FR4
 XX WO2004056312-A2.
 PN
 XX
 PD 08-JUL-2004.
 XX
 PF 16-DEC-2003; 2003WO-US040426.
 XX
 XX 16-DEC-2002; 2002US-0434115P.
 PR 01-DEC-2003; 2003US-0526163P.
 XX
 PA (GETH) GENENTECH INC.
 PI Adams CM, Chan AC, Crowley CM, Lowman HB, Nakamura GR, Presta LG;
 XX WPI: 2004-500261/47.
 DR
 XX
 XX New humanized anti-CD20 antibodies, useful for treating a CD20 positive
 PT cancer (e.g. B cell lymphoma, leukemia, or non-Hodgkin's lymphoma) or
 PT autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis or
 PT psoriasis).
 XX
 PS Example 1; SEQ ID NO 7; 108bp; English.
 XX
 CC The present invention describes a humanised antibody (I) that binds human
 CC CD20 or its antigen-binding fragment, which depletes primate B cells in
 CC vivo, and comprises in the H chain Variable region (VH) at least a CDR3
 CC sequence consisting of 9 amino acids (SEQ ID NO:12, ADP79605) from an
 CC anti-human CD20 antibody and substantially the human consensus framework
 CC (FR) residues of human heavy chain subgroup III (VHIII). (I) has
 CC cytosolic, antirheumatic, antiarthritic, immunosuppressive,
 CC antiinflammatory, haemostatic, neuroprotective, antipsoriatic, muscular,
 CC antidiabetic, antianaemic, nephrotropic, hepatotropic and CNS
 CC activities, and can be used as a CD20 inhibitor. The humanised CD20
 CC binding antibody (I) can be used for treating a CD20 positive cancer
 CC (e.g. B cell lymphoma, leukemia, non-Hodgkin's lymphoma, lymphocyte
 CC predominant Hodgkin's disease, chronic lymphocytic leukemia or SLL), and
 CC autoimmune disease (e.g. rheumatoid arthritis, juvenile rheumatoid
 CC arthritis, systemic lupus erythematosus, Wegener's disease, inflammatory
 CC bowel disease, idiopathic thrombocytopenic purpura, thrombotic
 CC thrombocytopenic purpura, autoimmune thrombocytopenia, multiple
 CC sclerosis, psoriasis, Iga nephropathy, Igm polyneuropathies, myasthenia
 CC gravis, vasculitis, diabetes mellitus, Reynaud's syndrome, Sjogren's
 CC syndrome, glomerulonephritis, dermatomyositis, Wegner's granulomatosis,
 CC ANCA (included under vasculitis), Aplastic anaemia, Autoimmune haemolytic
 CC anaemia, factor VIII deficiency, haemophilia A, autoimmune neutropenia,
 CC Castleman's syndrome, Goodpasture's syndrome, solid organ transplant
 CC rejection, graft versus host disease, Igm mediated, Hashimoto's
 CC thyroiditis, autoimmune hepatitis, lymphoid interstitial pneumonitis,
 CC bronchiolitis obliterans (non-transplant) vs NSIP, Guillain-Barre
 CC syndrome, large vessel vasculitis, giant cell (Takayasu's) arteritis,
 CC medium vessel vasculitis, Kawasaki's Disease, or polyarteritis nodosa).
 CC The present sequence represents the 2H7 anti-CD20 murine monoclonal
 CC antibody heavy chain variable (VH) domain amino acid sequence, which is
 CC used in an example from the present invention.
 XX
 XX Sequence 122 AA;
 SQ
 Query Match 80.9%; Score 72; DB 8; Length 122;
 Best Local Similarity 81.2%; Pred. No. 0.00081;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

DT 04-NOV-2004 (first entry)
 XX
 XX Humanised 2H7.v16 variant heavy chain variable domain SEQ ID NO:8.
 DE
 XX humanised antibody; anti-human CD20 antibody; cytosolic; antirheumatic;
 KW antirheumatic; immunosuppressive; antiinflammatory; haemostatic;
 KW neuroprotective; antipsoriatic; muscular; antidiabetic; antianaemic;
 KW nephrotropic; hepatotropic; CNS; CD20 inhibitor;
 KW humanised CD20 binding antibody; CD20 positive cancer; leukemia;
 KW autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
 KW inflammatory bowel disease; thrombocytopenic purpura;
 KW myasthenia gravis; vasculitis; diabetes mellitus; glomerulonephritis;
 KW autoimmune haemolytic anaemia.
 KW
 XX Mus sp.
 OS Homo sapiens.
 OS Synthetic.
 OS
 XX Key
 FH Region
 FT Location/Qualifiers
 FT 1..25
 FT /label= FR1
 FT 26..35
 FT /label= CDR1
 FT 36..49
 FT /label= FR2
 FT 50..66
 FT /label= CDR2
 FT 67..98
 FT /label= FR3
 FT 99..111
 FT /label= CDR3
 FT 112..122
 FT /label= FR4
 FT
 XX WO2004056312-A2.
 XX
 XX 08-JUL-2004.
 XX
 XX 16-DEC-2003; 2003WO-US040426.
 XX
 XX 16-DEC-2002; 2002US-0434115P.
 XX 01-DEC-2003; 2003US-0526163P.
 XX
 XX (GETH) GENENTECH INC.
 XX
 PI Adams CM, Chan AC, Crowley CM, Lowman HB, Nakamura GR, Presta LG;
 XX WPI: 2004-500261/47.
 XX
 XX New humanized anti-CD20 antibodies, useful for treating a CD20 positive
 PT cancer (e.g. B cell lymphoma, leukemia, or non-Hodgkin's lymphoma) or
 PT autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis or
 PT psoriasis).
 PT
 PS Example 1; SEQ ID NO 8; 108bp; English.
 XX
 XX The present invention describes a humanised antibody (I) that binds human
 CC CD20 or its antigen-binding fragment, which depletes primate B cells in
 CC vivo, and comprises in the H chain Variable region (VH) at least a CDR3
 CC sequence consisting of 9 amino acids (SEQ ID NO:12, ADP79605) from an
 CC anti-human CD20 antibody and substantially the human consensus framework
 CC (FR) residues of human heavy chain subgroup III (VHIII). (I) has
 CC cytosolic, antirheumatic, antiarthritic, immunosuppressive,
 CC antiinflammatory, haemostatic, neuroprotective, antipsoriatic, muscular,
 CC antidiabetic, antianaemic, nephrotropic, hepatotropic and CNS
 CC activities, and can be used as a CD20 inhibitor. The humanised CD20
 CC binding antibody (I) can be used for treating a CD20 positive cancer
 CC (e.g. B cell lymphoma, leukemia, non-Hodgkin's lymphoma, lymphocyte
 CC predominant Hodgkin's disease, chronic lymphocytic leukemia or SLL), and
 CC autoimmune disease (e.g. rheumatoid arthritis, juvenile rheumatoid
 CC arthritis, systemic lupus erythematosus, Wegener's disease, inflammatory
 CC bowel disease, idiopathic thrombocytopenic purpura, thrombotic

RESULT 38
ADV21492
ID ADV21492 standard; protein; 122 AA.
XX
AC ADV21492;
DT 24-FEB-2005 (first entry)
XX
DE Human antibody VH domain SEQ ID No:201.
XX
KW Antibody engineering; binding molecule; antibody; humanized antibody;
KW proliferative disorder; tumor; inflammation; immune disorder;
KW autoimmune disease; infectious disease; viral infection; infection;
KW allergy; parasitic reaction; graft versus host disease; cytostatic;
KW antitumor; immunosuppressive; antimicrobial; virucide;
KW antiallergic; antiparasitic; heavy chain variable region; VH.
XX
OS Homo sapiens.
XX
PN WO2004106380-A2.
XX
PD 09-DEC-2004.
XX
PF 26-MAY-2004; 2004WO-EP005684.
XX
PR 31-MAY-2003; 2003EP-00012132.
XX
PA (MICR-) MICROMET AG.
XX
PI Kufer P, Raum T, Berry M, Kischel R, Mangold S, Krinner E;
PI Kohleisen B, Zeman S, Itin C, Baeuerle P;
XX
DR WPI: 2005-021269/02.
XX
PT Preparing human binding molecule specifically binding to human CD3
PT complex, comprises selecting molecules specifically binding to
PT extracellular domain of recombinant epsilon-chain and preparing
PT identified selected binding molecule.
XX
PS Disclosure; SEQ ID NO 201; 350pp; English.
XX
CC The invention relates to a method of preparing a human binding molecule,
CC fragment or its derivative which specifically binds to the human CD3
CC complex. The method comprises selecting molecules specifically binding to
CC or interacting with the extracellular domain of recombinant epsilon-chain
CC expressed independent of the human CD3 complex in the absence of other
CC members of the CD3 complex, from a population of candidate polypeptides
CC encoded by a library, selecting molecules from a population identified in
CC the above step for binding to the human CD3 complex, and preparing the
CC selected binding molecule. The binding molecule is an antibody molecule,
CC antibody fragment or its derivative or an antibody construct. Also
CC disclosed is a nucleic acid sequence encoding a human binding molecule, a
CC vector comprising such a nucleic acid, a host transformed or transfected
CC with such a vector, a composition comprising a human binding molecule,
CC and optionally a proteaceous compound capable of providing an
CC activation signal for immune effector cells, and a kit comprising a human
CC binding molecule. The method further involves recombinant expression of
CC the binding molecule, fragment or its derivative encoded by a nucleic
CC acid sequence chosen from the identified nucleic acid sequence, a nucleic
CC acid sequence hybridizing with the complementary strand of the identified
CC nucleic acid sequence under stringent hybridization conditions, and a
CC nucleic acid sequence which is degenerate as a result of the genetic code
CC to the above mentioned nucleotide sequences. The antibody molecule,
CC antibody fragment or its derivative or construct comprises a further
CC antigen-interaction-site and/or a further effector domain, and is
CC humanized and/or delaminized in an additional step. The further antigen-
CC interaction-site is specific for one or more cell surface molecule such
CC as a tumor specific marker. The antigen-interaction-site is further scFv,
CC which specifically binds to or interacts with an antigen chosen from
CC BpCAM, CCR5, CD19, EphA2, HER-2 neu, HER-3, HER-4, EGFR, PSMA, CEA, MUC-1
CC (mucin), MUC2, MUC3, MUC4, MUC5AC, MUC5B, MUC7, beta2MG, Lewis Y, CD30,
CC CD33, CD30, ganglioside GD3, 9-O-Acetyl-GD3, GM2, Globo H, fucosyl GM1,

CC Poly SA, GD2, carboanhydrase IX (MN/CA IX), CD44v6, Sonic hedgehog (Shh),
CC Mu-1, plasma cell antigen, (membrane-bound) IGE, melanoma chondroitin
CC sulfate proteoglycan (MSP), CCR8, TNF-alpha precursor, STEAP,
CC mesothelin, A33 antigen, prostate stem cell antigen (PSCA), Ly-6,
CC desmoglein 4, E-cadherin neopeptide, fetal acetylcholine receptor, CD25,
CC CA19-9 marker, CA-125 marker and muellerian inhibitory substance (MIS)
CC receptor type II, srm (sialylated Tn antigen; TAG-72), PAP (fibroblast
CC activated antigen), endostatin, EGFRvIII, Ig, SAS and CD63. In a human
CC binding molecule, the antibody molecule, antibody fragment or its
CC derivative or an antibody construct, comprises a heavy chain variable
CC (VH) region, a light chain variable (VL) region, complementarily
CC determining regions 1-3 (CDR1-3) of a VH-region, and CDR1-3 of a VL-
CC region. The method is useful for preparing a human binding molecule,
CC fragment or its derivative which specifically binds to the human CD3
CC complex. The human binding molecule polypeptide sequences, and the
CC polynucleotide sequences encoding them are useful for the prevention,
CC treatment or amelioration of proliferative disease, tumorous disease,
CC inflammatory disease, immunological disorder, autoimmune disease,
CC infectious disease, viral disease, allergic reactions, parasitic
CC reactions, graft-versus-host diseases or host-versus-graft diseases, or
CC for preparation of a pharmaceutical composition for the prevention,
CC treatment or amelioration of the above mentioned diseases. This sequence
CC represents a VH domain of a human antibody.
XX
SQ Sequence 122 AA:
XX
Query Match 80.9%; Score 72; DB 9; Length 122;
Best Local Similarity 81.2%; Pred. No. 0.00081;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 IYFGNDISYNOKFXG 17
Db 51 IYFGNDISYNOKFXG 66
XX
RESULT 39
ADM03408
ID ADM03408 standard; protein; 122 AA.
XX
AC ADM03408;
XX
DT 24-MAR-2005 (first entry)
XX
DE Humanized anti-CD20 antibody heavy chain variable region - SEQ ID 14.
XX
KW B-lymphocyte; b-cell lymphoma; autoimmune disease; immunosuppressive;
KW non-hodgkin lymphoma; hodgkins disease; cytostatic;
KW chronic lymphocytic leukemia; hairy cell leukemia; rheumatoid arthritis;
KW antirheumatic; antirheumatic; systemic lupus erythematosus;
KW wegener granulomatosis; antiallergic; antiinflammatory; vasotropic;
KW inflammatory bowel disease; gastrointestinal-gen.;
KW idiopathic thrombocytopenic purpura; hemostatic; multiple sclerosis;
KW aetna; antiaesthetic; psoriasis; antipsoriatic; myasthenia gravis;
KW muscular-gen.; neuroprotective; vasculitis; diabetes; antidiabetic;
KW glomerulonephritis; nephrotropic; antibody; heavy chain variable region;
KW anti-CD20.
XX
OS Synthetic.
OS Undefined.
OS
PN WO2005000351-A2.
XX
PD 06-JAN-2005.
XX
PF 04-JUN-2004; 2004WO-US017693.
XX
XX 05-JUN-2003; 2003US-0476414P.
PR 05-JUN-2003; 2003US-0476481P.
PR 06-JUN-2003; 2003US-0476531P.
XX
PA (GETH) GENENTECH INC.
XX
PI Chan A, Gong Q, Martin F;

XX WPI, 2005-058069/06.
DR
XX
XX Depleting B cells from a mixed population of cells by contacting the
PT cells with a BlyS antagonist and a CD20 binding antibody, useful for
PT treating B cell malignancies and autoimmune disorders.
XX
XX Disclosure; SEQ ID NO 14; 114pp; English.
PS
XX The invention comprises a method of depleting B cells from a mixed
CC population of cells, the method involves contacting the mixed population
CC of cells with BlyS antagonist (e.g. an immunoadhesin) and a CD20 binding
CC antibody (e.g. hu2H7.v16). The method of the invention is useful for
CC treating B cell malignancies and autoimmune disorders, such as: non-
CC Hodgkin's lymphoma, Hodgkin's disease, follicular center cell lymphomas,
CC lymphocytic leukemia, hairy cell leukemia, rheumatoid arthritis, systemic
CC lupus erythematosus, Wegener's disease, inflammatory bowel disease,
CC idiopathic thrombocytopenic purpura, multiple sclerosis, asthma,
CC psoriasis, IgA nephropathy, myasthenia gravis, vasculitis, diabetes and
CC glomerulonephritis. The present amino acid sequence represents a
CC humanized anti-CD20 antibody (hu2H7.v16) heavy chain variable region.
XX
SQ Sequence 122 AA;
Query Match 80.9%; Score 72; DB 9; Length 122;
Best Local Similarity 81.2%; Pred. No. 0.00081;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 2 IYPGNDISYNQKFXG 17
Db 51 IYPGNGDTSYNQKFXG 66
RESULT 40
ID ADW21310 standard; protein; 122 AA.
XX
XX ADW21310;
XX
XX 07-APR-2005 (first entry)
XX
XX Mouse anti-CD20 antibody 2H7 VH, humanized clone v16.
XX
XX Humanized antibody; immune disorder; cancer; cytostatic; neoplasm;
KW rheumatoid arthritis; multiple sclerosis; systemic lupus erythematosus;
KW phage display; Antirheumatic; Antiarthritic; Neuroprotective;
KW Antiinflammatory; Dermatological; Immunosuppressive; leukemia; lymphoma;
KW myeloma; heavy chain variable region; CD20.
XX
XX Mus musculus.
OS Homo sapiens.
OS Chimeric.
OS
XX WO2005005462-A2.
XX
XX 20-JAN-2005.
XX
XX 04-JUN-2004; 2004WO-US017682.
XX
XX 05-JUN-2003; 2003US-0476414P.
PR 05-JUN-2003; 2003US-0476481P.
PR 06-JUN-2003; 2003US-0476531P.
XX
XX (GETH) GENENTECH INC.
XX
XX Chan AC, Gordon NC, Kelley RF, Koehler MFT, Starovasnik MA;
PI WPI, 2005-092059/10.
XX
XX New polypeptide or BlyS antagonist, for treating an immune-related
PT condition (e.g. rheumatoid arthritis, multiple sclerosis or systemic
PT lupus erythematosus) or cancer (e.g. leukemia or lymphoma).
XX
XX

PS Disclosure; SEQ ID NO 48; 226pp; English.
XX
XX The invention relates to a polypeptide comprising sequences of formula I,
CC I or II, (detailed in the claims) which are antagonists of BlyS (B cell
CC stimulator). Also included are a nucleic acid molecule encoding the
CC polypeptide, a vector comprising the nucleic acid molecule, a host cell
CC comprising the nucleic acid molecule, a method for producing a
CC polypeptide, a composition comprising the polypeptide optionally further
CC comprising a physiological carrier, a method for detecting an inhibitor
CC of BlyS binding to BR3 (BlyS receptor 3) in vitro, a method for
CC inhibiting BlyS binding to BR3 in a mammal, a method for inhibiting BlyS
CC signaling in a mammal and a method for treating an immune-related
CC condition or cancer in a mammal. The sequence of Formula I, II or III is
CC a sequence fused or conjugated to an immunoadhesion protein or to an
CC antibody, where the antibody is a Fab antibody, Fab' 2 antibody, a
CC scv antibody, a humanized antibody or multispecific antibody, e.g.
CC antibodies directed against CD20. The polypeptide is conjugated to an
CC agent, e.g. a growth inhibitory agent, a cytotoxic agent, a detection
CC agent, an agent that improves the bioavailability of the polypeptide and
CC an agent that improves the half-life of the polypeptide, where the
CC cytotoxic agent is a toxin, an antibiotic or a radioactive isotope. The
CC polypeptide, composition and methods are useful for treating an immune-
CC related condition (many examples given in the specification), e.g.
CC rheumatoid arthritis, multiple sclerosis or systemic lupus erythematosus
CC or for treating cancer (many examples given in the specification), e.g.
CC leukemia, lymphoma or myeloma. The present sequence represents the light
CC or heavy chain variable region of a humanized mouse antibody directed
CC against human CD20.
XX
SQ Sequence 122 AA;
Query Match 80.9%; Score 72; DB 9; Length 122;
Best Local Similarity 81.2%; Pred. No. 0.00081;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 2 IYPGNDISYNQKFXG 17
Db 51 IYPGNGDTSYNQKFXG 66
RESULT 41
ID ADW21309 standard; protein; 122 AA.
XX
XX ADW21309;
XX
XX 07-APR-2005 (first entry)
XX
XX Mouse anti-CD20 antibody 2H7 VH.
XX
XX Antibody; immune disorder; cancer; cytostatic; neoplasm;
KW rheumatoid arthritis; multiple sclerosis; systemic lupus erythematosus;
KW phage display; Antirheumatic; Antiarthritic; Neuroprotective;
KW Antiinflammatory; Dermatological; Immunosuppressive; leukemia; lymphoma;
KW myeloma; heavy chain variable region; CD20.
XX
XX Mus musculus.
XX
XX WO2005005462-A2.
XX
XX 20-JAN-2005.
XX
XX 04-JUN-2004; 2004WO-US017682.
XX
XX 05-JUN-2003; 2003US-0476414P.
PR 05-JUN-2003; 2003US-0476481P.
PR 06-JUN-2003; 2003US-0476531P.
XX
XX (GETH) GENENTECH INC.
XX
XX Chan AC, Gordon NC, Kelley RF, Koehler MFT, Starovasnik MA;
PI WPI, 2005-092059/10.
XX
XX

XX New polypeptide or Blyes antagonist, for treating an immune-related
 PT condition (e.g. rheumatoid arthritis, multiple sclerosis or systemic
 PT lupus erythematosus) or cancer (e.g. leukemia or lymphoma).
 XX
 PS Disclosure; SEQ ID NO 47; 226pp; English.

XX The invention relates to a polypeptide comprising sequences of formula I,
 CC I or II, (detailed in the claims) which are antagonists of Blyes (B cell
 CC stimulator). Also included are a nucleic acid molecule encoding the
 CC polypeptide, a vector comprising the nucleic acid molecule, a host cell
 CC comprising the nucleic acid molecule, a method for producing a
 CC polypeptide, a composition comprising the polypeptide optionally further
 CC comprising a physiological carrier, a method for detecting an inhibitor
 CC of Blyes binding to BR3 (Blyes receptor 3) in vitro, a method for
 CC inhibiting Blyes binding to BR3 in a mammal, a method for inhibiting Blyes
 CC signaling in a mammal and a method for treating an immune-related
 CC condition or cancer in a mammal. The sequence of Formula I, II or III is
 CC a sequence fused or conjugated to an immunoadhesion protein or to an
 CC antibody, where the antibody is a F(ab) antibody, F(ab')₂ antibody, a
 CC scfv antibody, a humanized antibody or multispecific antibody, e.g.
 CC antibodies directed against CD20. The polypeptide is conjugated to an
 CC agent, e.g. a growth inhibitory agent, a cytotoxic agent, a detection
 CC agent, an agent that improves the bioavailability of the polypeptide and
 CC an agent that improves the half-life of the polypeptide, where the
 CC cytotoxic agent is a toxin, an antibiotic or a radioactive isotope. The
 CC polypeptide, composition and methods are useful for treating an immune-
 CC related condition (many examples given in the specification), e.g.
 CC rheumatoid arthritis, multiple sclerosis or systemic lupus erythematosus
 CC or for treating cancer (many examples given in the specification), e.g.
 CC leukemia, lymphoma or myeloma. The present sequence represents the light
 CC or heavy chain variable region of a mouse antibody directed against human
 CC CD20.
 XX

SQ Sequence 122 AA;

Query Match 80.9%; Score 72; DB 9; Length 122;
 Best Local Similarity 81.2%; Pred. No. 0.00081;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGNDISYNOKFXG 17
 |||||
 Db 51 IYPGNGDTSYNOKFXG 66

RESULT 42

ADX00803
 ID ADX00803 standard; protein; 122 AA.

AC ADX00803;

DT 21-APR-2005 (first entry)

DE Humanized 2H7 v16 antibody heavy chain variable region, SEQ ID 2.

XX Antirheumatic; Antiarthritic; Antiinflammatory; Antiallergic;
 KW Dermatological; Immunosuppressive; Gastrointestinal-Gen.; Hemostatic;
 KW Antiproliferative; Nephroretroic; Neuroprotective; Muscular-Gen.; Vasotropic;
 KW Antidiabetic; Antianemic; Anti-HIV; Cytostatic; CD20 antagonist;
 KW antibody; antibody identification; antibody therapy; humanized antibody;
 KW humanized 2H7 v16 antibody; autoimmune disease; rheumatoid arthritis;
 KW systemic lupus erythematosus; inflammatory bowel disease;
 KW idiopathic thrombocytopenia purpura; thrombocytopenic purpura;
 KW thrombocytopenia; multiple sclerosis; psoriasis; myasthenia gravis;
 KW vasculitis; diabetes mellitus; Sjogrens syndrome; glomerulonephritis;
 KW autoimmune hemolytic anemia; Hodgkins disease; non-Hodgkin lymphoma;
 KW lymphoma; leukemia; acute lymphoblastic leukemia;
 KW chronic lymphocytic leukemia; hairy cell leukemia;
 KW lymphoplasmacytoid lymphoma; mantle cell lymphoma; multiple myeloma;
 KW heavy chain variable region.
 XX
 OS Synthetic.

PN US2005032130-A1.

XX 10-FEB-2005.

PP 24-JUN-2004; 2004US-00877363.

PR 29-JUL-2003; 2003US-0490678P.

PA (GENTH) GENTECH INC.

PI Beresini M, Song A;

DR WPI; 2005-161657/17.

XX Detecting neutralizing antibodies to a therapeutic antibody, useful in
 PT evaluating the efficacy of (anti-CD20) immunotherapy, comprises
 PT determining the ability of a sample from a patient treated with the
 PT antibody to block antibody activity.

PS Disclosure; SEQ ID NO 2; 18pp; English.

XX The present invention relates to a method (M1) for detecting neutralizing
 CC antibodies to a therapeutic antibody. The method comprises contacting
 CC cells expressing the antigen recognized by the therapeutic antibody with
 CC complement and with a sample from a patient treated with the therapeutic
 CC antibody, and determining complement-dependent cytotoxicity (CDC) of the
 CC therapeutic antibody, where a reduction in CDC indicates the presence of
 CC neutralizing antibodies in the sample. Also claimed is a method (M2) for
 CC evaluating the efficacy of an antibody that binds CD20, e.g. humanized
 CC 2H7 v16 antibody. The present sequence is a heavy chain variable region
 CC sequence of humanized 2H7 v16 antibody. In (M2) the anti-CD20 antibody is
 CC preferably administered to treat an autoimmune disease or B cell
 CC malignancy. The autoimmune disease is rheumatoid arthritis, systemic
 CC lupus erythematosus, Wegeners disease, inflammatory bowel disease,
 CC idiopathic or immune thrombocytopenic purpura, thrombotic
 CC thrombocytopenic purpura, autoimmune thrombocytopenia, multiple
 CC sclerosis, psoriasis, immunoglobulin A nephropathy, IGM polyneuropathies,
 CC myasthenia gravis, vasculitis, diabetes mellitus, Reynaud's syndrome,
 CC Sjogren's syndrome, glomerulonephritis or autoimmune hemolytic anemia.
 CC The B cell malignancy is chosen from Hodgkin's disease, non-Hodgkin's
 CC disease, follicular center cell lymphoma, acute lymphocytic leukemia,
 CC chronic lymphocytic leukemia, hairy cell leukemia, plasmacytoid
 CC lymphocytic lymphoma, mantle cell lymphoma, AIDS or HIV-related lymphoma,
 CC multiple myeloma, central nervous system lymphoma, post-transplant
 CC lymphoproliferative disorder, Waldenstrom's mucosa-associated lymphoid
 CC tissue lymphoma and marginal zone lymphoma/leukemia.
 XX

SQ Sequence 122 AA;

Query Match 80.9%; Score 72; DB 9; Length 122;
 Best Local Similarity 81.2%; Pred. No. 0.00081;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGNDISYNOKFXG 17
 |||||
 Db 51 IYPGNGDTSYNOKFXG 66

RESULT 43

ADY21867
 ID ADY21867 standard; protein; 122 AA.

AC ADY21867;

DT 05-MAY-2005 (first entry)

DE Human antibody 2H7 VH L11S mutant.

XX Antibacterial; Virucide; Antiparasitic; Fungicide; Immunotherapy;
 KW antibody engineering; cancer; neoplasia; cytostatic; immune disorder;
 KW graves disease; antithyroid; endocrine disease; hashimoto's disease;
 KW immunosuppressive; rheumatoid arthritis; antiarthritic; antirheumatic;
 KW inflammation; musculoskeletal disease; systemic lupus erythematosus;

KW antiinflammatory; dermatological; dermatological disease;
 KW metabolic disorder; sjogrens syndrome; ocular disease;
 KW thrombocytopenic purpura; hemostatic; hematological disease;
 KW multiple sclerosis; neuroprotective; neurobiological disease;
 KW myasthenia gravis; muscular-gen.; bacterial infection; fungal infection;
 KW fungicide; viral infection; virucide; parasitic infection; antiparasitic;
 KW fusion protein.
 OS Homo sapiens;
 OS Synthetic.
 PN WO2005017148-A1.
 XX
 XX 24-FEB-2005.
 PD
 PF 24-DEC-2003; 2003WO-US041600.
 XX
 PR 26-JUL-2003; 2003US-00627556.
 XX
 PA (TRUB-) TRUBION PHARM INC.
 PI Ledbetter JA, Hayden-Ledbetter MS, Thompson PA,
 DR WPI; 2005-182370/19.
 DR N-PSDB; ADY21866.
 XX
 PT New non-naturally occurring single chain protein comprising polypeptides
 PT with binding domain, connecting regions and N-terminally truncated
 PT immunoglobulin, having immunological activity, useful for neutralizing
 PT infectious agent.
 XX
 PS Disclosure; Page 368; 590pp; English.
 XX
 XX The invention relates to a non-naturally occurring single chain protein
 CC (1) comprising a first polypeptide having a binding domain polypeptide
 CC capable of binding to a target molecule, the binding domain polypeptide
 CC comprising a heavy chain variable region, which comprises an amino acid
 CC substitution or deletion at one or more amino acid residues, a second
 CC polypeptide comprising a connecting region attached to the first
 CC polypeptide, and a third polypeptide comprising an N-terminally truncated
 CC immunoglobulin heavy chain constant region polypeptide attached to the
 CC second polypeptide, where the non-naturally occurring single-chain
 CC protein is capable of an immunological activity. Also included are
 CC reducing a target cell population in a subject (involving administering
 CC to the subject a protein that is less than 150 kD, which involves
 CC treating the target cell population with a first protein or peptide that
 CC binds to cells within the target cell population, and treating the target
 CC cell population with a second protein or peptide that capable of at least
 CC one of binding an Fc receptor, inducing target cell apoptosis, or fix
 CC complements, where the first protein or peptide molecule is directly
 CC connected to the second protein or peptide molecule or, optionally, the
 CC first protein or peptide molecule and the second protein or peptide
 CC molecule are linked by a third protein or peptide molecule, and where the
 CC protein molecule is not an antibody, a member of the TNF family or the
 CC TNF receptor family, and is not conjugated with a bacterial toxin, a
 CC cytotoxic drug, or a radioisotope), depleting cells in an animal
 CC (involving administering a modified IgG protein into the blood stream of
 CC an animal), a polynucleotide that encodes the polypeptide of the
 CC invention, a cell containing the polynucleotide, a recombinant vector
 CC capable of expressing the polypeptide, expressing the polypeptide, a
 CC composition comprising the polypeptide) in combination with one or more
 CC additional therapeutic compounds, displaying recombinant molecules (which
 CC molecules include a native or engineered immunoglobulin heavy chain
 CC variable region, the improvement comprising an immunoglobulin heavy chain
 CC region that includes one or more mutation, substitution, alteration,
 CC and/or deletion at one or more amino acid residue corresponding to
 CC positions 9, 10, 11, 12, 108, 110, and 112 in the heavy chain variable
 CC region) and a non-naturally occurring single chain antigen-binding
 CC protein comprising protein having a mutation chosen from a list given in
 CC the specification. The polypeptides of the invention comprise single
 CC chain antibodies (scfv, with or without mutated residues) linked via an
 CC immunoglobulin hinge region (wild-type or mutants where the cysteines are
 CC changed to serines/prolines and denoted (SSS-P/H, (CSC-S/H etc) to an

CC immunoglobulin (IgG, IgE or IgA) heavy chain constant region (CH) which
 CC may also have mutations in CH2 (e.g., T26N) or a truncated CH3 (e.g., T4
 CC CH3, a 4 amino acid deletion). The polypeptide may be further linked to a
 CC non-antibody protein such as the transmembrane and cytoplasmic tail
 CC (TN/CT) of caspase-3, caspase-8 or CD80. The fusion polypeptides are
 CC useful for neutralization of an infectious agent (where the infectious
 CC agent is a bacterium, a virus, a parasite, or a fungus) and also for
 CC treatment of cancer, immune disorders, Grave's disease, Hashimoto's
 CC disease, rheumatoid arthritis, systemic lupus erythematosus, Sjogren's
 CC syndrome, thrombocytopenic purpura, multiple sclerosis and myasthenia
 CC gravis. The present sequence is an antibody peptide or fragment (scfv,
 CC hinge, CH region, VL or VH) used in a fusion protein of the invention.
 XX

SO Sequence 122 AA;

Query Match 80.9%; Score 72; DB 9; Length 122;
 Best Local Similarity 81.2%; Pred. No. 0.00081;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYFGNDISYNOKEFXG 17
 DB 51 IYFGNDISYNOKEFXG 66

RESULT 44
 ADX16331
 ID ADX16331 standard; protein; 122 AA.
 XX
 AC ADX16331;
 XX
 DT 05-MAY-2005 (first entry)
 XX

DE Modified Leu16 antibody heavy chain variable region.
 XX

XX immunosuppressive; cytostatic; Antirheumatic; Arthritis;
 KW CD20 modulator; antibody; pharmaceutical; autoimmune disease;
 KW proliferative disorder; leukemia; lymphoma; rheumatoid arthritis;
 KW immune disorder; hematological disease; neoplasm; inflammation;
 KW musculoskeletal disease; hyperproliferation; antibody engineering;
 KW mutin.
 KW
 OS Homo sapiens.
 OS Synthetic.
 XX

XX Key Location/Qualifiers

FT Misc-difference 12 /note= "Wild type Val substituted by Lys"
 FT Misc-difference 20 /note= "Wild type Met substituted by Val"
 FT Misc-difference 68 /note= "Wild type Ala substituted by Thr"
 FT Misc-difference 82 /note= "Wild type Gln substituted by Glu"
 FT Misc-difference 87 /note= "Wild type Thr substituted by Arg"
 FT Misc-difference 91 /note= "Wild type Thr substituted by Arg"
 FT Misc-difference 93 /note= "Wild type Ser substituted by Thr"
 FT Misc-difference 114 /note= "Wild type Asp substituted by Val"
 FT Misc-difference 114 /note= "Wild type Ala substituted by Thr"
 XX
 PN WO2005016969-A2.
 XX
 XX 24-FEB-2005.
 PD
 PF 16-AUG-2004; 2004WO-EP009033.
 XX
 PR 14-AUG-2003; 2003EP-00018480.
 PR 14-NOV-2003; 2003US-0520171P.
 XX
 PA (MERCK) MERCK PATENT GMBH.
 XX

PI Carr FU, Williams S, Gallies SD;
 XX WPI; 2005-196054/20.
 DR
 XX
 PT New CD20-binding polypeptide (chimeric antibody), useful for treating
 PT autoimmune diseases and proliferative disorders such as leukemia,
 PT lymphomas and rheumatoid arthritis.
 XX
 PS Claim 1; Page: 64pp; English.
 CC The invention relates to a polypeptide composition having the ability to
 CC bind to CD20 antigen. The CD20-binding polypeptide composition is in the
 CC form of a chimeric antibody and further including a human heavy chain
 CC constant region and a human light chain constant region, where the human
 CC heavy chain constant region is an Igg constant region, specifically an
 CC IgG1 constant region, and where the human light chain constant region is
 CC a human kappa light chain constant region. The polypeptide is fused to a
 CC cytokine, i.e. interleukin-2 (IL2). The C-terminus of the polypeptide is
 CC fused to the N-terminus of the cytokine. The polypeptides are in the form
 CC of a whole antibody, a Fab antibody fragment, a single-chain Fv antibody
 CC fragment, or a minbody. The polypeptide composition or a pharmaceutical
 CC composition is useful for manufacturing a medicament for the treatment of
 CC an autoimmune disease. The composition and method are useful for treating
 CC proliferative disorders such as leukemia, lymphomas, rheumatoid
 CC arthritis, and other autoimmune diseases. The present sequence represents
 CC the modified leu16 antibody heavy chain variable region used in the CD20-
 CC binding polypeptide composition of the invention. Note: The present
 CC sequence is not shown in the specification but is derived from the leu16
 CC antibody heavy chain variable region sequence given in figure 1 (see
 CC seqid:9) and information given in claim 1.
 CC
 SO Sequence 122 AA;
 OY
 Query Match 80.9%; Score 72; DB 9; Length 122;
 Best Local Similarity 81.2%; Pred. No. 0.00081;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Db 51 IYPNGDTSYNOKFXG 66
 2 IYPNGDTSYNOKFXG 17
 ||||| |||||
 51 IYPNGDTSYNOKFXG 66
 RESULT 45
 ADX16294
 ID ADX16294 standard; protein; 122 AA.
 AC ADX16294;
 XX
 DT 05-MAY-2005 (first entry)
 XX
 DE Lue16 antibody heavy chain variable region.
 XX
 KW immunosuppressive; Cytostatic; Antirheumatic; Antiarthritic;
 KW CD20 modulator; antibody; pharmaceutical; autoimmune disease;
 KW proliferative disorder; leukemia; lymphoma; rheumatoid arthritis;
 KW immune disorder; hematological disease; neoplasm; inflammation;
 KW musculoskeletal disease; hyperproliferation; antibody engineering;
 KW heavy chain variable region; Lue16.
 XX
 OS Homo sapiens.
 XX
 PN WO2005016969-A2.
 XX
 PD 24-FEB-2005.
 XX
 PF 16-AUG-2004; 2004WO-EP009033.
 XX
 PR 14-AUG-2003; 2003EP-00018480.
 XX
 PR 14-NOV-2003; 2003US-0520171P.
 XX
 PA (MERE) MERCK PATENT GMBH.
 XX
 PI Carr FU, Williams S, Gallies SD;

XX
 DR WPI; 2005-196054/20.
 XX
 XX
 PT New CD20-binding polypeptide (chimeric antibody), useful for treating
 PT autoimmune diseases and proliferative disorders such as leukemia,
 PT lymphomas and rheumatoid arthritis.
 XX
 PS Claim 1; Fig 3; 64pp; English.
 CC The invention relates to a polypeptide composition having the ability to
 CC bind to CD20 antigen. The CD20-binding polypeptide composition is in the
 CC form of a chimeric antibody and further including a human heavy chain
 CC constant region and a human light chain constant region, where the human
 CC heavy chain constant region is an Igg constant region, specifically an
 CC IgG1 constant region, and where the human light chain constant region is
 CC a human kappa light chain constant region. The polypeptide is fused to a
 CC cytokine, i.e. interleukin-2 (IL2). The C-terminus of the polypeptide is
 CC fused to the N-terminus of the cytokine. The polypeptides are in the form
 CC of a whole antibody, a Fab antibody fragment, a single-chain Fv antibody
 CC fragment, or a minbody. The polypeptide composition or a pharmaceutical
 CC composition is useful for manufacturing a medicament for the treatment of
 CC an autoimmune disease. The composition and method are useful for treating
 CC proliferative disorders such as leukemia, lymphomas, rheumatoid
 CC arthritis, and other autoimmune diseases. The present sequence represents
 CC a CD20-binding polypeptide of the invention.
 CC
 SO Sequence 122 AA;
 OY
 Query Match 80.9%; Score 72; DB 9; Length 122;
 Best Local Similarity 81.2%; Pred. No. 0.00081;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Db 51 IYPNGDTSYNOKFXG 66
 2 IYPNGDTSYNOKFXG 17
 ||||| |||||
 51 IYPNGDTSYNOKFXG 66
 RESULT 46
 ADX16295
 ID ADX16295 standard; protein; 122 AA.
 AC ADX16295;
 XX
 DT 05-MAY-2005 (first entry)
 XX
 DE VhY light chain variable region.
 XX
 KW immunosuppressive; Cytostatic; Antirheumatic; Antiarthritic;
 KW CD20 modulator; antibody; pharmaceutical; autoimmune disease;
 KW proliferative disorder; leukemia; lymphoma; rheumatoid arthritis;
 KW immune disorder; hematological disease; neoplasm; inflammation;
 KW musculoskeletal disease; hyperproliferation; antibody engineering;
 KW light chain variable region; VhY.
 XX
 OS Homo sapiens.
 XX
 PN WO2005016969-A2.
 XX
 PD 24-FEB-2005.
 XX
 PF 16-AUG-2004; 2004WO-EP009033.
 XX
 PR 14-AUG-2003; 2003EP-00018480.
 XX
 PR 14-NOV-2003; 2003US-0520171P.
 XX
 PA (MERE) MERCK PATENT GMBH.
 XX
 PI Carr FU, Williams S, Gallies SD;
 XX
 DR WPI; 2005-196054/20.
 XX
 PT New CD20-binding polypeptide (chimeric antibody), useful for treating
 PT autoimmune diseases and proliferative disorders such as leukemia,

PT lymphomas and rheumatoid arthritis.
XX
PS Claim 8, Fig 3, 64pp; English.
XX
CC The invention relates to a polypeptide composition having the ability to
CC bind to CD20 antigen. The CD20-binding polypeptide composition is in the
CC form of a chimeric antibody and further including a human heavy chain
CC constant region and a human light chain constant region, where the human
CC heavy chain constant region is an IgG constant region, specifically an
CC IgG1 constant region, and where the human light chain constant region is
CC a human kappa light chain constant region. The polypeptide is fused to a
CC cytokine, i.e. interleukin-2 (IL2). The C-terminus of the polypeptide is
CC fused to the N-terminus of the cytokine. The polypeptides are in the form
CC of a whole antibody, a Fab antibody fragment, a single-chain Fv antibody
CC fragment, or a minibody. The polypeptide composition or a pharmaceutical
CC composition is useful for manufacturing a medicament for the treatment of
CC an autoimmune disease. The composition and method are useful for treating
CC proliferative disorders such as leukemia, lymphomas, rheumatoid
CC arthritis, and other autoimmune diseases. The present sequence represents
CC a CD20-binding polypeptide of the invention.
XX
SQ Sequence 122 AA;
XX
Query Match 80.9%; Score 72; DB 9; Length 122;
Best Local Similarity 81.2%; Pred. No. 0.00081;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
QY 2 IYPGNDISYNQKFXG 17
Db 51 IYPGNGDTSYNQKFXG 66
XX
RESULT 47
ADY62623
ID ADY62623 standard; protein; 122 AA.
XX
AC ADY62623;
XX
DT 19-MAY-2005 (first entry)
XX
DE Humanized 2H7 antibody variable heavy chain.
XX
XX Antibody therapy; ocular disease; ophthalmological; uveitis; retinopathy;
KM Wegener granulomatosis; iritis; ocular pemphigoid; onchocerciasis;
KM episcleritis; scleritis; sjogren's syndrome; antibody; heavy chain;
KM immunoglobulin.
XX
XX Homo sapiens,
OS Chimeric.
OS Unidentified.
XX
FN US2005053602-A1.
XX
PD 10-MAR-2005.
XX
PE 20-AUG-2004; 2004US-00922651.
XX
PR 29-AUG-2003; 2003US-0498791P.
XX
PA (GETH) GENENTECH INC.
XX
PI Brunetta PG;
XX
DR WPI; 2005-202206/21.
XX
PT Treating an ocular disease in a mammal, such as uveitis, iritis, thyroid
XX eye disease, comprises administering a CD20 antagonist to the mammal.
XX
PS Disclosure; SEQ ID NO 2, 11pp; English.
XX
XX The invention relates to a method for treating an ocular disease by
CC administering a CD20 antagonist which comprises an antibody to the mammal
CC in an amount effective to treat the ocular disorder. The method and the

CC antagonist are useful for treating an ocular disease, such as uveitis,
CC iritis, thyroid eye disease or Grave's ophthalmology, ocular Behcet's
CC disease, ocular myasthenia gravis, ocular pemphigoid, autoimmune
CC retinopathy, onchocerciasis, episcleritis, scleritis, relapsing steroid
CC dependent optic neuritis, ocular involvement of Wegener's granulomatosis,
CC Sjogren's eye complication, melanoma associated retinopathy and cancer
CC associated retinopathy. The present sequence is the humanized 2H7
CC antibody variable heavy chain that binds to CD20 antigen.
XX
SQ Sequence 122 AA;
XX
Query Match 80.9%; Score 72; DB 9; Length 122;
Best Local Similarity 81.2%; Pred. No. 0.00081;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
QY 2 IYPGNDISYNQKFXG 17
Db 51 IYPGNGDTSYNQKFXG 66
XX
RESULT 48
AD283548
ID AD283548 standard; protein; 122 AA.
XX
AC AD283548;
XX
DT 14-JUL-2005 (first entry)
XX
DE CD20 VH.
XX
KM neoplasm; inflammation; immune disorder; infection; allergy;
KM graft versus host disease; cytostatic; Antiinflammatory;
KM immunosuppressive; Virucide; Antibacterial; Antiallergic; Antiparasitic;
KM CD20.
XX
XX Synthetic.
OS
XX WO2005040220-A1.
XX
FN 06-MAY-2005.
XX
PD 15-OCT-2004; 2004WO-EP011646.
XX
PE 16-OCT-2003; 2003EP-00023581.
XX
PR (MICR-) MICROMET AG.
XX
PA Hofmeister R, Kohleisen B, Lenkkeri-Schuetz U, Itin C, Baewerle P,
XX Carr PJ, Hamilton AA, Williams S;
XX
DR WPI; 2005-333494/34.
XX
DR N-PSDB: AD283547.
XX
XX New cytotoxically active CD3 specific binding construct comprises a first
XX domain specifically binding to human CD3 and an Ig-derived second binding
XX domain, useful for treating, preventing, or ameliorating, e.g.
XX proliferative disease.
XX
PS Disclosure; SEQ ID NO 170, 639pp; English.
XX
XX The invention relates to a cytotoxically active CD3 specific binding
XX construct comprising a first domain specifically binding to human CD3 and
XX an Ig-derived second binding domain. The CD3 specific binding construct
XX above or the construct produced by the process, nucleic acid molecule,
XX vector, or host is useful for the preparation of a pharmaceutical
XX composition for the prevention, treatment, or amelioration of a
XX proliferative disease, a tumor, an inflammatory disease, an immunological
XX disorder, an autoimmune disease, an infectious disease, viral disease,
XX allergic reactions, parasitic reactions, graft-versus-host diseases, or
XX host-versus-graft diseases. The cytotoxically active CD3 specific binding
XX construct is useful for treating, preventing, or ameliorating
XX proliferative disease, a tumor, an inflammatory disease, an immunological
XX disorder, an autoimmune disease, an infectious disease, viral disease,

CC allergic reactions, parasitic reactions, graft-versus-host diseases, or
CC host-versus-graft diseases. The present sequence represents the amino
CC acid sequence of a CD20 VH.
XX

Sequence 122 AA;

Query Match 80.9%; Score 72; DB 9; Length 122;
Best Local Similarity 81.2%; Pred. No. 0.00081;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGNDISTYNQKFXG 17
| | | | | | | | | | | | | | | | | | | | |
Db 51 IYPGNDISTYNQKFXG 66

RESULT 49

AE827726
ID AE827726 standard; protein; 122 AA.

AC AEB27726;

DT 08-SEP-2005 (first entry)

DE Humanized 2H7 antibody heavy chain variable region sequence.

XX Antibody therapy; autoimmune disease;
XX B-lymphocyte-restricted differentiation antigen; Bp35; arthritis;
KW immunosuppressive; anti-rheumatic; antiarthritic; anti-inflammatory;
KW dermatological; gastrointestinal; antitumor; antitubercular;
KW antiarteriosclerotic; vasotropic; thyromimetic; antidiabetic;
KW nephrotropic; neuroprotective; cardiac; CD20-antagonist.

OS Homo sapiens.
OS Synthetic.

XX WO2005060999-A2.

PD 07-JUL-2005.

XX 07-DEC-2004; 2004WO-US040949.

XX 19-DEC-2003; 2003US-0531363P.

PA (GETH) GENENTECH INC.

PI Brunetta PG;

XX WPI; 2005-488599/49.

XX Treating autoimmune diseases, such as rheumatoid arthritis, psoriasis,
PT inflammatory bowel disease, Crohn's disease, ulcerative colitis, eczema,
PT asthma, lupus, atherosclerosis and diabetes, using CD20 antagonists or
PT antibodies.

XX Disclosure; SEQ ID NO 2; s1pp; English.

XX The invention relates to treating autoimmune disease in a patient. The
CC method involves detecting CD20 antigen (also called human B-lymphocyte-
CC restricted differentiation antigen, Bp35) or CD20-positive B cells in a
CC sample from the patient. When CD20 or CD20-positive B cells is detected
CC in the sample, a CD20 antagonist or antibody is administered to the
CC patient to treat the autoimmune disease. Also disclosed are CD20
CC proteins, nucleic acids and antibodies used in the methods of the
CC invention. The CD20 antagonist in treating autoimmune disease comprises
CC an antibody that is not conjugated with a cytotoxic agent and comprises
CC rituximab or humanized 2H7. The antibody is also conjugated with a
CC cytotoxic agent. The methods and compositions of the present invention
CC are useful for diagnosing or treating autoimmune diseases, such as
CC rheumatoid arthritis, psoriasis, inflammatory bowel disease, Crohn's
CC disease, ulcerative colitis, eczema, asthma, lupus, atherosclerosis,
CC aplastic anemia, Sjogren's syndrome, autoimmune thyroiditis, diabetes,
CC Guillain-Barre syndrome, glomerulonephritis and coronary artery disease.
CC The method consists essentially of administering the antagonist to the

CC mammal. The CD20 protein or nucleic acid is detected in the initial step.
CC The present sequence represents the heavy chain variable region sequence
CC of a humanized 2H7 antibody.
XX

Sequence 122 AA;

Query Match 80.9%; Score 72; DB 9; Length 122;
Best Local Similarity 81.2%; Pred. No. 0.00081;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGNDISTYNQKFXG 17
| | | | | | | | | | | | | | | | | | | | |
Db 51 IYPGNDISTYNQKFXG 66

RESULT 50

AE817636
ID AE817636 standard; peptide; 122 AA.

AC AEB17636;

DT 08-SEP-2005 (first entry)

DE Variable heavy peptide sequence of humanized 2H7 antibody.

XX Transplant rejection; immunosuppressive; CD20;
KW human B-lymphocyte-restricted differentiation antigen; Bp35; B-lymphocyte;
KW CD20 antagonist; antibody therapy; autoimmune disease; rituximab;
KW humanized antibody.

OS Mus sp.

OS Homo sapiens.

OS Chimeric.

XX WO2005061542-A2.

PD 07-JUL-2005.

XX 07-DEC-2004; 2004WO-US040947.

XX 19-DEC-2003; 2003US-0531594P.

PA (GETH) GENENTECH INC.

PI Brunetta PG;

XX WPI; 2005-522180/53.

XX Treating transplant rejection, such as grafts from bone marrow, skin,
PT heart, liver, spleen, pancreas, thyroid, lung, kidney and tubular organs,
PT using CD20 antagonists or antibodies.

XX Disclosure; SEQ ID NO 2; 47pp; English.

XX The present invention relates to treating a patient suffering from
CC transplant rejection with a therapy based on the presence of CD20 in a
CC sample taken from the patient. The method of treating transplant
CC rejection in a patient comprises detecting CD20 or a CD20-positive B
CC cells in a sample from the patient, and where CD20 or CD20-positive B
CC cells is detected in the sample, administering a CD20 antagonist or
CC antibody to the patient to treat the autoimmune disease. Also disclosed
CC as new are CD20 proteins, nucleic acids and antibodies used in the
CC methods of the invention. The sample is from a biopsy taken from the
CC patient prior to transplantation or from a biopsy of a transplanted
CC organ. The solid organ transplant rejection is treated, where the solid
CC organ is a lung. The antagonist comprises an antibody that is not
CC conjugated with a cytotoxic agent. The antibody comprises rituximab or
CC humanized 2H7, and is conjugated with a cytotoxic agent. The CD20 protein
CC or nucleic acid is detected in the initial step. Acute or chronic
CC rejection is treated in the following step. CD20-antagonist. The methods
CC and compositions of the present invention are useful for diagnosing or
CC treating transplant rejection, such as grafts from bone marrow, skin,
CC heart, liver, spleen, pancreas, thyroid, lung, kidney and tubular organs.

CC The present sequence is the variable heavy peptide sequence of humanized
CC 2H7 antibody,
CC
CC

CC 2H7 antibody.
xy

XX

SQ Sequence 122 AA;

Query Match	80.9%;	Score 72;	DB 9;	Length 122;
Best Local similarity	81.3%;	Pred NO	0.00081.	

Best Local Similarity 81.2%; Pred. No. 0.00081;
Matches 13: Conservative 0: Mismatches 3

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGNDISYNÖKFXG 17
|||||

Db 51 IYPGNGDTSYNQKFKG 66

Search completed: May 4, 2006, 12:57:42
Job time : 172.111 secs

Job time : 172.111 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 4, 2006, 13:00:03 ; Search time 24.2857 Seconds
(without alignments)
67.352 Million cell updates/sec

Title: US-10-700-632-2

Perfect score: 89

Sequence: 1 VLYPNDSDYNOKFXG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 1000 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	73	82.0	91	2	Ig heavy chain V r
2	73	82.0	117	2	Ig heavy chain V r
3	72	80.9	93	2	Ig gamma chain V r
4	72	80.9	94	2	Ig gamma chain V r
5	72	80.9	95	2	Ig gamma chain V r
6	72	80.9	97	2	Ig gamma chain V r
7	72	80.9	101	2	Ig gamma chain V r
8	72	80.9	102	2	Ig gamma chain V r
9	72	80.9	102	2	Ig gamma chain V r
10	70	78.7	109	2	Ig heavy chain V r
11	68	76.4	133	2	Ig heavy chain V r
12	61	68.5	112	2	Ig heavy chain V r
13	60	67.4	115	2	Ig heavy chain V r
14	59	66.3	102	2	Ig heavy chain V r
15	59	66.3	108	2	Ig heavy chain V r
16	58	65.2	123	2	Ig heavy chain V r
17	58	65.2	123	2	Ig heavy chain V r
18	58	65.2	138	2	Ig heavy chain V r
19	58	65.2	140	2	Ig heavy chain V r
20	57	64.0	112	2	Ig heavy chain V r
21	57	64.0	115	2	Ig heavy chain V r
22	57	64.0	118	2	Ig heavy chain V r
23	57	64.0	119	2	Ig heavy chain V r
24	55	61.8	67	2	Ig heavy chain V r
25	55	61.8	107	2	Ig heavy chain V r
26	55	61.8	109	2	Ig heavy chain V r
27	55	61.8	111	2	Ig heavy chain V r
28	55	61.8	127	2	Ig heavy chain V r
29	55	61.8	246	2	Ig heavy chain V r

30	61.8	446	2	S40295	Ig gamma-2a chain
31	60.7	104	2	S26466	Ig heavy chain V r
32	60.7	110	2	PI0244	Ig heavy chain V r
33	60.7	112	2	PI0245	Ig heavy chain V r
34	60.7	117	1	HVMS02	Ig heavy chain pre
35	60.7	117	1	HVMSA1	Ig heavy chain pre
36	60.7	119	2	PL0089	Ig heavy chain V r
37	60.7	120	2	B22769	Ig heavy chain V r
38	60.7	126	2	PI1424	Ig heavy chain V r
39	60.7	140	2	S04575	Ig heavy chain pre
40	59.6	76	2	B28572	Ig heavy chain V r
41	59.6	84	2	PI1487	Ig heavy chain V r
42	59.6	96	2	PI1165	Ig heavy chain V r
43	59.6	102	2	PI1490	Ig heavy chain V r
44	59.6	106	2	PI1002	Ig heavy chain V r
45	59.6	109	2	PI1001	Ig heavy chain V r
46	59.6	110	2	PI1000	Ig heavy chain V r
47	59.6	118	2	A24754	Ig heavy chain V r
48	59.6	123	2	E48677	Ig heavy chain V-D
49	59.6	140	1	HVMSG7	Ig heavy chain pre
50	59.6	140	2	PI1486	Ig heavy chain V r
51	59.6	140	2	PI1489	Ig heavy chain V r
52	59.6	140	2	PI1489	Ig heavy chain V r
53	58.4	50	2	S26941	Ig heavy chain V r
54	58.4	102	2	PI1491	Ig heavy chain V r
55	58.4	117	2	PL0237	Ig heavy chain V r
56	58.4	117	2	PL0235	Ig heavy chain V r
57	58.4	117	2	S03305	Ig heavy chain V r
58	58.4	119	2	PI1518	Ig heavy chain V r
59	58.4	119	2	S19664	Ig heavy chain V r
60	58.4	119	2	PI1516	Ig heavy chain V r
61	58.4	119	2	PI1519	Ig heavy chain V r
62	58.4	122	2	A27635	Ig heavy chain pre
63	58.4	123	2	F48677	Ig heavy chain V-D
64	58.4	135	2	PI1494	Ig heavy chain V r
65	58.4	137	2	PI1227	Ig heavy chain pre
66	58.4	139	2	A27609	Ig heavy chain pre
67	58.4	140	2	PI1488	Ig heavy chain V r
68	57.3	66	2	S36384	Ig heavy chain V r
69	57.3	96	2	H28195	Ig heavy chain V r
70	57.3	101	2	PH0983	Ig heavy chain V r
71	57.3	101	2	PH0982	Ig heavy chain V r
72	57.3	102	2	PI1254	Ig heavy chain V r
73	57.3	104	2	PH0981	Ig heavy chain V r
74	57.3	112	2	S26473	Ig heavy chain V-D
75	57.3	116	2	S09962	Ig heavy chain V r
76	57.3	120	2	F28185	Ig heavy chain V r
77	57.3	121	2	A30551	Ig heavy chain V r
78	57.3	122	2	S32185	Ig heavy chain V r
79	57.3	127	2	PI1411	Ig heavy chain pre
80	57.3	135	2	A30577	Ig heavy chain pre
81	57.3	138	2	E32513	Ig heavy chain pre
82	57.3	140	2	S09216	Ig heavy chain pre
83	56.2	90	2	PI1485	Ig heavy chain V r
84	56.2	95	2	S26469	Ig heavy chain V r
85	56.2	98	2	PI1274	Ig heavy chain V r
86	56.2	98	2	S26907	Ig heavy chain V r
87	56.2	101	2	S12428	Ig heavy chain V r
88	56.2	101	2	S12424	Ig heavy chain V r
89	56.2	101	2	F37262	Ig heavy chain V r
90	56.2	102	2	PI1266	Ig heavy chain V r
91	56.2	102	2	PI1279	Ig heavy chain V r
92	56.2	102	2	PI1281	Ig heavy chain V r
93	56.2	102	2	PI1281	Ig heavy chain V r
94	56.2	102	2	PI1277	Ig heavy chain V r
95	56.2	102	2	PI1244	Ig heavy chain V r
96	56.2	102	2	PI1267	Ig heavy chain V r
97	56.2	102	2	PI1272	Ig heavy chain V r
98	56.2	102	2	PI1282	Ig heavy chain V r
99	56.2	102	2	PI1248	Ig heavy chain V r
100	56.2	102	2	PI1280	Ig heavy chain V r
101	56.2	102	2	PI1258	Ig heavy chain V r
102	56.2	102	2	PI1264	Ig heavy chain V r

103	50	56.2	102	2	PH1259	Ig heavy chain V r
104	50	56.2	102	2	PH1273	Ig heavy chain V r
105	50	56.2	102	2	PH1265	Ig heavy chain V r
106	50	56.2	102	2	PH1249	Ig heavy chain V r
107	50	56.2	102	2	PH1271	Ig heavy chain V r
108	50	56.2	102	2	PH1278	Ig heavy chain V r
109	50	56.2	104	2	B36006	Ig heavy chain V r
110	50	56.2	105	2	PH0976	Ig heavy chain V r
111	50	56.2	109	2	PH0973	Ig heavy chain V r
112	50	56.2	111	2	PH0968	Ig heavy chain V r
113	50	56.2	113	2	PH1428	Ig heavy chain V r
114	50	56.2	113	2	S55530	Ig heavy chain V r
115	50	56.2	115	2	PH1557	Ig heavy chain V r
116	50	56.2	117	1	MEMSAB	Ig heavy chain V r
117	50	56.2	117	1	MEMS57	Ig heavy chain V r
118	50	56.2	117	1	A28846	Ig heavy chain pre
119	50	56.2	117	2	S19670	Ig heavy chain V r
120	50	56.2	117	2	S19666	Ig heavy chain V r
121	50	56.2	118	1	MEMS38	Ig heavy chain V r
122	50	56.2	119	2	B30562	Ig heavy chain V r
123	50	56.2	120	2	PD0008	Ig heavy chain V r
124	50	56.2	120	2	F45722	anti-glycoprotein
125	50	56.2	120	2	E45722	Ig heavy chain V r
126	50	56.2	123	2	PH1423	Ig heavy chain - h
127	50	56.2	123	2	S38492	Ig heavy chain V r
128	50	56.2	123	2	C36006	Ig heavy chain V r
129	50	56.2	127	2	PH1414	Ig heavy chain V r
130	50	56.2	127	2	PH1409	Ig heavy chain V r
131	50	56.2	128	2	S16685	Ig heavy chain V r
132	50	56.2	128	2	S17267	Ig heavy chain V r
133	50	56.2	134	2	PH1422	Ig heavy chain V r
134	50	56.2	136	2	A49047	Ig heavy chain V r
135	50	56.2	136	2	PH1559	Ig heavy chain V r
136	50	56.2	136	2	PH0208	Ig heavy chain pre
137	50	56.2	137	2	F29380	Ig heavy chain pre
138	50	56.2	139	2	PH1558	Ig heavy chain V r
139	50	56.2	140	2	PH1498	Ig heavy chain V r
140	50	56.2	140	2	T01407	Ig heavy chain (my
141	49	55.1	86	2	S12580	Ig heavy chain V r
142	49	55.1	88	2	C25155	Ig heavy chain V r
143	49	55.1	88	2	E25155	Ig heavy chain V r
144	49	55.1	88	2	G25155	Ig heavy chain V r
145	49	55.1	88	2	F25155	Ig heavy chain V r
146	49	55.1	109	2	PH0233	Ig heavy chain V r
147	49	55.1	112	2	S09957	Ig heavy chain V-D
148	49	55.1	113	2	PH0974	Ig heavy chain V r
149	49	55.1	113	2	S55528	Ig heavy chain V r
150	49	55.1	113	2	S55532	Ig heavy chain V r
151	49	55.1	113	2	S55531	Ig heavy chain V r
152	49	55.1	115	2	A56700	Ig heavy chain (an
153	49	55.1	116	2	S20645	Ig heavy chain V r
154	49	55.1	117	2	PH0234	Ig heavy chain V r
155	49	55.1	119	2	S36257	Ig heavy chain V r
156	49	55.1	120	2	A54256	Ig heavy chain V r
157	49	55.1	121	2	PL0281	Ig heavy chain V r
158	49	55.1	123	2	B30560	Ig heavy chain V r
159	49	55.1	127	2	PH1421	Ig heavy chain V r
160	49	55.1	141	2	A39276	Ig heavy chain pre
161	49	53.9	98	2	PH0877	Ig heavy chain V r
162	48	53.9	98	2	S17604	Ig heavy chain V r
163	48	53.9	106	2	F32513	Ig heavy chain V r
164	48	53.9	110	2	A32189	Ig heavy chain V r
165	48	53.9	114	2	S26319	Ig heavy chain V r
166	48	53.9	117	1	HVMS3	Ig heavy chain pre
167	48	53.9	118	2	S38717	Ig heavy chain V r
168	48	53.9	122	2	S06825	Ig heavy chain V r
169	48	53.9	125	2	PH1410	Ig heavy chain V r
170	48	53.9	135	2	S50057	Ig heavy chain pre
171	48	53.9	475	2	S01321	Ig gamma-2b chain
172	47	52.8	94	2	S42185	Ig gamma chain V r
173	47	52.8	94	2	PH0996	Ig heavy chain V r
174	47	52.8	96	2	D5155	Ig heavy chain V r
175	47	52.8	97	2	S17603	Ig heavy chain V r
176	47	52.8	98	2	A28572	Ig heavy chain V r
177	47	52.8	98	2	S26313	Ig heavy chain V r
178	47	52.8	98	2	S26312	Ig heavy chain V r
179	47	52.8	101	2	S26311	Ig heavy chain V r
180	47	52.8	101	2	S26310	Ig heavy chain V r
181	47	52.8	102	2	PH1247	Ig heavy chain V r
182	47	52.8	102	2	PH1252	Ig heavy chain V r
183	47	52.8	104	2	PH0991	Ig heavy chain V r
184	47	52.8	109	2	PH0989	Ig heavy chain V r
185	47	52.8	109	2	PH1094	Ig heavy chain V r
186	47	52.8	109	2	PH1096	Ig heavy chain V r
187	47	52.8	110	2	PH0995	Ig heavy chain V r
188	47	52.8	111	2	PH0990	Ig heavy chain V r
189	47	52.8	111	2	PH0993	Ig heavy chain V r
190	47	52.8	111	2	PH0994	Ig heavy chain V r
191	47	52.8	111	2	PH0992	Ig heavy chain V r
192	47	52.8	112	2	A30502	Ig heavy chain V r
193	47	52.8	114	2	PH1523	Ig heavy chain V r
194	47	52.8	114	2	PH1522	Ig heavy chain V r
195	47	52.8	116	2	S15672	Ig heavy chain V r
196	47	52.8	117	1	HVMS8A	Ig heavy chain pre
197	47	52.8	117	2	S25176	Ig heavy chain V r
198	47	52.8	118	2	S38565	Ig heavy chain V r
199	47	52.8	119	2	PH1505	Ig heavy chain V r
200	47	52.8	119	2	PH1517	Ig heavy chain V r
201	47	52.8	119	2	S09955	Ig heavy chain V-D
202	47	52.8	119	2	PH1502	Ig heavy chain V r
203	47	52.8	119	2	PH1521	Ig heavy chain V r
204	47	52.8	119	2	PH1504	Ig heavy chain V r
205	47	52.8	119	2	PH1504	Ig heavy chain V r
206	47	52.8	119	2	PH1520	Ig heavy chain V r
207	47	52.8	119	2	PH1512	Ig heavy chain V r
208	47	52.8	119	2	C30562	Ig heavy chain V r
209	47	52.8	121	2	A26405	Ig heavy chain V r
210	47	52.8	123	2	PH1413	Ig heavy chain V r
211	47	52.8	131	2	S66537	Ig heavy chain V r
212	47	52.8	135	2	E29380	Ig heavy chain pre
213	47	52.8	140	2	PH1482	Ig heavy chain V r
214	47	52.8	144	2	B30502	Ig heavy chain V r
215	47	52.8	150	2	FN0444	Ig heavy chain V r
216	47	52.8	150	2	AG0859	Outer membrane ush
217	47	52.8	75	2	A25155	Ig heavy chain V r
218	46	51.7	116	2	184704	gene VH104B protei
219	46	51.7	146	2	D82748	stringent starvati
220	46	51.7	558	2	T37567	probable NADPH cyt
221	46	50.6	56	2	PH1158	Ig heavy chain V r
222	45	50.6	72	2	C37263	Ig heavy chain V r
223	45	50.6	88	2	PH1161	Ig heavy chain V r
224	45	50.6	94	2	G32513	Ig heavy chain V r
225	45	50.6	102	2	PH1238	Ig heavy chain V r
226	45	50.6	102	2	PH1263	Ig heavy chain V r
227	45	50.6	102	2	B37263	Ig heavy chain V r
228	45	50.6	111	2	S26463	Ig heavy chain V r
229	45	50.6	116	2	S26309	Ig heavy chain V r
230	45	50.6	117	1	HVMS23	Ig heavy chain pre
231	45	50.6	119	2	D30562	Ig heavy chain V r
232	45	50.6	122	2	S24287	Ig heavy chain V r
233	45	50.6	136	1	HVMSB1	Ig heavy chain pre
234	45	50.6	158	2	F82305	ecrington starvati
235	45	50.6	214	2	PC4202	monoclonal antibod
236	45	50.6	335	2	T39391	meu14. RING zinc f
237	45	50.6	1220	2	S64916	probable membrane
238	45	49.4	71	2	PH1167	Ig heavy chain V r
239	44	49.4	96	2	S17608	Ig heavy chain V r
240	44	49.4	113	2	S55533	Ig heavy chain V r
241	44	49.4	113	2	S55535	Ig heavy chain V r
242	44	49.4	120	2	S09956	Ig heavy chain V-D
243	44	49.4	125	2	PH0100	Ig heavy chain V r
244	44	49.4	127	2	PH1420	Ig heavy chain V r
245	44	49.4	212	2	S77369	hypothetical prote
246	44	49.4	212	2	S37483	Ig gamma-2a chain
247	44	49.4	249	2	S04845	Ig heavy chain pre
248	44	49.4	549	2		

249	44	49.4	1286	2	T18734	hypothetical prote
250	43	48.3	86	2	S54912	Ig heavy chain V r
251	43	48.3	102	2	PH1275	Ig heavy chain V r
252	43	48.3	102	2	PH1260	Ig heavy chain V r
253	43	48.3	103	2	PH0986	Ig heavy chain V r
254	43	48.3	117	2	S19669	Ig heavy chain V r
255	43	48.3	126	2	PH1416	Ig heavy chain V r
256	43	48.3	126	2	PH1417	Ig heavy chain V r
257	43	48.3	126	2	PH1418	Ig heavy chain V r
258	43	48.3	126	2	PH1419	Ig heavy chain V r
259	43	48.3	259	2	T36157	probable secreted
260	43	48.3	356	2	T27733	hypothetical prote
261	43	48.3	477	2	AC1923	site-specific DNA-
262	42.5	47.8	580	2	JC7502	choline transpor
263	42	47.2	90	2	S03306	Ig heavy chain V r
264	42	47.2	91	2	PI0242	Ig heavy chain V r
265	42	47.2	96	2	S17609	Ig heavy chain V r
266	42	47.2	102	2	PH1268	Ig heavy chain V r
267	42	47.2	102	2	PH1276	Ig heavy chain V r
268	42	47.2	107	2	PI0240	Ig heavy chain V r
269	42	47.2	107	2	PI0243	Ig heavy chain V r
270	42	47.2	107	2	PI0241	Ig heavy chain V r
271	42	47.2	113	2	S55534	Ig heavy chain V r
272	42	47.2	116	2	S22558	Ig heavy chain V r
273	42	47.2	119	2	PI0086	Ig heavy chain V r
274	42	47.2	119	2	S45714	Ig heavy chain V r
275	42	47.2	126	2	PH1412	Ig heavy chain V r
276	42	47.2	221	2	S49220	Ig gamma-1 chain -
277	42	47.2	400	2	C97147	probable glycosyl
278	42	47.2	422	2	S04911	yopA protein - Yer
279	42	47.2	422	2	T38990	cell division cont
280	42	47.2	455	2	S04912	yopA protein - Yer
281	42	47.2	505	2	G75197	lacZ expression re
282	42	47.2	505	2	F71230	hypothetical prote
283	41.5	46.6	2391	2	T18410	cardamoyl-phosphat
284	41.5	46.6	4342	2	H83343	probable non-ribos
285	41	46.1	31	2	S22023	Ig mu chain - mous
286	41	46.1	86	2	A25150	Ig heavy chain V r
287	41	46.1	102	2	PH1243	Ig heavy chain V r
288	41	46.1	102	2	PH1262	Ig heavy chain V r
289	41	46.1	105	2	PH0978	Ig heavy chain V r
290	41	46.1	117	2	S18553	Ig heavy chain V r
291	41	46.1	117	2	S01822	Ig heavy chain V-D
292	41	46.1	117	2	S09961	Ig heavy chain V-D
293	41	46.1	118	2	S37201	Ig heavy chain V r
294	41	46.1	122	2	S36276	Ig heavy chain V r
295	41	46.1	125	2	S20639	Ig heavy chain V r
296	41	46.1	171	2	A10432	probable stringen
297	41	46.1	273	2	C85966	hypothetical prote
298	41	46.1	273	2	AD0892	bactiracin resista
299	41	46.1	273	2	G65093	bactiracin resista
300	41	46.1	273	2	DN1121	bactiracin resista
301	41	46.1	277	2	T49784	hypothetical prote
302	41	46.1	567	2	B69166	hypothetical prote
303	41	46.1	593	2	C97848	ABC transporter AT
304	41	46.1	629	2	C64180	hypothetical prote
305	41	46.1	849	2	DB4675	hypothetical prote
306	41	46.1	849	2	S61962	probable membrane
307	41	46.1	1138	2	E71615	probable amine tra
308	41	46.1	1378	2	T47605	RING finger-like p
309	40.5	45.5	560	2	I18065	gene NMB protein -
310	40	44.9	69	2	D25150	Ig heavy chain V r
311	40	44.9	85	2	E37262	Ig heavy chain V r
312	40	44.9	87	2	PH1162	Ig heavy chain V r
313	40	44.9	95	2	G37262	Ig heavy chain V r
314	40	44.9	98	2	S26920	Ig heavy chain V r
315	40	44.9	98	2	PH1154	Ig heavy chain V r
316	40	44.9	98	2	PH1160	Ig heavy chain V r
317	40	44.9	99	2	D34964	Ig heavy chain V-V
318	40	44.9	102	2	PH1237	Ig heavy chain V r
319	40	44.9	102	2	PH1241	Ig heavy chain V r
320	40	44.9	107	2	PH0971	Ig heavy chain V r
321	40	44.9	116	2	S53751	antibody Fab vcl 1
322	40	44.9	117	1	HVH0HG	Ig heavy chain pre
323	40	44.9	119	2	F30502	Ig heavy chain V r
324	40	44.9	119	2	S20640	Ig heavy chain V r
325	40	44.9	121	2	A21854	Ig heavy chain V r
326	40	44.9	121	2	AD2492	hypothetical prote
327	40	44.9	122	2	PC4279	anti-SS-A/Ro 60K p
328	40	44.9	122	2	PC4280	anti-SS-A/Ro 60K p
329	40	44.9	123	2	S60067	Ig heavy chain V r
330	40	44.9	137	2	H32513	Ig heavy chain V r
331	40	44.9	256	2	T40964	probable hydroxyc
332	40	44.9	361	1	SYEBKR	choirismate synthas
333	40	44.9	361	1	SYEBKR	choirismate synthas
334	40	44.9	361	2	AF0804	choirismate synthas
335	40	44.9	361	2	E91030	choirismate synthas
336	40	44.9	361	2	F85874	choirismate synthas
337	40	44.9	361	2	AG0315	choirismate synthas
338	40	44.9	362	2	T33502	hypothetical prote
339	40	44.9	474	1	G2MS11	Ig gamma-2b chain
340	40	44.9	499	2	S41599	cytochrome P450 77
341	40	44.9	502	2	T25263	hypothetical prote
342	40	44.9	579	2	S46757	hypothetical prote
343	40	44.9	754	2	T18238	lysophospholipase
344	40	44.9	804	2	T18014	hypothetical prote
345	39.5	44.4	415	2	A32129	carboxypeptidase B
346	39.5	44.4	503	2	JN0524	toxin co-regulated
347	39.5	44.4	503	2	F82275	Ig heavy chain V r
348	39	43.8	69	2	H25114	Ig heavy chain V r
349	39	43.8	98	2	PH1108	Ig heavy chain V r
350	39	43.8	98	2	PH1124	Ig heavy chain V r
351	39	43.8	98	2	PH1157	Ig heavy chain V r
352	39	43.8	98	2	I28833	Ig kappa chain V r
353	39	43.8	107	2	PH0987	Ig heavy chain V r
354	39	43.8	107	2	PH0984	Ig heavy chain V r
355	39	43.8	108	2	PH0985	Ig heavy chain V r
356	39	43.8	114	2	G81353	hypothetical prote
357	39	43.8	116	2	B28814	Ig heavy chain V r
358	39	43.8	117	2	S03289	Ig heavy chain pre
359	39	43.8	119	2	PH1510	Ig heavy chain V r
360	39	43.8	119	2	PH1503	Ig heavy chain V r
361	39	43.8	120	1	MMMS15	Ig heavy chain V r
362	39	43.8	128	2	C37267	Ig heavy chain V r
363	39	43.8	140	2	PH1463	Ig heavy chain V r
364	39	43.8	142	2	A32483	Ig heavy chain V r
365	39	43.8	181	2	AC0505	fibinrial chain lim
366	39	43.8	188	2	S31626	cell fusion protei
367	39	43.8	235	1	E69883	phage-related repl
368	39	43.8	242	2	E83738	hypothetical prote
369	39	43.8	251	2	A64755	probable membrane
370	39	43.8	251	2	B85519	hypothetical prote
371	39	43.8	251	2	G90668	hypothetical prote
372	39	43.8	277	2	T27275	hypothetical prote
373	39	43.8	287	1	B64201	hypothetical prote
374	39	43.8	349	2	A97007	probable membrane
375	39	43.8	350	1	DEZPA	alcohol dehydrogen
376	39	43.8	357	1	F82115	choirismate synthas
377	39	43.8	361	2	F82115	choirismate synthas
378	39	43.8	372	1	A55510	choirismate synthas
379	39	43.8	372	1	T47514	hypothetical prote
380	39	43.8	411	2	T17750	hypothetical prote
381	39	43.8	426	2	B81351	hypothetical prote
382	39	43.8	430	2	C81402	probable integral
383	39	43.8	440	2	G96600	protein P14016..24
384	39	43.8	563	2	T38766	probable transcrip
385	39	43.8	566	2	T16375	hypothetical prote
386	39	43.8	809	2	S67153	probable membrane
387	39	43.8	837	2	T119271	hypothetical prote
388	39	43.8	849	2	I50617	protein-tyrosine k
389	39	43.8	885	2	T38387	hypothetical prote
390	39	43.8	1043	2	S38034	PSI1 protein - Yea
391	39	43.8	1577	2	A35140	hemolysin A precu
392	39	43.8	1881	2	H95076	zinc metalloprotei
393	39	43.8	2573	2	D71614	hypothetical prote
394	38.5	43.3	344	2	T49259	hypothetical prote

395	38.5	43.3	449	2	H97249	protein containing
396	38	42.7	54	2	PH163	Ig heavy chain V r
397	38	42.7	80	2	PH166	Ig heavy chain V r
398	38	42.7	98	2	B24754	Ig heavy chain V r
399	38	42.7	98	2	PH164	Ig heavy chain V r
400	38	42.7	98	2	PH111	Ig heavy chain V r
401	38	42.7	98	2	PH156	Ig heavy chain V r
402	38	42.7	104	2	PH165	Ig heavy chain V r
403	38	42.7	108	2	PH0972	Ig heavy chain V r
404	38	42.7	109	2	S26318	Ig heavy chain V r
405	38	42.7	111	2	H70308	hypothetical prote
406	38	42.7	114	2	PH167	Ig heavy chain V r
407	38	42.7	118	2	PH166	Ig heavy chain V r
408	38	42.7	119	2	PH0513	hypothetical prote
409	38	42.7	120	2	S25175	Ig heavy chain V r
410	38	42.7	121	1	GYMS11	Ig heavy chain V r
411	38	42.7	122	2	S20643	Ig heavy chain V r
412	38	42.7	128	2	T18104	hypothetical prote
413	38	42.7	131	2	A27472	Ig heavy chain pre
414	38	42.7	141	2	F65086	hypothetical prote
415	38	42.7	234	2	G84790	hypothetical prote
416	38	42.7	260	2	AC3456	hydroxylases of the
417	38	42.7	261	2	AF1939	hypothetical prote
418	38	42.7	273	2	H82092	HeaA/Moeb/ThiF fam
419	38	42.7	274	2	S70130	hypothetical prote
420	38	42.7	295	2	D91114	hypothetical prote
421	38	42.7	308	2	D85959	probable enzyme Z4
422	38	42.7	337	1	ZHBP4	gene H protein - p
423	38	42.7	345	2	T24570	hypothetical prote
424	38	42.7	386	2	T36425	probable sugar iso
425	38	42.7	438	2	B69023	conserved hypotet
426	38	42.7	491	2	F96818	hypothetical prote
427	38	42.7	525	2	AI3103	ribitol kinase [im
428	38	42.7	525	2	A96183	D-ribitol kinase (EC
429	38	42.7	528	2	E71525	probable ABC trans
430	38	42.7	539	2	T22041	hypothetical prote
431	38	42.7	563	1	CZCLBM	cellulase (EC 3.2.
432	38	42.7	565	2	E90561	hypothetical prote
433	38	42.7	573	2	D90561	hypothetical prote
434	38	42.7	620	2	D71825	probable type III
435	38	42.7	650	2	T38692	probable serine/th
436	38	42.7	673	2	Q01744	hypothetical 77.2K
437	38	42.7	758	1	A39343	calpain (EC 3.4.22
438	38	42.7	764	2	T05409	hypothetical prote
439	38	42.7	768	2	AF0147	probable amino aci
440	38	42.7	1046	2	T30199	chitinase (EC 3.2.
441	38	42.7	1153	2	S00551	leukocyte surface
442	38	42.7	1364	2	T40839	hypothetical prote
443	38	42.7	2401	2	T28676	riophy protein -
444	38	42.7	4544	1	S02392	alpha-2-macroglobu
445	38	42.7	4545	1	S25111	alpha-2-macroglobu
446	37.5	42.1	405	2	T41593	hypothetical prote
447	37.5	42.1	443	2	H83293	probable two-compo
448	37.5	42.1	450	2	G96670	hypothetical prote
449	37.5	42.1	478	2	G84576	probable beta-1,3-
450	37.5	42.1	506	2	T01292	hypothetical prote
451	37	41.6	93	2	C86754	hypothetical prote
452	37	41.6	97	2	PH155	Ig heavy chain V r
453	37	41.6	102	2	PH1232	Ig heavy chain V r
454	37	41.6	111	2	S25051	Ig heavy chain V r
455	37	41.6	114	2	S20707	Ig heavy chain V r
456	37	41.6	118	2	S25174	Ig heavy chain V r
457	37	41.6	119	2	PH0099	Ig heavy chain V r
458	37	41.6	120	2	S31999	Ig heavy chain V r
459	37	41.6	120	2	S41394	Ig heavy chain V r
460	37	41.6	134	2	T23217	hypothetical prote
461	37	41.6	136	2	S04576	Ig heavy chain pre
462	37	41.6	165	2	B91141	stringent starvati
463	37	41.6	165	2	JS0666	stringent starvati
464	37	41.6	165	2	H85986	stringent starvati
465	37	41.6	166	2	AD0908	stringent starvati
466	37	41.6	178	2	D64036	hypothetical prote
467	37	41.6	179	2	A12386	hypothetical prote
468	37	41.6	183	1	R5BY32	ribosomal protein
469	37	41.6	217	2	T28343	hypothetical prote
470	37	41.6	226	2	AE1650	hypothetical prote
471	37	41.6	226	2	AF1589	hypothetical prote
472	37	41.6	227	2	G89807	exotoxin 14 [impor
473	37	41.6	239	2	B89967	serine proteinase
474	37	41.6	242	2	A12246	hypothetical prote
475	37	41.6	255	2	S34144	lipase - Serratia
476	37	41.6	257	2	T33648	hypothetical prote
477	37	41.6	260	2	E75448	transcription regu
478	37	41.6	272	2	AD0080	undecaprenol kinas
479	37	41.6	291	2	G97337	short-chain alcoh
480	37	41.6	319	2	S32923	phospholipase A1 (
481	37	41.6	334	2	S20026	beta-glucanase - r
482	37	41.6	335	2	H72420	oligopeptide ABC t
483	37	41.6	335	2	A46678	endoglycosidase F2
484	37	41.6	353	2	T49440	alcohol dehydrogen
485	37	41.6	354	1	S51779	endo-1,4-beta-xyla
486	37	41.6	355	2	AD3101	hypothetical prote
487	37	41.6	355	2	F98185	hypothetical prote
488	37	41.6	392	2	F96937	cell wall-associat
489	37	41.6	393	2	D96577	hypothetical prote
490	37	41.6	404	2	D42094	bwa protein - smut
491	37	41.6	416	2	F90076	hypothetical prote
492	37	41.6	434	2	S04534	invasin precursor
493	37	41.6	444	2	C70444	biotin carboxylase
494	37	41.6	520	2	T06625	hypothetical prote
495	37	41.6	520	2	T50518	DNA binding protei
496	37	41.6	590	2	E70843	probable flavoprot
497	37	41.6	642	2	T39839	beta-hexosaminidas
498	37	41.6	690	2	S64646	biotin-lacetyl-CoA
499	37	41.6	696	2	AB1566	hypothetical prote
500	37	41.6	754	2	H84710	Mutator-like trans
501	37	41.6	758	2	S65169	hypothetical prote
502	37	41.6	820	2	A86247	hypothetical prote
503	37	41.6	820	2	H86246	hypothetical prote
504	37	41.6	979	2	JH0589	glutamate receptor
505	37	41.6	979	2	JH0592	glutamate receptor
506	37	41.6	980	2	I57936	glutamate receptor
507	37	41.6	1027	2	AC1841	glycerophosphoryl
508	37	41.6	1032	2	D95177	Shf2 family protei
509	37	41.6	1032	2	F98043	SMF/SMF Family ATP
510	37	41.6	1249	2	T47885	beta-tubulin cotac
511	37	41.6	1460	2	S48457	nucleoporin RAI7 -
512	37	41.6	1499	2	AC2555	hypothetical prote
513	37	41.6	1518	2	T28880	hypothetical prote
514	37	41.6	1644	2	T13803	DNA-directed RNA p
515	37	41.6	2013	2	AD1129	probable peptidogl
516	36.5	41.0	118	2	PL0084	Ig heavy chain V r
517	36.5	41.0	184	2	D64460	hypothetical prote
518	36.5	41.0	306	1	CPBOB	carboxypeptidase B
519	36.5	41.0	382	2	S13237	tail fiber protein
520	36.5	41.0	416	1	A42332	carboxypeptidase B
521	36.5	41.0	431	2	B82119	citrate synthase V
522	36.5	41.0	460	2	G83421	cysteineL-tRNA syn
523	36.5	41.0	919	2	S24842	Tl6G12.2 protein -
524	36.5	41.0	1374	2	T30809	plasmidogen relate
525	36.5	41.0	2911	2	T20566	hypothetical prote
526	36	40.4	82	2	A36025	Ig heavy chain V r
527	36	40.4	99	2	D37282	Ig heavy chain V r
528	36	40.4	101	2	S42183	Ig gamma chain V r
529	36	40.4	107	2	S26320	Ig heavy chain V r
530	36	40.4	109	2	A89990	hypothetical prote
531	36	40.4	117	2	S18552	Ig heavy chain V r
532	36	40.4	117	2	S09950	Ig heavy chain V-D
533	36	40.4	120	2	S03471	Ig heavy chain V-D
534	36	40.4	122	1	D71156	hypothetical prote
535	36	40.4	122	2	S06823	Ig heavy chain V r
536	36	40.4	122	2	A75006	hypothetical prote
537	36	40.4	123	2	PH1403	Ig heavy chain V r
538	36	40.4	126	2	C64155	hypothetical prote
539	36	40.4	138	2	PH0105	acti-digoxin trans
540	36	40.4	144	2	E41287	Ig heavy chain pre

541	36	40.4	146	2	C42520	A2BL16.3K protein	614	35	39.3	88	2	D58932	ribosomal protein
542	36	40.4	149	2	B97838	ABC transporter su	615	35	39.3	96	2	S17230	Ig heavy chain V r
543	36	40.4	156	2	AB1511	hypothetical prote	616	35	39.3	96	2	S17614	Ig heavy chain V r
544	36	40.4	163	2	G89793	conserved hypotnet	617	35	39.3	96	2	S17620	Ig heavy chain V r
545	36	40.4	166	2	DB8794	conserved hypotnet	618	35	39.3	96	2	S17618	Ig heavy chain V r
546	36	40.4	188	1	JC2393	phospholipase A2 1	619	35	39.3	96	2	S17610	Ig heavy chain V r
547	36	40.4	204	2	G90239	phosphoribosyl ant	620	35	39.3	101	2	S26314	Ig heavy chain V r
548	36	40.4	205	2	AT0967	conserved hypotnet	621	35	39.3	106	2	S26315	Ig heavy chain V r
549	36	40.4	207	2	T49218	hypothetical prote	622	35	39.3	109	2	PH1672	Ig heavy chain V r
550	36	40.4	211	2	T34216	NADH2 dehydrogenas	623	35	39.3	110	2	G84629	hypothetical prote
551	36	40.4	218	2	T05593	hypothetical prote	624	35	39.3	116	2	S55342	Ig heavy chain V r
552	36	40.4	237	2	D64514	hypothetical prote	625	35	39.3	117	2	T29963	hypothetical prote
553	36	40.4	240	2	C89967	serine proteinase	626	35	39.3	118	2	PL0200	anti-DNA autoantib
554	36	40.4	250	1	A41330	acid phosphatase (627	35	39.3	119	2	PL0085	Ig heavy chain V r
555	36	40.4	256	2	S77176	cell-cell signalin	628	35	39.3	136	2	PN0536	Ig heavy chain V r
556	36	40.4	256	2	T39108	probable hydroxyac	629	35	39.3	151	2	PL0011	Ig heavy chain pre
557	36	40.4	289	2	A12464	hypothetical prote	630	35	39.3	158	2	T37446	probable 17.9K pro
558	36	40.4	295	2	C89916	dihydrodipicolinat	631	35	39.3	166	2	JQ1804	B10R 18.9K protein
559	36	40.4	307	2	E70082	glucose 1-dehydrog	632	35	39.3	171	2	S23623	Ig heavy chain V r
560	36	40.4	309	2	F82936	thioredoxin reduct	633	35	39.3	175	2	C84674	similar to termina
561	36	40.4	326	2	AB3198	hypothetical prote	634	35	39.3	177	2	T01346	hypothetical prote
562	36	40.4	327	2	G72411	hypothetical prote	635	35	39.3	200	1	A54020	Crotalus neutraliz
563	36	40.4	332	2	B90522	hypothetical prote	636	35	39.3	206	2	B72407	ABC transporter, A
564	36	40.4	335	1	H71071	hypothetical prote	637	35	39.3	209	2	G69321	conserved hypotnet
565	36	40.4	361	2	UX0152	D-amino-acid oxida	638	35	39.3	212	2	S78185	ribosomal protein
566	36	40.4	387	2	T31748	hypothetical prote	639	35	39.3	216	2	S72825	hypothetical prote
567	36	40.4	420	2	A59304	methyviologen-red	640	35	39.3	225	2	T20335	hypothetical prote
568	36	40.4	464	2	I17227	cyclin-dependent k	641	35	39.3	225	2	H90085	hypothetical prote
569	36	40.4	465	2	H87301	conserved hypotnet	642	35	39.3	229	2	T51587	filamentous flower
570	36	40.4	478	2	AC1383	chitinase and chit	643	35	39.3	233	2	T34793	hypothetical prote
571	36	40.4	515	2	T52610	glucose-6-phosphat	644	35	39.3	237	2	D82133	conserved hypotnet
572	36	40.4	517	1	A40872	aldehyde dehydroge	645	35	39.3	239	2	H89967	serine proteinase
573	36	40.4	524	2	T46310	hypothetical prote	646	35	39.3	239	2	H89966	serine proteinase
574	36	40.4	530	2	E72129	ABC transporter pr	647	35	39.3	240	2	AD2006	glucose-6-P-dehydr
575	36	40.4	530	2	AB6494	ABC transporter pr	648	35	39.3	261	1	I40437	stage III sporulat
576	36	40.4	546	2	C86071	Probable ubiquitin	649	35	39.3	267	2	AG2352	hypothetical prote
577	36	40.4	546	2	D65188	Probable ubiquitin	650	35	39.3	272	2	T23671	hypothetical prote
578	36	40.4	546	2	E91224	Probable ubiquitin	651	35	39.3	272	2	B71094	hypothetical prote
579	36	40.4	612	2	G69797	conserved hypotnet	652	35	39.3	275	2	G70914	hypothetical prote
580	36	40.4	633	2	B86271	protein FlcA1.4 l	653	35	39.3	282	2	T19393	hypothetical prote
581	36	40.4	648	2	T41915	hypothetical prote	654	35	39.3	285	2	T35195	probable serine pr
582	36	40.4	677	1	RDPC04	NADPH-ferrithempro	655	35	39.3	288	2	T44603	hypothetical prote
583	36	40.4	677	1	AE0557	NADPH-ferrithempro	656	35	39.3	290	2	B90205	conserved hypotnet
584	36	40.4	678	1	RDRT04	NADPH-ferrithempro	657	35	39.3	294	2	S60991	hypothetical prote
585	36	40.4	679	2	A25505	NADPH-ferrithempro	658	35	39.3	297	2	D86827	dihydrodipicolinat
586	36	40.4	715	2	S08450	hypothetical prote	659	35	39.3	308	2	F75485	conserved hypotnet
587	36	40.4	725	1	Z1BP22	gene 1 protein - p	660	35	39.3	319	2	C81390	hypothetical prote
588	36	40.4	779	2	S64011	3-isopropylmalate	661	35	39.3	319	2	AC2536	hypothetical prote
589	36	40.4	883	2	T03577	DNA topoisomerase	662	35	39.3	325	2	B72760	hypothetical prote
590	36	40.4	939	2	T32521	fibribrial prote	663	35	39.3	340	1	C64096	aldose 1-epimerase
591	36	40.4	1050	2	S57488	hypothetical prote	664	35	39.3	348	2	B97720	hypothetical prote
592	36	40.4	1100	2	T21544	hypothetical prote	665	35	39.3	349	2	S60760	polysialic acid ca
593	36	40.4	1175	2	S39951	chitin synthase (E	666	35	39.3	351	2	S47635	penicilliolysin - p
594	36	40.4	1176	2	S66771	hypothetical prote	667	35	39.3	356	2	T41557	hypothetical prote
595	36	40.4	1333	2	S30356	CDG25 protein homo	668	35	39.3	359	2	T06604	succinyl-diaminopi
596	36	40.4	1416	2	D71350	probable DNA-direc	669	35	39.3	377	2	C82113	hypothetical prote
597	36	40.4	1770	2	S56221	hypothetical prote	670	35	39.3	377	2	C71048	hypothetical prote
598	36	40.4	1941	2	T30554	ubiquitin-protein	671	35	39.3	377	2	T19603	hypothetical prote
599	36	40.4	2021	2	AB4771	similar to Ch-TOG	672	35	39.3	381	2	T22334	hypothetical prote
600	36	40.4	4199	2	S76412	hypothetical prote	673	35	39.3	381	2	JC4378	sugar isomerase -
601	35.5	39.9	189	2	B89837	hypothetical prote	674	35	39.3	383	2	A72299	metalloproteinase
602	35.5	39.9	210	2	F70125	conserved hypotnet	675	35	39.3	390	1	ACBPMG	maturatation protein
603	35.5	39.9	281	2	T27471	hypothetical prote	676	35	39.3	395	2	T25651	hypothetical prote
604	35.5	39.9	281	2	S39745	ywlL protein - Bac	677	35	39.3	400	2	E69446	hypothetical prote
605	35.5	39.9	396	1	AD2224	protein-export mem	678	35	39.3	417	2	F88637	protein F53H1.3 li
606	35.5	39.9	631	2	AD6433	hypothetical prote	679	35	39.3	423	2	A55797	collagen precursor
607	35.5	39.9	886	2	S43562	K08E5.3 protein -	680	35	39.3	432	2	T08771	hypothetical prote
608	35.5	39.9	859	2	C96504	protein F9C16.23 l	681	35	39.3	442	2	T38691	hypothetical prote
609	35.5	39.9	997	1	I54390	phosphoinositide-s	682	35	39.3	443	2	C81271	biotin carboxylase
610	35.5	39.9	1093	2	A31758	phosphorylase kina	683	35	39.3	444	2	T01548	protein kinase hom
611	35.5	39.9	1093	2	B40793	phosphorylase kina	684	35	39.3	453	2	S67089	hypothetical prote
612	35.5	39.9	1096	1	S62358	insitol 1,4,5-Cri	685	35	39.3	455	2	G71860	biotin carboxylase
613	35.5	39.9	1749	2	S75138	hypothetical prote	686	35	39.3	458	2	B64566	biotin carboxylase

687	35	39.3	458	2	C97151	hypothetical prote	760	34	38.2	98	2	S26938	Ig heavy chain V r
688	35	39.3	458	2	AD2249	two-component sens	761	34	38.2	98	2	A46026	group I intron end
689	35	39.3	460	2	S34969	outer membrane por	762	34	38.2	101	2	T37252	Ig heavy chain V r
690	35	39.3	478	2	AF1758	chitinase and chit	763	34	38.2	102	2	S26471	Ig heavy chain V r
691	35	39.3	483	2	T23312	hypothetical prote	764	34	38.2	106	2	PH1005	Ig heavy chain V r
692	35	39.3	485	2	C86143	hypothetical prote	765	34	38.2	108	1	S73448	hypothetical prote
693	35	39.3	500	2	B83910	hypothetical prote	766	34	38.2	108	2	PH0977	Ig heavy chain V r
694	35	39.3	500	2	H71075	hypothetical prote	767	34	38.2	110	1	MMV214	14k cell fusion pr
695	35	39.3	519	2	T27711	hypothetical prote	768	34	38.2	110	1	MMV220	14k cell fusion pr
696	35	39.3	522	2	C90073	hypothetical prote	769	34	38.2	110	2	S37262	cell fusion protei
697	35	39.3	525	2	B83913	hypothetical prote	770	34	38.2	110	2	S37275	cell fusion protei
698	35	39.3	537	2	AC2930	hypothetical prote	771	34	38.2	110	2	S37281	cell fusion protei
699	35	39.3	537	2	C98352	hypothetical prote	772	34	38.2	110	2	T37413	14k membrane prote
700	35	39.3	543	1	WZBEM5	hypothetical prote	773	34	38.2	110	2	J01833	2L protein - vario
701	35	39.3	604	2	T08211	gene 19 protein - H	774	34	38.2	110	2	D72167	A3L protein - var
702	35	39.3	606	2	B84889	glycoprotein G - H	775	34	38.2	110	2	D36851	cell fusion protei
703	35	39.3	608	2	AH2531	hypothetical prote	776	34	38.2	114	2	S51053	ribosomal protein
704	35	39.3	610	2	S67701	hypothetical prote	777	34	38.2	114	4	A47271	ribosephenyl phosph
705	35	39.3	619	2	A84411	hypothetical prote	778	34	38.2	117	1	HVHU35	Ig heavy chain pre
706	35	39.3	635	2	T30788	hypothetical prote	779	34	38.2	117	2	S31680	Ig heavy chain V r
707	35	39.3	635	2	B72155	hypothetical prote	780	34	38.2	117	2	S18511	Ig heavy chain V r
708	35	39.3	635	2	T28474	hypothetical prote	781	34	38.2	117	2	S37274	cell fusion protei
709	35	39.3	635	2	H42507	F12L protein - vac	782	34	38.2	118	2	S36265	Ig heavy chain V r
710	35	39.3	635	2	G36840	C16L protein - var	783	34	38.2	120	2	S03484	Ig heavy chain V-D
711	35	39.3	637	2	AC1860	two-component sens	784	34	38.2	121	2	S19969	Ig heavy chain V r
712	35	39.3	679	2	H95036	glycosyl hydrolase	785	34	38.2	123	2	S20646	Ig heavy chain V r
713	35	39.3	698	2	S73085	probable oxidoredu	786	34	38.2	129	2	S46393	Ig heavy chain V r
714	35	39.3	737	2	D97907	alpha-xylosidase (787	34	38.2	131	2	PH1425	Ig heavy chain V r
715	35	39.3	740	2	D71602	hypothetical prote	788	34	38.2	134	2	E90422	hypothetical prote
716	35	39.3	760	2	S10888	ERCC2 protein - hu	789	34	38.2	135	2	S49530	anti-Sm antibody V
717	35	39.3	767	2	A55732	excision repair pr	790	34	38.2	135	2	PH1492	Ig heavy chain V r
718	35	39.3	767	2	A49546	DNA topoisomerase	791	34	38.2	138	2	PN0538	Ig heavy chain V r
719	35	39.3	767	2	JU0144	DNA topoisomerase	792	34	38.2	138	2	B84329	hypothetical prote
720	35	39.3	798	2	T00131	xylian 1,4-beta-xy	793	34	38.2	147	2	AE1321	pH5 system enzyme
721	35	39.3	803	2	H71457	probable protein k	794	34	38.2	148	1	MMV2M2	HN2 protein - snee
722	35	39.3	809	2	G95239	probable adenylate	795	34	38.2	148	2	G64466	hypothetical prote
723	35	39.3	829	2	S72366	DNA topoisomerase	796	34	38.2	150	2	D64123	stringent starvati
724	35	39.3	848	2	T16430	hypothetical prote	797	34	38.2	162	1	Z3BP17	gene 3 protein - p
725	35	39.3	850	2	H82886	topoisomerase IV s	798	34	38.2	168	2	A72057	Holliday junction
726	35	39.3	869	2	T44440	chitinase (Ec 3.2.	799	34	38.2	168	2	B86568	crossover junction
727	35	39.3	920	2	T26650	hypothetical prote	800	34	38.2	181	2	T27261	hypothetical prote
728	35	39.3	929	2	T32492	hypothetical prote	801	34	38.2	184	2	H90386	hypothetical prote
729	35	39.3	952	2	I50612	protein-tyrosine k	802	34	38.2	188	2	T31006	hypothetical prote
730	35	39.3	971	2	T09210	starch phosphoryl	803	34	38.2	197	2	G86900	DNA helicase Ruva
731	35	39.3	984	2	A39753	protein-tyrosine k	804	34	38.2	220	2	AD0426	two-component syst
732	35	39.3	1007	2	D75012	hypothetical prote	805	34	38.2	225	2	S63048	hypothetical prote
733	35	39.3	1007	2	H81670	conserved hypotet	806	34	38.2	227	2	E97526	30S ribosomal prot
734	35	39.3	1069	2	S27922	nuclear antigen EB	807	34	38.2	228	2	F90417	conserved hypotet
735	35	39.3	1090	2	AG1749	glycosidase homolo	808	34	38.2	229	2	T33627	hypothetical prote
736	35	39.3	1095	2	T00329	hypothetical prote	809	34	38.2	230	2	H97296	probable membrane
737	35	39.3	1144	2	F84725	probable inositol	810	34	38.2	231	2	B69477	ABC transporter, A
738	35	39.3	1146	2	SA0311	integrin - fruit f	811	34	38.2	231	2	S60387	decappling enzyme c
739	35	39.3	1153	1	RWMH1B	cell surface glyco	812	34	38.2	234	2	A11852	hypothetical prote
740	35	39.3	1171	2	E97295	transcription -rep	813	34	38.2	241	2	AC0128	30S ribosomal prot
741	35	39.3	1203	2	T21275	hypothetical prote	814	34	38.2	242	2	C82097	30S ribosomal protei
742	35	39.3	1208	2	T00362	hypothetical prote	815	34	38.2	244	2	B84957	probable phosphoe
743	35	39.3	1215	2	B48281	cytochrome-oxasociat	816	34	38.2	248	1	E75186	conserved hypotet
744	35	39.3	1241	2	T37190	nephxin - human	817	34	38.2	253	2	D95121	conserved hypotet
745	35	39.3	1320	2	B59092	hypothetical prote	818	34	38.2	253	2	H97980	conserved hypotet
746	35	39.3	1483	2	S10015	hypothetical prote	819	34	38.2	255	2	AP2745	30S ribosomal prot
747	35	39.3	1549	2	S50705	hypothetical prote	820	34	38.2	257	2	C69862	conserved hypotet
748	35	39.3	1607	2	T21982	hypothetical prote	821	34	38.2	260	2	E64619	adhesin A - Helico
749	35	39.3	1651	1	C3NJ	complement C3 prec	822	34	38.2	261	2	G69152	polyferredoxin 1 -
750	35	39.3	2339	2	A45597	DNA-directed RNA p	823	34	38.2	261	2	A69142	hypothetical prote
751	35	38.8	1332	2	A69314	hypothetical prote	824	34	38.2	263	2	SS3468	water-stress-induc
752	34.5	38.8	296	2	AF1170	probable sugar ABC	825	34	38.2	264	2	F75386	ribosomal protein
753	34.5	38.8	296	2	AH1527	probable sugar ABC	826	34	38.2	264	2	C70560	hypothetical prote
754	34.5	38.8	566	2	B81404	acetylacetate synth	827	34	38.2	281	2	H97786	ribonuclease III (
755	34.5	38.8	654	2	F85057	receptor-like prot	828	34	38.2	283	2	T24794	hypothetical prote
756	34	38.2	34	2	HS3480	melanoma antigen-s	829	34	38.2	285	2	AG0270	hypothetical prote
757	34	38.2	70	2	AD0298	probable membrane	830	34	38.2	292	2	AG1457	p45 related protei
758	34	38.2	98	2	S26910	Ig heavy chain V r	831	34	38.2	293	2	B97193	dihydrodipicolinat
759	34	38.2	98	2	S26912	Ig heavy chain V r	832	34	38.2	293	2	D70231	conserved hypotet

833	34	38.2	294	2	AH1725	oxidoreductase hom
834	34	38.2	296	2	B43819	immediate-early tr
835	34	38.2	297	2	T38161	hypothetical prote
836	34	38.2	305	2	FE6905	conserved hypotnet
837	34	38.2	306	2	E69970	uncharacterized pr
838	34	38.2	308	2	G64401	hypothetical prote
839	34	38.2	319	2	S72379	transposase - Ente
840	34	38.2	321	2	G96921	oligoposase ABC t
841	34	38.2	326	2	S76986	hypothetical prote
842	34	38.2	330	1	ZHBP33	gene H protein - p
843	34	38.2	332	1	WMBP16	gene 16 protein -
844	34	38.2	332	1	WMBP26	gene 16 protein -
845	34	38.2	333	2	JC4807	G1 progession neg
846	34	38.2	335	2	A54458	estradiol 17beta-d
847	34	38.2	344	2	S62652	alcohol dehydrogen
848	34	38.2	346	2	JC1376	alcohol dehydrogen
849	34	38.2	346	2	H70860	alcohol dehydrogen
850	34	38.2	346	2	FE9786	glycoprotein endop
851	34	38.2	350	2	AE1227	phenylalany- <i>t</i> -RNA s
852	34	38.2	350	2	AG1580	phenylalany- <i>t</i> -RNA s
853	34	38.2	353	2	T01542	hypothetical prote
854	34	38.2	354	2	H84940	chlorimate synthas
855	34	38.2	354	2	B97120	DNA uptake protein
856	34	38.2	354	2	C71057	hypothetical prote
857	34	38.2	356	1	A42053	gap junction prote
858	34	38.2	357	2	B95399	probable ROK-famil
859	34	38.2	358	2	S23111	connexin 40 - mus
860	34	38.2	359	2	B84674	hypothetical prote
861	34	38.2	364	2	T47899	dhidrodiolpicolinat
862	34	38.2	364	2	S46304	dhidrodiolpicolinat
863	34	38.2	365	2	E84890	probable dihydrodi
864	34	38.2	365	2	JC4379	metalloproteinas
865	34	38.2	367	1	S62746	alcohol dehydrogen
866	34	38.2	371	2	A81319	probable N-acetyl
867	34	38.2	373	2	T13332	hypothetical prote
868	34	38.2	374	2	B82690	chorimate synthas
869	34	38.2	378	2	FE4446	chorimate synthas
870	34	38.2	380	1	WZMP	dhidrodiolpicolinat
871	34	38.2	380	2	G97248	uncharacterized co
872	34	38.2	382	2	A46229	pre-mRNA splicing
873	34	38.2	386	2	T84612	sensory epithelia
874	34	38.2	386	2	T28375	ORF MSV214 SCG gen
875	34	38.2	387	2	S19885	immediate-early tr
876	34	38.2	389	2	H71152	hypothetical prote
877	34	38.2	394	2	AC3094	conserved hypotnet
878	34	38.2	394	2	G98192	hypothetical prote
879	34	38.2	405	2	H97130	FEK-like DNA segr
880	34	38.2	408	1	A69819	alanine- <i>t</i> -RNA ligas
881	34	38.2	410	2	S77844	probable nucleosid
882	34	38.2	418	2	E71848	pyrimidine nucleos
883	34	38.2	418	2	DE4667	hypothetical prote
884	34	38.2	427	2	A85789	hypothetical prote
885	34	38.2	427	2	E90940	hypothetical prote
886	34	38.2	427	2	H64938	hypothetical prote
887	34	38.2	428	2	AE0712	conserved hypotnet
888	34	38.2	428	2	A82873	potassium channel
889	34	38.2	429	2	T47717	beta-1,3-glucanas
890	34	38.2	437	2	H90265	heterodisulfite re
891	34	38.2	438	2	T35789	probable secreted
892	34	38.2	441	2	D90855	hypothetical prote
893	34	38.2	445	2	T32366	hypothetical prote
894	34	38.2	446	2	T33986	hypothetical prote
895	34	38.2	450	2	T40337	probable saccharop
896	34	38.2	451	2	FE7230	probable maltodext
897	34	38.2	452	2	E90011	phosphoglucosamine
898	34	38.2	452	2	AH0964	probable PTS syste
899	34	38.2	455	2	B64860	YMN protein - Esc
900	34	38.2	462	2	T25726	hypothetical prote
901	34	38.2	478	2	T39532	hypothetical prote
902	34	38.2	480	2	S49182	beta-glucosidase (
903	34	38.2	511	1	S60287	endo-1,4-beta-xyla
904	34	38.2	513	2	H69735	glucose-6-phosphat
905	34	38.2	515	1	S57785	glucose-6-phosphat
906	34	38.2	516	2	F90318	acyl-CoA dehydroge
907	34	38.2	516	2	A86148	hypothetical prote
908	34	38.2	523	2	T50478	neurotin - goldfif
909	34	38.2	527	2	T51258	hypothetical prote
910	34	38.2	529	2	G70140	oligopeptide ABC t
911	34	38.2	539	2	T36660	proteinase - Stre
912	34	38.2	543	2	JC4812	hyaluronan synthas
913	34	38.2	547	2	FE9964	amino acid degrad
914	34	38.2	574	2	A99189	glycyl- <i>t</i> -RNA synthe
915	34	38.2	576	2	S36702	hypothetical prote
916	34	38.2	581	1	H64532	2',3'-cyclic-nucle
917	34	38.2	582	2	T24545	intermediate filam
918	34	38.2	583	2	C72544	probable glycyl-tr
919	34	38.2	600	2	D95899	probable dipeptide
920	34	38.2	604	2	H81924	probable integral
921	34	38.2	604	2	A81181	hypothetical prote
922	34	38.2	609	2	H97040	ATP-dependent DNA
923	34	38.2	617	2	A90644	probable membrane
924	34	38.2	617	2	A85495	hypothetical prote
925	34	38.2	643	2	S69681	ABC-type transport
926	34	38.2	647	2	FE4170	paraoporal cryetal
927	34	38.2	652	2	A27323	NADPH-ferritinopro
928	34	38.2	678	2	S27158	MEK kinase - mouse
929	34	38.2	687	2	A46212	NADH2 dehydrogenas
930	34	38.2	702	2	T12146	conserved membrane
931	34	38.2	704	2	S61612	conserved hypotnet
932	34	38.2	717	2	H72208	hypothetical prote
933	34	38.2	737	2	T16737	maltoephosphoryla
934	34	38.2	751	2	E86834	hypothetical prote
935	34	38.2	757	2	C89946	hypothetical prote
936	34	38.2	760	2	I51720	probable DNA helic
937	34	38.2	783	2	T01015	probable subtilisi
938	34	38.2	785	2	A82123	chemotaxis protein
939	34	38.2	796	2	UC7355	peroxisome prolife
940	34	38.2	797	2	A83410	organic solvent co
941	34	38.2	809	2	B70692	hypothetical prote
942	34	38.2	831	2	T23812	hypothetical prote
943	34	38.2	839	2	T41826	p55 ctf83 - Bombyx
944	34	38.2	846	2	A86663	antipeptidase N [
945	34	38.2	846	2	JN0324	lysine aminopeptid
946	34	38.2	846	2	S23157	membrane alanyl am
947	34	38.2	847	2	D72860	viral capsid assoc
948	34	38.2	850	2	FE9260	ABC transporter, p
949	34	38.2	850	2	A98126	conserved hypotnet
950	34	38.2	870	2	T09137	extensin homolog -
951	34	38.2	874	2	S25530	glycoprotein B - b
952	34	38.2	893	2	T36795	probable penicilli
953	34	38.2	902	2	T26775	hypothetical prote
954	34	38.2	903	2	A87704	aconitlate hydrat
955	34	38.2	904	2	T04377	probable pullulana
956	34	38.2	918	2	D71407	hypothetical prote
957	34	38.2	933	2	G70166	probable zinc prot
958	34	38.2	936	2	FE6508	hypothetical prote
959	34	38.2	939	2	B82121	peptidase, insulin
960	34	38.2	942	2	T13014	cytochrome b245 be
961	34	38.2	950	2	T09076	hypothetical prote
962	34	38.2	955	2	FE4914	hypothetical prote
963	34	38.2	964	2	T49038	hypothetical prote
964	34	38.2	971	2	C75503	hypothetical prote
965	34	38.2	974	2	S34189	receptor tyrosine
966	34	38.2	985	2	I51672	hypothetical prote
967	34	38.2	988	2	FE6316	probable secreted
968	34	38.2	991	2	A99334	hypothetical prote
969	34	38.2	1022	2	T48358	hypothetical prote
970	34	38.2	1035	2	G86342	hypothetical prote
971	34	38.2	1041	2	B81281	probable secreted
972	34	38.2	1045	2	FE90365	hypothetical prote
973	34	38.2	1083	2	S54293	regulator protein
974	34	38.2	1091	2	G59435	DIC-1 (deleted in
975	34	38.2	1091	2	AP1380	glycosidase homolo
976	34	38.2	1108	2	T41188	probable ubiquitin
977	34	38.2	1169	2	H70178	exodeoxyribonuclea
978	34	38.2	1189	1	JC2366	protein-tyrosine-p

979 34 38.2 1206 2 F72233 conserved hypochet
980 34 38.2 1233 1 G71612 novel serine/threo
981 34 38.2 1238 2 S63247 probable membrane
982 34 38.2 1244 2 S25327 cytoskeleton assem
983 34 38.2 1245 2 D71613 GAF domain protein
984 34 38.2 1309 2 P66509 protein F27F5.19 [d
985 34 38.2 1337 2 T30291 dextranase - Strept
986 34 38.2 1367 2 S74285 BUD3 protein - Yea
987 34 38.2 1430 2 D82533 RNA polymerase bet
988 34 38.2 1474 2 B85168 retrotransposon 11
989 34 38.2 1493 2 T10757 MAP kinase kinase
990 34 38.2 1509 1 A27224 myosin heavy chain
991 34 38.2 1529 2 S69688 hypothetical prote
992 34 38.2 1547 2 A12043 hypothetical prote
993 34 38.2 1584 2 T18276 protein-tyrosine k
994 34 38.2 1720 2 T07258 cell division prot
995 34 38.2 1822 2 T14106 probable GTPase-ac
996 34 38.2 1859 1 A34092 DNA-directed RNA p
997 34 38.2 1862 2 T29959 DNA-directed RNA p
998 34 38.2 2088 2 E71436 hypothetical prote
999 34 38.2 2135 2 T14602 variant-specific s
1000 34 38.2 2493 2 A55481 adenylate cyclase

ALIGNMENTS

RESULT 1

PH1004 Ig heavy chain V region (clone 165.5) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PH1004 R:Titman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both IGM and Igg anti-DNA antibodies are the products of clonally selective B c

A:Reference number: PH0971; MUID:92381444; PMID:1512540

A:Accession: PH1004

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-91 <TIL>

A:Cross-references: UNIPARC:UPI0000176ACD

A:Experimental source: B cell, strain [NZB x NZW]F1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 82.0%; Score 73; DB 2; Length 91; Best Local Similarity 81.2%; Pred. No. 6.9e-05; Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IYPGNDISTYNQKFXG 17
| | | | | | | | | | | | | | | | |
Db 33 IYPGNDISTYNQKFXG 48

RESULT 2

S55541 Ig heavy chain V region pel - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999

C:Accession: S55541 R:Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.

J. Mol. Biol. 247, 932-946, 1995

A:Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies usin

utations in the variable region genes.

A:Reference number: S55528; MUID:95239763; PMID:7536850

A:Accession: S55541

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-117 <BOE>

A:Cross-references: UNIPARC:UPI00001161F8; EMBL:X82580; NID:9854286; PIDN:CAAS7916.1; PI

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:14-97/Domain: immunoglobulin homology <IMM>

Query Match 82.0%; Score 73; DB 2; Length 117; Best Local Similarity 81.2%; Pred. No. 6e-05; Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IYPGNDISTYNQKFXG 17
| | | | | | | | | | | | | | | | |
Db 50 IYPGNDISTYNQKFXG 65

RESULT 3

S42182 Ig gamma chain V region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 28-Sep-1994 #sequence_revision 21-Jul-1995 #text_change 23-Jul-1999

C:Accession: S42182 R:Mo, J.A.; Bona, C.A.; Holmdahl, R.

Eur. J. Immunol. 23, 2503-2510, 1993

A:Title: Variable region gene selection of immunoglobulin G-expressing B cells with spec

A:Reference number: S42176; MUID:94009207; PMID:7691608

A:Accession: S42182

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-93 <MOJ>

A:Cross-references: UNIPARC:UPI0000116564; EMBL:Z25453; NID:9407822; PIDN:CAAB0940.1; PI

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

F:8-91/Domain: immunoglobulin homology <IMM>

RESULT 4

S42177 Ig gamma chain V region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 28-Sep-1994 #sequence_revision 21-Jul-1995 #text_change 23-Jul-1999

C:Accession: S42177 R:Mo, J.A.; Bona, C.A.; Holmdahl, R.

Eur. J. Immunol. 23, 2503-2510, 1993

A:Title: Variable region gene selection of immunoglobulin G-expressing B cells with spec

A:Reference number: S42176; MUID:94009207; PMID:7691608

A:Accession: S42177

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-94 <MOJ>

A:Cross-references: UNIPARC:UPI000011655B; EMBL:Z25443; NID:9407812; PIDN:CAAB0930.1; PI

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

F:8-91/Domain: immunoglobulin homology <IMM>

RESULT 5

S42178 Ig gamma chain V region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 28-Sep-1994 #sequence_revision 21-Jul-1995 #text_change 23-Jul-1999

C:Accession: S42178

R;Mo, J.A.; Bona, C.A.; Holmdahl, R.
Eur. J. Immunol. 23, 2503-2510, 1993
A;Title: Variable region gene selection of immunoglobulin G-expressing B cells with spec
A;Reference number: S42176; MUID:94009207; PMID:7691608
A;Accession: S42178
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-95 <MOJ>
A;Cross-references: UNIPARC:UPI000011655D; EMBL:Z25445; NID:9407814; PIDN:CAA80932.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 80.9%; Score 72; DB 2; Length 95;
Best Local Similarity 81.2%; Pred. No. 0.00011;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 IYPGNDISTYNQKFXG 17
|||||
Db 44 IYPGNGDTSYNQKFXG 59

RESULT 6

S42181
Ig gamma chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 28-Sep-1994 #sequence_revision 21-Jul-1995 #text_change 23-Jul-1999
C;Accession: S42181
R;Mo, J.A.; Bona, C.A.; Holmdahl, R.
Eur. J. Immunol. 23, 2503-2510, 1993
A;Title: Variable region gene selection of immunoglobulin G-expressing B cells with spec
A;Reference number: S42176; MUID:94009207; PMID:7691608
A;Accession: S42181
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-97 <MOJ>
A;Cross-references: UNIPARC:UPI0000116563; EMBL:Z25451; NID:9407820; PIDN:CAA80938.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;8-91/Domain: immunoglobulin homology <IMM>

Query Match 80.9%; Score 72; DB 2; Length 97;
Best Local Similarity 81.2%; Pred. No. 0.00011;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 IYPGNDISTYNQKFXG 17
|||||
Db 44 IYPGNGDTSYNQKFXG 59

RESULT 7

S42184
Ig gamma chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 28-Sep-1994 #sequence_revision 21-Jul-1995 #text_change 06-Jun-1997
C;Accession: S42184
R;Mo, J.A.; Bona, C.A.; Holmdahl, R.
Eur. J. Immunol. 23, 2503-2510, 1993
A;Title: Variable region gene selection of immunoglobulin G-expressing B cells with spec
A;Reference number: S42176; MUID:94009207; PMID:7691608
A;Accession: S42184
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-101 <MOJ>
A;Cross-references: UNIPARC:UPI0000176E59; EMBL:Z25457
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 80.9%; Score 72; DB 2; Length 101;
Best Local Similarity 81.2%; Pred. No. 0.00011;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 IYPGNDISTYNQKFXG 17
|||||
Db 51 IYPGNGDTSYNQKFXG 66

RESULT 8

S42179
Ig gamma chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 28-Sep-1994 #sequence_revision 21-Jul-1995 #text_change 23-Jul-1999
C;Accession: S42179
R;Mo, J.A.; Bona, C.A.; Holmdahl, R.
Eur. J. Immunol. 23, 2503-2510, 1993
A;Title: Variable region gene selection of immunoglobulin G-expressing B cells with spec
A;Reference number: S42176; MUID:94009207; PMID:7691608
A;Accession: S42179
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-101 <MOJ>
A;Cross-references: UNIPARC:UPI000011655F; EMBL:Z25447; NID:9407816; PIDN:CAA80934.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 80.9%; Score 72; DB 2; Length 101;
Best Local Similarity 81.2%; Pred. No. 0.00011;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 IYPGNDISTYNQKFXG 17
|||||
Db 51 IYPGNGDTSYNQKFXG 66

RESULT 9

S42180
Ig gamma chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 28-Sep-1994 #sequence_revision 21-Jul-1995 #text_change 23-Jul-1999
C;Accession: S42180
R;Mo, J.A.; Bona, C.A.; Holmdahl, R.
Eur. J. Immunol. 23, 2503-2510, 1993
A;Title: Variable region gene selection of immunoglobulin G-expressing B cells with spec
A;Reference number: S42176; MUID:94009207; PMID:7691608
A;Accession: S42180
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-102 <MOJ>
A;Cross-references: UNIPARC:UPI0000116561; EMBL:Z25449; NID:9407818; PIDN:CAA80936.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 80.9%; Score 72; DB 2; Length 102;
Best Local Similarity 81.2%; Pred. No. 0.00011;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 IYPGNDISTYNQKFXG 17
|||||
Db 51 IYPGNGDTSYNQKFXG 66

RESULT 10

PH1003
Ig heavy chain V region (clone 178-c5) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH1003
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B c
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH1003
A;Status: nucleic acid sequence not shown

A:Molecule type: mRNA
A:Residues: 1-109 <TIL>
A:Cross-references: UNIPARC:UPI0000176D14
A:Experimental source: B cell, strain [NZB x NZM]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 78.7%; Score 70; DB 2; Length 109;
Best Local Similarity 75.0%; Pred. No. 0.00026;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGNDISYNQKFXG 17
|||:|||||
Db 51 IYPGNSDTNYQKFKG 66

RESULT 11
PC1155
Ig heavy chain precursor V region (B72.3) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: PC1155
R:Whittle, N.; Adair, J.; Lloyd, C.; Jenkins, L.; Devine, J.; Schlom, J.; Raubitschek, A.
Protein Eng. 1, 499-505, 1987
A:Title: Expression in COS cells of a mouse-human chimeric B72.3 antibody.
A:Reference number: PC1155; MUID:89220990; PMID:3508296
A:Accession: PC1155
A:Molecule type: mRNA
A:Residues: 1-133 <WHI>
A:Cross-references: UNIPARC:UPI000002B8BF
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-133/Product: Ig heavy chain V region (B72.3) #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 76.4%; Score 68; DB 2; Length 133;
Best Local Similarity 75.0%; Pred. No. 0.00069;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGNDISYNQKFXG 17
|||:|||||
Db 70 IYPGNDIKYNEKFKG 85

RESULT 12
PH0979
Ig heavy chain V region (clone 17s-c4) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PH0979
R:Tillman, D.W.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both Igm and Igg anti-DNA antibodies are the products of clonally selective B c
A:Reference number: PH0971; MUID:92381444; PMID:1512540
A:Accession: PH0979
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-112 <TIL>
A:Cross-references: UNIPARC:UPI0000176CFP
A:Experimental source: B cell, strain [NZB x NZM]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 68.5%; Score 61; DB 2; Length 112;
Best Local Similarity 68.8%; Pred. No. 0.0081;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 IYPGNDISYNQKFXG 17
|||:|||||
Db 51 IYPGDDIKYNGKFKG 66

RESULT 13
A54378
Ig heavy chain V region anti-triplex DNA - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C:Accession: A54378
R:Agazie, Y.M.; Lee, J.S.; Burkholder, G.D.
J. Biol. Chem. 269, 7019-7023, 1994
A:Title: Characterization of a new monoclonal antibody to triplex DNA and immunofluoresce
A:Reference number: A54378; MUID:94165109; PMID:7509814
A:Accession: A54378
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-115 <AGA>
A:Cross-references: UNIPARC:UPI0000176E3F; GB:S68961; NID:G545744; PIDN:AAB30095.1; PID:G
A:Experimental source: spleen and myeloma cell line MOPC 315.43
A>Note: sequence inconsistent with nucleotide translation
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 67.4%; Score 60; DB 2; Length 115;
Best Local Similarity 62.5%; Pred. No. 0.012;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IYPGNDISYNQKFXG 17
|||:|||||
Db 51 IYPGNGTKYNEKFKG 66

RESULT 14
S42176
Ig gamma chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 28-Sep-1994 #sequence_revision 21-Jul-1995 #text_change 23-Jul-1999
C:Accession: S42176
R:Mo, J.A.; Bona, C.A.; Holmdahl, R.
Eur. J. Immunol. 23, 2503-2510, 1993
A:Title: Variable region gene selection of immunoglobulin G-expressing B cells with spec
A:Reference number: S42176; MUID:94009207; PMID:7651608
A:Accession: S42176
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-102 <MOI>
A:Cross-references: UNIPARC:UPI0000116559; EMBL:Z25441; NID:G407810; PIDN:CAA80928.1; PII
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 66.3%; Score 59; DB 2; Length 102;
Best Local Similarity 68.8%; Pred. No. 0.016;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 IYPGNDISYNQKFXG 17
|||:|||||
Db 51 IYPNGGTSTYQKFKG 66

RESULT 15
PH0975
Ig heavy chain V region (clone 163.72) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PH0975
R:Tillman, D.W.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both Igm and Igg anti-DNA antibodies are the products of clonally selective B c
A:Reference number: PH0971; MUID:92381444; PMID:1512540
A:Accession: PH0975
A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA
A:Residues: 1-108 <TTL>
A:Cross-references: UNIPARC:UPI0000176CPD
A:Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 66.3%; Score 59; DB 2; Length 108;
Best Local Similarity 68.8%; Pred. No. 0.017;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 IYPGNDISYNOKFXG 17
| | | | |
51 IYPNNGTSYNOKFXG 66

RESULT 16

G48677

Ig heavy chain V-D-J region (419.1) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 17-Mar-1999

C:Accession: G48677

R:Assignment: J.; Brait, M.; Jamila, I.; Urbain, J.; Gottlieb, P.; Brown, A.; Hasemann, C

Proc. Natl. Acad. Sci. U.S.A. 90, 9508-9512, 1993

A:Title: Molecular characterization of monoclonal CRI-A-positive anti-arsenate antibodies

A:Reference number: A48677; MUID:94022404; PMID:8415731

A:Accession: G48677

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-123 <TAS>

A:Cross-references: UNIPARC:UPI0000176DC0

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 66.3%; Score 59; DB 2; Length 123;
Best Local Similarity 68.8%; Pred. No. 0.019;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 IYPGNDISYNOKFXG 17
| | | | |
51 IYPGNDYIKYNEKFXG 66

RESULT 17

G28195

Ig heavy chain V region (anti-haloperidol antibody B) - mouse

C:Species: Mus musculus (house mouse)

C>Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 23-Jul-1999

C:Accession: G28195

R:Sherman, M.A.; Deane, R.J.; Bolger, M.B.

J. Biol. Chem. 263, 4059-4063, 1988

A:Title: Haloperidol binding to monoclonal antibodies. Hypervariable region amino acid s

A:Reference number: A28195; MUID:88153717; PMID:3267217

A:Accession: G28195

A:Molecule type: mRNA

A:Residues: 1-120 <SHF>

A:Cross-references: UNIPARC:UPI0000114D6F; GB:M19772; NID:G195520; PIDN:AAA38340.1; PID:

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 65.2%; Score 58; DB 2; Length 120;
Best Local Similarity 62.5%; Pred. No. 0.027;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IYPGNDISYNOKFXG 17
| | | | |
51 IYPGNVTKYNEKFXG 66

RESULT 18

S21810
Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999

C:Accession: S21810

R:Ostermeyer, M.; Brack, C.H.; Trautnecker, A.; Koehler, G.

submitted to the EMBL Data Library, January 1991

A:Description: Nucleotide sequence of a rearranged VDJ-region of a mouse Ig mu heavy chain

A:Reference number: S21810

A:Accession: S21810

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-138 <OST>

A:Cross-references: UNIPARC:UPI000115ED6; EMBL:X56936; NID:954163; PIDN:CAA40257.1; PID:

C:Genetics:

A:Insertions: 15/3

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 65.2%; Score 58; DB 2; Length 138;
Best Local Similarity 62.5%; Pred. No. 0.031;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IYPGNDISYNOKFXG 17
| | | | |
51 IYPGNVTKYNEKFXG 85

RESULT 19

PH1484

Ig heavy chain V region (clones X7-3C5 and X7-3C5H) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999

C:Accession: PH1484; PH1497

R:Giusti, A.M.; Manser, T.

J. Exp. Med. 177, 797-809, 1993

A:Title: Hypermutation is observed only in antibody H chain V region transgenes that have

d for somatic mutation.

A:Reference number: PH1482; MUID:93171820; PMID:8436910

A:Accession: PH1484

A>Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-140 <GIU>

A:Cross-references: UNIPARC:UPI0000176BA4

A:Experimental source: hybridoma cell

C:Genetics:

A:Insertions: 16/1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 65.2%; Score 58; DB 2; Length 140;
Best Local Similarity 68.8%; Pred. No. 0.032;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 IYPGNDISYNOKFXG 17
| | | | |
51 IYPGNDYIKYNEKFXG 85

RESULT 20

PL0232

Ig heavy chain V region (anti-DNA, DP7VH) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996

C:Accession: PL0232

R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A

J. Exp. Med. 171, 265-297, 1990

A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic n

A:Reference number: PL0231; MUID:90111618; PMID:2104919

A:Accession: PL0232

A:Molecule type: mRNA

```

A:Residues: 1-112 <SHL>
A:Cross-references: UNIPARC:UPI0000176C56
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-30/Region: framework 1
F:15-98/Domain: immunoglobulin homology <IMM>
F:31-35/Region: complementarity-determining 1
F:36-49/Region: framework 2
F:50-66/Region: complementarity-determining 2
F:67-96/Region: framework 3
F:97-104/Region: complementarity-determining 3
F:105-112/Region: framework 4

Query Match          64.0%; Score 57; DB 2; Length 112;
Best Local Similarity 62.5%; Pred. No. 0.037;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IYPGNDDISYNOKEXG 17
   |||:|:|:|:|:|
Db 51 IYPGDGDTNYNGKFKG 66

RESULT 21
PI0238
Ig heavy chain V region (anti-DNA, 6NWH and 6QVH) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
C:Accession: PI0238
R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Plisetsky, D.; Marshak-Rothstein, A.
J. Exp. Med. 171, 265-297, 1990
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A:Reference number: PI0231; MUID:90111618; PMID:2104919
A:Accession: PI0238
A:Molecule type: mRNA
A:Residues: 1-115 <SHL>
A:Cross-references: UNIPARC:UPI0000176C53
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-30/Region: framework 1
F:15-98/Domain: immunoglobulin homology <IMM>
F:31-35/Region: complementarity-determining 1
F:36-49/Region: framework 2
F:50-66/Region: complementarity-determining 2
F:67-98/Region: framework 3
F:99-107/Region: complementarity-determining 3
F:108-115/Region: framework 4

Query Match          64.0%; Score 57; DB 2; Length 115;
Best Local Similarity 62.5%; Pred. No. 0.038;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IYPGNDDISYNOKEXG 17
   |||:|:|:|:|:|
Db 51 IYPGDGDTNYNGKFKG 66

RESULT 22
PI0231
Ig heavy chain V region (anti-DNA, D20VH) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Plisetsky, D.; Marshak-Rothstein, A.
J. Exp. Med. 171, 265-297, 1990
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A:Reference number: PI0231; MUID:90111618; PMID:2104919
A:Accession: PI0231
A:Molecule type: mRNA
A:Residues: 1-118 <SHL>
A:Cross-references: UNIPARC:UPI0000176C54
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-30/Region: framework 1

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F:15-98/Domain: immunoglobulin homology <IMM>
F:31-35/Region: complementarity-determining 1
F:36-49/Region: framework 2
F:50-66/Region: complementarity-determining 2
F:67-98/Region: framework 3
F:99-110/Region: complementarity-determining 3
F:111-118/Region: framework 4

Query Match          64.0%; Score 57; DB 2; Length 118;
Best Local Similarity 62.5%; Pred. No. 0.039;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      2 IYPGNDDISYNOKEFXG 17
      |||:|:|:|:|
DB      51 IYPGDGDTYNGKFKG 66

RESULT 23
A:24672
Ig heavy chain precursor V region (VMU-3.2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 23-Jul-1999
C:Accession: A24672
R:Winter, E.; Radbruch, A.; Krawinkel, U.
EMBO J. 4, 2861-2867, 1985
A:Reference number: A91022; MUID:86055722; PMID:2598759
A:Accession: A24672
A:Molecule type: DNA
A:Residues: 1-119 <WIN>
A:Cross-references: UNIPARC:UPI0000113755; GB:X03088; NID:952378; PIDN:CAA26881.1; PID:97
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:4-119/Product: Ig heavy chain V region VMU-3.2 #status predicted <MAT>
F:18-101/Domain: immunoglobulin homology <IMM>

Query Match          64.0%; Score 57; DB 2; Length 119;
Best Local Similarity 62.5%; Pred. No. 0.039;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      2 IYPGNDDISYNOKEFXG 17
      |||:|:|:|:|
DB      54 IYPGDGDTYNGKFKG 69

RESULT 24
H28833
Ig kappa chain V region (HP22.202.16) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-May-1997
C:Accession: H28833
R:Corbett, S.; Hirth, M.; Roth, C.; Theze, J.; Fougereau, M.; Schiffl, C.
J. Immunol. 141, 779-784, 1988
A:Title: Allele-specific manipulation of the GAT idiotypic cascade. Immunization of C57BL/6 m
A:Reference number: A92827; MUID:88285674; PMID:3135311
A:Accession: H28833
A:Molecule type: mRNA
A:Residues: 1-67 <COR>
A:Cross-references: UNIPARC:UPI0000176D5E
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin

Query Match          61.8%; Score 55; DB 2; Length 67;
Best Local Similarity 56.2%; Pred. No. 0.046;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY      2 IYPGNDISYNOKEFXG 17
      |||:|:|:|:|
DB      20 IYPGSGNTKYNEKFKG 35

RESULT 25
PH0999

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Ig heavy chain V region (clone 74-c1) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C/Accession: PH0999
R/Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A/Title: Both Igm and IgG anti-DNA antibodies are the products of clonally selective B
A/Reference number: PH0971; MUID:92381444; PMID:1512540
A/Accession: PH0999
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-107 <TIL>
A/Cross-references: UNIPARC:UPI0000176D10
A/Experimental source: B cell, strain [NZB x NZW]F1
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F,14-97/Domain: immunoglobulin homology <IMM>

Query Match 61.8%; Score 55; DB 2; Length 107;
Best Local Similarity 56.2%; Pred. No. 0.075;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Oy 2 IYPGNDISYNQKFXG 17
|||: : ||: ||
Db 50 IYPSGNTKYNKEKFG 65

RESULT 26
PH0997
Ig heavy chain V region (clone 178-c2) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C/Accession: PH0997
R/Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A/Title: Both Igm and IgG anti-DNA antibodies are the products of clonally selective B
A/Reference number: PH0971; MUID:92381444; PMID:1512540
A/Accession: PH0997
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-109 <TIL>
A/Cross-references: UNIPARC:UPI0000176D0E
A/Experimental source: B cell, strain [NZB x NZW]F1
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F,15-98/Domain: immunoglobulin homology <IMM>

Query Match 61.8%; Score 55; DB 2; Length 109;
Best Local Similarity 56.2%; Pred. No. 0.076;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Oy 2 IYPGNDISYNQKFXG 17
|||: : ||: ||
Db 51 IYPSGNTKYNKEKFG 66

RESULT 27
PH0998
Ig heavy chain V region (clone 165-3) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C/Accession: PH0998
R/Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A/Title: Both Igm and IgG anti-DNA antibodies are the products of clonally selective B
A/Reference number: PH0971; MUID:92381444; PMID:1512540
A/Accession: PH0998
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-111 <TIL>
A/Cross-references: UNIPARC:UPI0000176D0F
A/Experimental source: B cell, strain [NZB x NZW]F1
C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin
F,15-98/Domain: immunoglobulin homology <IMM>

Query Match 61.8%; Score 55; DB 2; Length 111;
Best Local Similarity 56.2%; Pred. No. 0.078;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Oy 2 IYPGNDISYNQKFXG 17
|||: : ||: ||
Db 51 IYPSGNTKYNKEKFG 66

RESULT 28
PH1415
Ig heavy chain V region (clone P1-57) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C/Accession: PH1415
R/van der Stoep, N.; van der Linden, J.; Logtenberg, T.
J. Exp. Med. 177, 99-107, 1993
A/Title: Molecular evolution of the human immunoglobulin E response: High incidence of
dermatitis.
A/Reference number: PH1409; MUID:93115676; PMID:8418213
A/Accession: PH1415
A/Molecule type: mRNA
A/Residues: 1-127 <VAN>
A/Cross-references: UNIPARC:UPI000017694F
A/Experimental source: PBMC
A/Note: the authors translated the codon TTG for residue 118 as Met
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F,15-98/Domain: immunoglobulin homology <IMM>

Query Match 61.8%; Score 55; DB 2; Length 127;
Best Local Similarity 52.9%; Pred. No. 0.09;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Oy 1 VIYPGNDISYNQKFXG 17
|||: : ||: ||
Db 50 IYPSGNTKYNKEKFG 66

RESULT 29
S38950
Ig gamma chain - mouse
C/Species: Mus musculus (house mouse)
C/Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999
C/Accession: S38950
R/Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Welgeberger, C.; Bi
Biol. Chem. Hoppe-Seyler 374, 993-1000, 1993
A/Title: Primary structure of the murine monoclonal IgG2a antibody mAb735 against alpha
A/Reference number: S38950; MUID:94128242; PMID:8257501
A/Accession: S38950
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-246 <KLE>
A/Cross-references: UNIPARC:UPI0000176F3B
C/Superfamily: immunoglobulin C region; immunoglobulin homology
F,137-201/Domain: immunoglobulin homology <IMM>

Query Match 61.8%; Score 55; DB 2; Length 246;
Best Local Similarity 56.2%; Pred. No. 0.18;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Oy 2 IYPGNDISYNQKFXG 17
|||: : ||: ||
Db 51 IYPSGNTKYNKEKFG 66

RESULT 30
S40295
Ig gamma-2a chain (mAb735) - mouse

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C/Species: Mus musculus (house mouse)
C/Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004
C/Accession: S40295
R/Kiebert, S.; Kitzlin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; Bi
submitted to the EMBL Data Library, January 1993
A/Description: Primary structure of the murine monoclonal IgG2a antibody mab735 against
A/Reference number: S40295
A/Accession: S40295
A/Molecule type: Protein
A/Residues: 1-446 <KLE>
A/Cross-references: UNIPROT:Q9JL25; UNIPARC:UPI0000176F38
C/Genetics:
A/Map position: 12
C/Superfamily: immunoglobulin C region; immunoglobulin homology
C/Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic acid
F,1-446/Product: Ig gamma-2a chain #status experimental <Mat>
F,1-117/Domain: V-D-J region <VDJ>
F,118-446/Domain: C region <CHR>
F,118-214/Domain: C1 region <CH1>
F,215-230/Region: hinge
F,231-340/Domain: C2 region <CH2>
F,341-446/Domain: C3 region <CH3>
F,360-427/Domain: immunoglobulin homology <IMM>
F,1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F,22-96,144-199,261-321,367-425/Disulfide bonds: #status predicted
F,132/Disulfide bonds: interchain (to light chain) #status predicted
F,224,227,229/Disulfide bonds: interchain #status predicted
F,297/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match          61.8%; Score 55; DB 2; Length 446;
Best Local Similarity 56.2%; Pred. No. 0.34;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Oy 2 IYPGNDISYNQKFXG 17
    |||:|:|:|:|
Db 51 IYPSGNTKYNKEKFG 66

RESULT 31
S26466
Ig heavy chain V region - mouse
C/Species: Mus musculus (house mouse)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C/Accession: S26466
R/Kavaler, J.
submitted to the EMBL Data Library, April 1991
A/Reference number: S26459
A/Accession: S26466
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-104 <KAV>
A/Cross-references: UNIPARC:UPI0000115F6A; EMBL:X59116; NID:G51933; PIDN:CAA41842.1; PIC
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F,3-86/Domain: immunoglobulin homology <IMM>

Query Match          60.7%; Score 54; DB 2; Length 104;
Best Local Similarity 56.2%; Pred. No. 0.11;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Oy 2 IYPGNDISYNQKFXG 17
    |||:|:|:|:|
Db 39 IYPSGNTKYNKEKFG 54

RESULT 32
PL0244
Ig heavy chain V region (anti-DNA, DP9VH) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
C/Accession: PL0244
R/Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A
J. Exp. Med. 171, 265-297, 1990

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A/Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic n
A/Reference number: PL0231; MUID:90111618; PMID:2104919
A/Accession: PL0244
A/Molecule type: mRNA
A/Residues: 1-110 <SHL>
A/Cross-references: UNIPARC:UPI0000176C5C
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F,1-23/Region: framework 1
F,8-91/Domain: immunoglobulin homology <IMM>
F,24-28/Region: complementarity-determining 1
F,29-42/Region: framework 2
F,43-59/Region: complementarity-determining 2
F,60-91/Region: framework 3
F,92-102/Region: complementarity-determining 3
F,103-110/Region: framework 4

Query Match          60.7%; Score 54; DB 2; Length 110;
Best Local Similarity 56.2%; Pred. No. 0.11;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Oy 2 IYPGNDISYNQKFXG 17
    |||:|:|:|:|
Db 44 IYSGSDNTKYNKEKFG 59

RESULT 33
PL0245
Ig heavy chain V region (anti-DNA, DP17VH) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
C/Accession: PL0245
R/Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A
J. Exp. Med. 171, 265-297, 1990
A/Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic n
A/Reference number: PL0231; MUID:90111618; PMID:2104919
A/Accession: PL0245
A/Molecule type: mRNA
A/Residues: 1-112 <SHL>
A/Cross-references: UNIPARC:UPI0000176C5D
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F,1-23/Region: framework 1
F,8-91/Domain: immunoglobulin homology <IMM>
F,24-28/Region: complementarity-determining 1
F,29-42/Region: framework 2
F,43-59/Region: complementarity-determining 2
F,60-91/Region: framework 3
F,92-102/Region: complementarity-determining 3
F,103-112/Region: framework 4

Query Match          60.7%; Score 54; DB 2; Length 112;
Best Local Similarity 56.2%; Pred. No. 0.11;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Oy 2 IYPGNDISYNQKFXG 17
    |||:|:~|:|:|
Db 44 IYSGSDNTKYNKEKFG 59

RESULT 34
HVMS02
Ig heavy chain precursor V region (102) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 09-Jul-2004
C/Accession: A02032
R/Bothwell, A.L.M.; Faskind, M.; Reih, M.; Imanishi-Kari, T.; Rajewsky, K.; Baltimore, D
Cell 24, 625-637, 1981
A/Title: Heavy chain variable region contribution to the NP(b) family of antibodies: som
A/Reference number: A90809; MUID:81234548; PMID:6788376
A/Accession: A02032
A/Molecule type: DNA
A/Residues: 1-117 <BOT>

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A:Cross-references: UNIPROT:P01750; UNIPARC:UP100000270BA
 A>Note: the sequence was determined from the germine gene
 A>Note: the germine gene, cloned from a library of strain C57BL/6 DNA, is one of a set
 1 (NDb antibodies)
 C:Genetics:
 A:Introns: 16/1
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-117/Product: Ig heavy chain V region (102) #status predicted <MAT>
 F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 60.7%; Score 54; DB 1; Length 117;
 Best Local Similarity 56.2%; Pred. No. 0.12;
 Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 IYPGNDISYNQKFXG 17
 |||:|:|:|:|:|:|
 Db 70 IHPSDSDTNVQKFKG 85

RESULT 35
 HWSAI
 Ig heavy chain precursor V region (A1/A4) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
 C:Accession: A02029
 R:Yancopoulos, G.D.; Alt, F.W.
 Cell 40, 271-281, 1985
 A>Title: Developmentally controlled and tissue-specific expression of unrearranged V-H g
 A:Reference number: A90860; MUID:85099340; PMID:2578321
 A:Accession: A02029
 A:Molecule type: DNA
 A:Residues: 1-117 <YAN>
 A:Cross-references: UNIPROT:P06327; UNIPARC:UP10000028A69; GB:M13787; NID:G196006; PIDN:
 A>Note: the sequence was determined from the germine gene
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-117/Product: Ig heavy chain V region (A1/A4) #status predicted <MAT>
 F:20-49/Region: framework 1
 F:34-117/Domain: immunoglobulin homology <IMM>
 F:50-54/Region: complementarity-determining 1
 F:55-68/Region: framework 2
 F:69-85/Region: complementarity-determining 2
 F:86-117/Region: framework 3
 F:41-115/Disulfide bonds: #status predicted

Query Match 60.7%; Score 54; DB 1; Length 117;
 Best Local Similarity 56.2%; Pred. No. 0.12;
 Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 IYPGNDISYNQKFXG 17
 |||:|:|:|:|:|:|
 Db 70 IYPGDSSTVYKFKG 85

RESULT 36
 PL0089
 Ig heavy chain V region (12S18-1) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 04-Mar-2000
 C:Accession: PL0089
 R:Meek, K.; Haemann, C.; Pollok, B.; Alkan, S.S.; Bralt, M.; Slouci, M.; Urbain, J.; Ca
 U. Exp. Med. 169, 519-533, 1989
 A>Title: Structural characterization of antidiabetic antibodies; evidence that Ab2s are
 A:Reference number: PL0080; MUID:89094248; PMID:2492056
 A:Accession: PL0089
 A:Molecule type: mRNA
 A:Residues: 1-119 <ME>
 A:Cross-references: UNIPARC:UP10000115F1B; GB:X58580; GB:Y00794; NID:G51591; PIDN:CAA414
 A>Note: the sequence shown here is from the VH region of an antidiabetic monoclonal and
 A>Note: sequences from two other clones (18S28-16 and 12S84-3) were almost identical to

C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 60.7%; Score 54; DB 2; Length 119;
 Best Local Similarity 64.3%; Pred. No. 0.12;
 Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 IYPGNDISYNQKFXG 15
 |||:|:|:|:|:|:|
 Db 51 IYPGSDITVYKFKG 64

RESULT 37
 B2769
 Ig heavy chain V region (B1-8.V1/V2) - mouse (tentative sequence)
 C:Species: Mus musculus (house mouse)
 C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 16-Aug-1996
 C:Accession: B2769
 R:Dildrop, R.; Bruggemann, M.; Radbruch, A.; Rajewsky, K.; Beyreuther, K.
 EMBO J. 1, 635-640, 1982
 A>Title: Immunoglobulin V region variants in hybridoma cells. II. Recombination between
 A:Reference number: A90971; MUID:84236026; PMID:7188353
 A:Accession: B2769
 A:Molecule type: protein
 A:Residues: 1-120 <DIL>
 A:Cross-references: UNIPARC:UP10000176B76
 A>Note: the sequences of two spontaneously arising somatic variants, B1-8.V1 and B1-8.V2
 A>Note: peptides and unsequenced residues were positioned by homology with the B1-8 sequ
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 60.7%; Score 54; DB 2; Length 120;
 Best Local Similarity 56.2%; Pred. No. 0.12;
 Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 IYPGNDISYNQKFXG 17
 |||:|:|:|:|:|:|
 Db 51 IHPSDSDTNVQKFKG 66

RESULT 38
 PH1424
 Ig heavy chain V region (clone P3-60) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
 C:Accession: PH1424
 R:van der Stoep, N.; van der Linden, J.; Logtenberg, T.
 J. Exp. Med. 177, 99-107, 1993
 A>Title: Molecular evolution of the human immunoglobulin B response: High incidence of s
 dermatitis.
 A:Reference number: PH1409; MUID:93115676; PMID:8418213
 A:Accession: PH1424
 A:Molecule type: mRNA
 A:Residues: 1-126 <VAN>
 A:Cross-references: UNIPARC:UP10000176A2P
 A:Experimental source: PBMC
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 60.7%; Score 54; DB 2; Length 126;
 Best Local Similarity 52.9%; Pred. No. 0.13;
 Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 IYPGNDISYNQKFXG 17
 |||:|:|:|:|:|:|
 Db 50 IYPGSDITVYKFKG 66

RESULT 39
 S04575

Ig heavy chain precursor V region (MRL-RF24) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 21-Jan-2000
C:Accession: S04575
R:Kotler, R.; Noonan, D.J.; Strchal, R.; Balderas, R.S.; Moller, N.P.H.; Dixon, F.J.; Th
Eur. J. Immunol. 17, 91-95, 1987
A:Title: Molecular analysis of the murine lupus-associated anti-self response: involveme
A:Reference number: S04573; MUID:87133856; PMID:3102255
A:Accession: S04575
A:Molecule type: mRNA
A:Residues: 1-140 <KOF>
A:Cross-references: UNIPARC:UPI0000115E00; EMBL:X14623; NID:G52398; PIDN:CAA32776.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence <status predicted <SIG>
F:20-140/Product: Ig kappa chain V region (fragment) #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 60.7%; Score 54; DB 2; Length 140;
Best Local Similarity 60.0%; Pred. No. 0.15;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 3 IYPGNDISYNQKFXG 17
: ||| : ||| :
Db 71 HPYNDTKYNEKFKG 85

RESULT 40

B28572
Ig heavy chain V regions (CR-Id 7, CR-Id 14) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 21-Jul-2000
C:Accession: B28572
R:Stekovitz, M.; Huang, S.Y.; Geffer, M.L.
Eur. J. Immunol. 13, 123-132, 1983
A:Title: The genetic basis of antibody production: a single heavy chain variable region
A:Reference number: A91262; MUID:83157801; PMID:6403356
A:Accession: B28572
A:Molecule type: DNA
A:Residues: 1-76 <SIE>
A:Cross-references: UNIPARC:UPI0000114908; GB:K02154; GB:M17032; NID:g196176; PIDN:AAA38
A:Note: this sequence was determined from the germ-line gene
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 59.6%; Score 53; DB 2; Length 76;
Best Local Similarity 56.2%; Pred. No. 0.11;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 2 IYPGNDISYNQKFXG 17
: ||| : ||| :
Db 36 IYPGNGYTAINEQFKG 51

RESULT 41

PH1487
Ig heavy chain V region (clone X20-4) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C:Accession: PH1487
R:Giusti, A.M.; Manser, T.
J. Exp. Med. 177, 797-809, 1993
A:Title: Hypermutation is observed only in antibody H chain V region transgenes that hav
d for somatic mutation.
A:Reference number: PH1482; MUID:93171820; PMID:8436910
A:Accession: PH1487
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-84 <GIU>
A:Cross-references: UNIPARC:UPI0000176A36
A:Experimental source: hybridoma cell
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 59.6%; Score 53; DB 2; Length 84;
Best Local Similarity 56.2%; Pred. No. 0.12;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 2 IYPGNDISYNQKFXG 17
: ||| : ||| :
Db 14 VNPNDYTKYNEKFKG 29

RESULT 42

PH1165
Ig heavy chain V region (clone 26F.1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 31-Dec-2004
C:Accession: PH1165
R:Schlitz, B.; Rajewsky, K.
J. Exp. Med. 176, 427-438, 1992
A:Title: Natural occurrence and origin of somatically mutated memory B cells in mice.
A:Reference number: PH1105; MUID:92364545; PMID:1500855
A:Accession: PH1165
A:Molecule type: DNA
A:Residues: 1-96 <SCH>
A:Cross-references: UNIPROT:Q9D8L4; UNIPARC:UPI0000176A41
A:Experimental source: B cell
C:Superfamily: immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-96/Domain: immunoglobulin homology <IMM>

Query Match 59.6%; Score 53; DB 2; Length 96;
Best Local Similarity 56.2%; Pred. No. 0.14;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 2 IYPGNDISYNQKFXG 17
: ||| : ||| :
Db 51 IYPGNGYTAINEKFKG 66

RESULT 43

PH1490
Ig heavy chain V region (clone XR6-1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C:Accession: PH1490
R:Giusti, A.M.; Manser, T.
J. Exp. Med. 177, 797-809, 1993
A:Title: Hypermutation is observed only in antibody H chain V region transgenes that have
d for somatic mutation.
A:Reference number: PH1482; MUID:93171820; PMID:8436910
A:Accession: PH1490
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-102 <GIU>
A:Cross-references: UNIPARC:UPI0000176A37
A:Experimental source: hybridoma cell
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 59.6%; Score 53; DB 2; Length 102;
Best Local Similarity 62.5%; Pred. No. 0.15;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 2 IYPGNDISYNQKFXG 17
: ||| : ||| :
Db 32 INPNGYINYNKFKG 47

RESULT 44

PH1002
Ig heavy chain V region (clone 165.45) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PH1002

R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
C;Title: Both IGM and Igg anti-DNA antibodies are the products of clonally selective B c
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH1002
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-106 <TIL>
A;Cross-references: UNIPARC:UPI0000176D13
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

Query Match 59.6%; Score 53; DB 2; Length 106;
Best Local Similarity 56.2%; Pred. No. 0.16;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Oy 2 IYPGNDISYNQKFXG 17
|||:|:|:|
Db 50 IYPGSGNTKYNKFKG 65

RESULT 45

PH1001
Ig heavy chain V region (clone 111.68) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH1001
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
C;Title: Both IGM and Igg anti-DNA antibodies are the products of clonally selective B c
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH1001
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-109 <TIL>
A;Cross-references: UNIPARC:UPI0000176D12
C;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 59.6%; Score 53; DB 2; Length 109;
Best Local Similarity 56.2%; Pred. No. 0.16;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Oy 2 IYPGNDISYNQKFXG 17
|||:|:|:|
Db 51 IYPGSGNTKYNKFKG 66

RESULT 46

PH1000
Ig heavy chain V region (clone 202.105) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH1000
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
C;Title: Both IGM and Igg anti-DNA antibodies are the products of clonally selective B c
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH1000
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-110 <TIL>
A;Cross-references: UNIPARC:UPI0000176D11
C;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 59.6%; Score 53; DB 2; Length 110;

Best Local Similarity 56.2%; Pred. No. 0.16;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Oy 2 IYPGNDISYNQKFXG 17
|||:|:|:|
Db 51 IYPGSGNTKYNKFKG 66

RESULT 47

A24754
Ig heavy chain V region (SE20.2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 28-Sep-1987 #sequence_revision 06-Nov-1992 #text_change 23-Jul-1999
C;Accession: A24754
R;Haba, S.; Rosen, E.M.; Meek, K.; Nisonoff, A.
J. Exp. Med. 164, 291-302, 1986
A;Reference number: A24754; MUID:86253060; PMID:3088196
A;Accession: A24754
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-118 <HAB>
A;Cross-references: UNIPARC:UPI0000114CID; db:M13647; MID:G195072; PIDN:AAA8149.1; PID:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 59.6%; Score 53; DB 2; Length 118;
Best Local Similarity 62.5%; Pred. No. 0.16;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Oy 2 IYPGNDISYNQKFXG 17
|||:|:|:|
Db 51 INPGNGYINVEKFKG 66

RESULT 48

E48677
Ig heavy chain V-D-J region (48) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 17-Mar-1999
C;Accession: E48677
R;Taasigmon, J.; Brail, M.; Jamila, I.; Urbahn, J.; Gottlieb, P.; Brown, A.; Hasemann, C
Proc. Natl. Acad. Sci. U.S.A. 90, 9508-9512, 1993
A;Title: Molecular characterization of monoclonal CRI-A-positive anti-arsenate antibody
A;Reference number: A48677; MUID:94022404; PMID:8415731
A;Accession: E48677
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-123 <RTAS>
A;Cross-references: UNIPARC:UPI0000176DC5
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 59.6%; Score 53; DB 2; Length 123;
Best Local Similarity 62.5%; Pred. No. 0.16;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Oy 2 IYPGNDISYNQKFXG 17
|||:|:~|:|:|
Db 51 INPGNGYINVEKFKG 66

RESULT 49

HVMSG7
Ig heavy chain precursor V region (93G7, 36-65) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Aug-1992 #sequence_revision 18-Aug-1992 #text_change 09-Jul-2004
C;Accession: A94264; A91261; A02028
R;Sims, J.; Rabbits, T.H.; Estess, P.; Slaughter, C.; Tucker, P.W.; Capra, J.D.
Science 216, 309-311, 1982
A;Title: Somatic mutation in genes for the variable portion of the immunoglobulin heavy
A;Reference number: A94264; MUID:82152818; PMID:6801765

A;Accession: A94264
 A;Molecule type: mRNA
 A;Residues: 1-140 <SIM>
 A;Cross-references: UNIPROT:P01746; UNIPARC:UPI0000270DA; GB:J00493; NID:g195006; PIDN:
 A;Experimental source: strain A/J, hybridoma 93G7
 R;Sekevit, M.; Gelfer, M.L.; Brodeur, P.; Riblet, R.; Marshak-Rothstein, A.
 Eur. J. Immunol. 12, 1023-1032, 1982
 A;Title: The genetic basis of antibody production: the dominant anti-arsenate idiotype
 A;Reference number: A91261; MUID:83131846; PMID:6186498
 A;Accession: A91261
 A;Molecule type: DNA
 A;Residues: 20-76, 'TK', '79-118', 'V', '120-125', 'Y', '127-134', 'T', '136-140' <SIE>
 A;Cross-references: UNIPARC:UPI000014DSB; GB:M19292; NID:g196201; PIDN:AAA38625.1; PID:
 A;Experimental source: strain A/J, hybridoma 36-65
 A;Note: the sequence was determined from the differentiated gene
 A;Note: from analysis of the sizes of several other differentiated genes that hybridize
 C;Genetics:
 A;Introns: 16//1
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; hybridoma; immunoglobulin
 F;1-19/Domain: signal sequence #status predicted <SIG>
 F;20-140/Product: Ig heavy chain V region (93G7) #status predicted <MAT>
 F;34-117/Domain: immunoglobulin homology <IMM>
 F;41-115/Disulfide bonds: #status predicted

Query Match 59.6%; Score 53; DB 1; Length 140;
 Best Local Similarity 62.5%; Pred. No. 0.21;
 Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IYPGNDISYNQKFXG 17
 |||||:|:|:|
 Db 70 INPGNGYINYNKFKG 85

RESULT 50

PH1486
 Ig heavy chain V region (clone X7-3D12) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
 C;Accession: PH1486
 R;Gustl, A.M.; Manser, T.
 J. Exp. Med. 177, 797-809, 1993
 A;Title: Hypermutation is observed only in antibody H chain V region transgenes that have
 d for somatic mutation.
 A;Reference number: PH1482; MUID:93171820; PMID:8436910
 A;Accession: PH1486
 A;Status: translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-140 <GIU>
 A;Cross-references: UNIPARC:UPI0000176BA6
 A;Experimental source: hybridoma cell
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 59.6%; Score 53; DB 2; Length 140;
 Best Local Similarity 62.5%; Pred. No. 0.21;
 Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IYPGNDISYNQKFXG 17
 |||||:|:|:|
 Db 70 INPGNGYINYNKFKG 85

Search completed: May 4, 2006, 13:08:43
 Job time : 38.2857 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 4, 2006, 12:46:39 ; Search time 159.206 Seconds
(without alignments)
75.336 Million cell updates/sec

Title: US-10-700-632-2
Perfect score: 89
Sequence: 1 VIYPNDISYNQKFXG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	72	80.9	120	Q5F211_MOUSE	Q5F211 mus musculus
2	68	76.4	487	Q6Z122_9MUR1	Q6Z122 mus sp. fv/
3	63	70.8	458	Q5B122_RAT	Q5B122 rattus norv
4	61	68.5	118	Q921C4_MOUSE	Q921C4 mus musculus
5	57	64.0	111	Q9D9B6_MOUSE	Q9D9B6 mus musculus
6	57	64.0	470	Q7TMK1_MOUSE	Q7TMK1 mus musculus
7	56	62.9	468	Q569W9_MOUSE	Q569W9 mus musculus
8	56	62.9	614	Q7TMT6_MOUSE	Q7TMT6 mus musculus
9	55	61.8	136	Q7TPE3_MOUSE	Q7TPE3 mus musculus
10	55	61.8	481	Q91WT1_MOUSE	Q91WT1 mus musculus
11	54	60.7	110	Q9JL83_MOUSE	Q9JL83 mus musculus
12	54	60.7	117	Q91183_MOUSE	Q91183 mus musculus
13	54	60.7	117	Q91183_MOUSE	Q91183 mus musculus
14	54	60.7	117	Q91183_MOUSE	Q91183 mus musculus
15	53	59.6	140	Q9DCD9_MOUSE	Q9DCD9 mus musculus
16	53	59.6	472	Q6P1A7_MOUSE	Q6P1A7 mus musculus
17	53	59.6	477	Q5B5E6_MOUSE	Q5B5E6 mus musculus
18	53	59.6	483	Q4VAB6_MOUSE	Q4VAB6 mus musculus
19	53	59.6	590	Q4V9V8_MOUSE	Q4V9V8 mus musculus
20	51	57.3	464	Q6P9S5_MOUSE	Q6P9S5 mus musculus
21	50	56.2	117	Q91183_MOUSE	Q91183 mus musculus
22	50	56.2	117	Q91183_MOUSE	Q91183 mus musculus
23	50	56.2	117	Q91183_MOUSE	Q91183 mus musculus
24	50	56.2	117	Q91183_MOUSE	Q91183 mus musculus
25	50	56.2	118	Q91183_MOUSE	Q91183 mus musculus
26	50	56.2	134	Q6S2R6_MOUSE	Q6S2R6 mus musculus
27	50	56.2	143	Q92400_MOUSE	Q92400 mus musculus
28	49	55.1	147	Q925S3_MOUSE	Q925S3 mus musculus
29	49	55.1	293	Q7VB33_PROMA	Q7VB33 prochloro
30	48.5	54.5	826	Q4YS38_PLABE	Q4YS38 plasmodium
31	48	53.9	117	Q91183_MOUSE	Q91183 mus musculus

32	48	53.9	463	Q991C4_MOUSE	Q991C4 mus musculus
33	48	53.9	483	Q5WMD6_CAEBR	Q5WMD6 caenorhabdi
34	47	52.8	109	Q91175_MOUSE	Q91175 mus musculus
35	47	52.8	117	Q91175_MOUSE	Q91175 mus musculus
36	47	52.8	118	Q91175_MOUSE	Q91175 mus musculus
37	47	52.8	120	Q91175_MOUSE	Q91175 mus musculus
38	47	52.8	488	Q91175_MOUSE	Q91175 mus musculus
39	47	52.8	613	Q91175_MOUSE	Q91175 mus musculus
40	47	52.8	891	Q91175_MOUSE	Q91175 mus musculus
41	47	52.8	899	Q91175_MOUSE	Q91175 mus musculus
42	47	52.8	899	Q91175_MOUSE	Q91175 mus musculus
43	47	52.8	899	Q91175_MOUSE	Q91175 mus musculus
44	47	52.8	899	Q91175_MOUSE	Q91175 mus musculus
45	46	51.7	146	Q91175_MOUSE	Q91175 mus musculus
46	46	51.7	146	Q91175_MOUSE	Q91175 mus musculus
47	46	51.7	158	Q91175_MOUSE	Q91175 mus musculus
48	46	51.7	158	Q91175_MOUSE	Q91175 mus musculus
49	46	51.7	158	Q91175_MOUSE	Q91175 mus musculus
50	46	51.7	158	Q91175_MOUSE	Q91175 mus musculus
51	46	51.7	158	Q91175_MOUSE	Q91175 mus musculus
52	46	51.7	158	Q91175_MOUSE	Q91175 mus musculus
53	46	51.7	158	Q91175_MOUSE	Q91175 mus musculus
54	46	51.7	158	Q91175_MOUSE	Q91175 mus musculus
55	46	51.7	158	Q91175_MOUSE	Q91175 mus musculus
56	46	51.7	158	Q91175_MOUSE	Q91175 mus musculus
57	46	51.7	158	Q91175_MOUSE	Q91175 mus musculus
58	46	51.7	158	Q91175_MOUSE	Q91175 mus musculus
59	46	51.7	158	Q91175_MOUSE	Q91175 mus musculus
60	46	51.7	158	Q91175_MOUSE	Q91175 mus musculus
61	46	51.7	158	Q91175_MOUSE	Q91175 mus musculus
62	46	51.7	158	Q91175_MOUSE	Q91175 mus musculus
63	46	51.7	158	Q91175_MOUSE	Q91175 mus musculus
64	46	51.7	158	Q91175_MOUSE	Q91175 mus musculus
65	46	51.7	158	Q91175_MOUSE	Q91175 mus musculus
66	46	51.7	158	Q91175_MOUSE	Q91175 mus musculus
67	46	51.7	158	Q91175_MOUSE	Q91175 mus musculus
68	46	51.7	158	Q91175_MOUSE	Q91175 mus musculus
69	46	51.7	158	Q91175_MOUSE	Q91175 mus musculus
70	46	51.7	158	Q91175_MOUSE	Q91175 mus musculus
71	46	51.7	158	Q91175_MOUSE	Q91175 mus musculus
72	46	51.7	158	Q91175_MOUSE	Q91175 mus musculus
73	46	51.7	158	Q91175_MOUSE	Q91175 mus musculus
74	46	51.7	158	Q91175_MOUSE	Q91175 mus musculus
75	46	51.7	158	Q91175_MOUSE	Q91175 mus musculus
76	46	51.7	158	Q91175_MOUSE	Q91175 mus musculus
77	46	51.7	158	Q91175_MOUSE	Q91175 mus musculus
78	46	51.7	158	Q91175_MOUSE	Q91175 mus musculus
79	46	51.7	158	Q91175_MOUSE	Q91175 mus musculus
80	46	51.7	158	Q91175_MOUSE	Q91175 mus musculus
81	46	51.7	158	Q91175_MOUSE	Q91175 mus musculus
82	46	51.7	158	Q91175_MOUSE	Q91175 mus musculus
83	46	51.7	158	Q91175_MOUSE	Q91175 mus musculus
84	46	51.7	158	Q91175_MOUSE	Q91175 mus musculus
85	46	51.7	158	Q91175_MOUSE	Q91175 mus musculus
86	46	51.7	158	Q91175_MOUSE	Q91175 mus musculus
87	46	51.7	158	Q91175_MOUSE	Q91175 mus musculus
88	46	51.7	158	Q91175_MOUSE	Q91175 mus musculus
89	46	51.7	158	Q91175_MOUSE	Q91175 mus musculus
90	46	51.7	158	Q91175_MOUSE	Q91175 mus musculus
91	46	51.7	158	Q91175_MOUSE	Q91175 mus musculus
92	46	51.7	158	Q91175_MOUSE	Q91175 mus musculus
93	46	51.7	158	Q91175_MOUSE	Q91175 mus musculus
94	46	51.7	158	Q91175_MOUSE	Q91175 mus musculus
95	46	51.7	158	Q91175_MOUSE	Q91175 mus musculus
96	46	51.7	158	Q91175_MOUSE	Q91175 mus musculus
97	46	51.7	158	Q91175_MOUSE	Q91175 mus musculus
98	46	51.7	158	Q91175_MOUSE	Q91175 mus musculus
99	46	51.7	158	Q91175_MOUSE	Q91175 mus musculus
100	46	51.7	158	Q91175_MOUSE	Q91175 mus musculus
101	46	51.7	158	Q91175_MOUSE	Q91175 mus musculus
102	46	51.7	158	Q91175_MOUSE	Q91175 mus musculus
103	46	51.7	158	Q91175_MOUSE	Q91175 mus musculus
104	46	51.7	158	Q91175_MOUSE	Q91175 mus musculus

251	40	44.9	361	1	AROC_SALPA	05pcc2 salmonella	324	39	43.8	188	2	Q9Q815_9POXY	Q9Q815 myxoma viru
252	40	44.9	361	1	AROC_YERPS	068bvs yersinia ps	325	39	43.8	194	2	Q833f8_ENTPA	Q833f8 enterococcu
253	40	44.9	361	1	Q83Q05_SHIFL	083q05 shigella fl	326	39	43.8	200	1	PLIGA_AGBKA	P82134 agkistrodon
254	40	44.9	362	2	Q965H7_CAEEL	0965h7 caenorhabdi	327	39	43.8	204	2	Q4LIF4_9BURK	Q4L1f4 burkholderi
255	40	44.9	364	2	Q95KX0_MACPA	095kx0 macaca fasc	328	39	43.8	221	2	Q9CAP3_ARATH	Q9CAP3 arabidopsis
256	40	44.9	366	1	AROC_SILPO	Q51xk0 silicibacte	329	39	43.8	226	2	Q58M09_9CAUD	Q58M09 cyanophaga
257	40	44.9	376	2	Q4W9X0_ASFPV	Q4W9X0 aspergillus	330	39	43.8	235	2	Q4PQF3_9GAMM	Q4PQF3 psychrobact
258	40	44.9	381	2	Q4N1F9_THIEPA	Q4N1f9 theileria p	331	39	43.8	235	2	Q8L964_ARATH	Q8L964 arabidopsis
259	40	44.9	388	2	Q4HMO3_GIBZE	Q4HMO3 gibberella	332	39	43.8	235	2	Q9FMC5_ARATH	Q9FMC5 arabidopsis
260	40	44.9	392	2	Q6FPX9_CANGA	Q6fpdx candida gla	333	39	43.8	235	2	Q9LPM5_ARATH	Q9LPM5 arabidopsis
261	40	44.9	401	2	Q4XRY7_PLACH	Q4xry7 plasmodium	334	39	43.8	235	2	Q31789_BACSU	Q31789 bacillus su
262	40	44.9	414	1	HISX_STAPB	08cg95 staphylococ	335	39	43.8	235	2	Q8PNZ0_XANAC	Q8PNZ0 xanthomonas
263	40	44.9	414	2	Q5HKN8_STAEQ	Q5hkn8 staphylococ	336	39	43.8	236	1	YAGV_ECOLI	P77263 escherichia
264	40	44.9	425	2	Q4UG11_THIEPA	Q4ug11 theileria a	337	39	43.8	242	2	Q5LC69_BACRN	Q5LC69 bacteroides
265	40	44.9	425	2	Q4N974_THIEPA	Q4N974 theileria p	338	39	43.8	242	2	Q9KEZ0_BACDH	Q9KEZ0 bacteroides
266	40	44.9	458	2	Q4Z3F9_PLABE	Q4z3f9 plasmodium	339	39	43.8	247	2	Q4YU12_PLABE	Q4YU12 plasmodium
267	40	44.9	481	2	Q91WT3_MOUSE	Q91wt3 mus musculu	340	39	43.8	248	2	Q8RBP6_THIEPA	Q8RBP6 thermoaer
268	40	44.9	487	2	Q7QIC1_ANOGA	Q7qic1 anopheles g	341	39	43.8	251	2	Q5PXN5_VIBCH	Q5PXN5 vibrio chol
269	40	44.9	492	2	Q74HL3_LACJO	Q74hl3 lactobacilli	342	39	43.8	251	2	Q8CWC2_ECOLI	Q8CWC2 escherichia
270	40	44.9	499	1	C77AI_SOLME	P37123 solanum mel	343	39	43.8	251	2	Q8XG16_ECOLI	Q8XG16 escherichia
271	40	44.9	512	2	Q5UEW6_9PROT	Q5uew6 uncultured	344	39	43.8	258	2	Q6CA02_YARLI	Q6CA02 yarrowia li
272	40	44.9	527	2	Q22770_CABER	Q22770 caenorhabdi	345	39	43.8	275	1	HEMK_BUCAP	Q8K9u9 buchnera ap
273	40	44.9	534	2	Q618A4_CABER	Q618a4 caenorhabdi	346	39	43.8	277	2	Q61074_TRYBR	Q61074 trypanosoma
274	40	44.9	562	2	Q9ZHH9_9BURK	Q9zhh9 burkholderi	347	39	43.8	277	2	Q57UX1_9TRYB	Q57UX1 trypanosoma
275	40	44.9	572	2	Q6B1D1_DEBHA	Q6b1d1 debaryomyce	348	39	43.8	277	2	Q9XWG0_CABER	Q9XWG0 caenorhabdi
276	40	44.9	579	1	YHVO_YEAST	Q81848 saccharomyc	349	39	43.8	283	2	Q9P7B5_SCHPO	Q9P7B5 schizosach
277	40	44.9	589	2	Q81BBS_PLAF7	Q81bbs plasmodium	350	39	43.8	287	1	Y01L_MYCCE	P47257 mycoplasma
278	40	44.9	616	2	Q5O4M7_MOUSE	Q5o4m7 mus musculu	351	39	43.8	289	2	Q7P543_RHIL0	Q7P543 rhizobium l
279	40	44.9	650	2	Q7R2P9_PLAYO	Q7r2p9 plasmodium	352	39	43.8	298	2	Q7P543_RHIL0	Q7P543 rhizobium l
280	40	44.9	669	2	Q41379_GIBZE	Q41379 gibberella	353	39	43.8	300	2	Q6FLB5_CANGA	Q6FLB5 candida gla
281	40	44.9	674	2	Q516M6_ENTHI	Q516m6 entamoeba h	354	39	43.8	305	2	Q4Y0X5_PLACH	Q4Y0X5 plasmodium
282	40	44.9	697	2	Q7NDN5_GLOVI	Q7ndn5 glioneobacter	355	39	43.8	317	2	Q6MB36_PARDW	Q6MB36 parachlamyd
283	40	44.9	737	2	Q4IMY1_GIBZE	Q4imyl gibberella	356	39	43.8	327	2	Q4IDC9_GIBZE	Q4IDC9 gibberella
284	40	44.9	746	2	Q8R3B2_MOUSE	Q8r3b2 mus musculu	357	39	43.8	331	2	Q82KS2_STRAW	Q82ks2 streptomyce
285	40	44.9	746	2	Q8C106_MOUSE	Q8c106 mus musculu	358	39	43.8	337	2	Q6MW91_NEUCR	Q6mw91 neurospora
286	40	44.9	754	1	PUB3_CANAL	Q9wvx1 candida alb	359	39	43.8	340	2	Q7QV09_GIADA	Q7QV09 giardia lam
287	40	44.9	754	2	Q5A760_CANAL	Q5a760 candida alb	360	39	43.8	344	2	Q8KGF5_CHLYE	Q8KGF5 chloretobium
288	40	44.9	754	2	Q5A7D5_CANAL	Q5a7d5 candida alb	361	39	43.8	349	2	Q97KP9_CLOAB	Q97kp9 clostridium
289	40	44.9	802	2	Q42810_EMENT	Q42810 emeritocella	362	39	43.8	350	1	ADH_SCHPO	P00332 schizosach
290	40	44.9	804	2	Q98562_CHVP1	Q98562 paramoecium	363	39	43.8	353	2	Q7SG68_NEUCR	Q7SG68 neurospora
291	40	44.9	879	2	Q89ZM4_BACTN	Q89zm4 bacteroides	364	39	43.8	357	1	AROC_HAEIN	P43875 haemophilus
292	40	44.9	883	2	Q54R11_DICDI	Q54r11 dictyosteli	365	39	43.8	357	1	AROC_PASMU	P57840 pasteurilla
293	40	44.9	987	2	Q7RCW6_PLAYO	Q7rcw6 plasmodium	366	39	43.8	357	2	Q4QNZ4_HAE18	Q4QNZ4 haemophilus
294	40	44.9	1016	2	Q8LHW9_ORYSA	Q8lhw9 oryza sativ	367	39	43.8	360	1	AROC_GLTOX	Q5fnp9 gluconobact
295	40	44.9	1183	2	Q5B516_EMENT	Q5b516 aspergillus	368	39	43.8	361	1	AROC_PHOPR	Q5lnt4 photobacter
296	40	44.9	1340	2	Q88CDG9_MOUSE	Q88cdg9 mus musculu	369	39	43.8	361	1	AROC_VIBAN	P919t8 vibrio angu
297	40	44.9	2456	2	Q81MG2_PLAF7	Q81mg2 plasmodium	370	39	43.8	361	1	AROC_VIBCH	Q9kgd5 vibrio chol
298	40	44.9	5561	2	Q81BH6_PLAF7	Q81bh6 plasmodium	371	39	43.8	361	1	AROC_VIBF1	Q87m9 vibrio fisc
299	39.5	44.4	120	2	Q920B8_MOUSE	Q920b8 mus musculu	372	39	43.8	361	1	AROC_VIBPA	Q87m9 vibrio para
300	39.5	44.4	415	1	CBP1_RAT	P19223 rattus norv	373	39	43.8	361	1	AROC_VIBVU	Q8dbt2 vibrio vuln
301	39.5	44.4	423	2	Q8LJ26_9CAUD	Q8lj26 virus phich	374	39	43.8	361	1	AROC_VIBVU	Q8dbt2 vibrio vuln
302	39.5	44.4	461	2	Q982U6_RHIL0	Q982u6 rhizobium l	375	39	43.8	368	2	Q5MSK3_LEGEL	Q4xx18 legionella
303	39.5	44.4	482	2	Q6M988_NEUCR	Q6m988 neurospora	376	39	43.8	373	2	Q4XX18_PLACH	Q4xx18 arabidopsis
304	39.5	44.4	503	2	TCPT_VIBCH	P29480 vibrio chol	377	39	43.8	376	2	Q9M169_ARATH	Q9m169 arabidopsis
305	39.5	44.4	503	2	Q93TTC3_VIBCH	Q93tct3 vibrio chol	378	39	43.8	403	2	Q93YV2_ARATH	Q93yv2 arabidopsis
306	39.5	44.4	503	2	Q7BGC2_VIBCH	Q7bgc2 vibrio chol	379	39	43.8	411	2	Q84573_CHVP1	Q84573 paramoecium
307	39.5	44.4	1439	2	Q7RZ95_NEUCR	Q7rzs5 neurospora	380	39	43.8	415	2	Q5HUX8_CAMJR	Q5hux8 campylobact
308	39	43.8	114	2	Q7AR87_CAMUR	Q7ar87 campylobact	381	39	43.8	415	2	Q6DHN4_BRAMB	Q6dhn4 brachydanio
309	39	43.8	120	1	HV50_MOUSE	P06332 mus musculu	382	39	43.8	423	2	Q4HTB4_CAMCO	Q4htb4 campylobact
310	39	43.8	140	2	Q924P8_MOUSE	Q924p8 mus musculu	383	39	43.8	426	2	Q7AR89_CAMJR	Q7ar89 campylobact
311	39	43.8	142	2	Q924Q1_MOUSE	Q924q1 mus musculu	384	39	43.8	428	2	Q5HVL1_CAMJR	Q5hvl1 campylobact
312	39	43.8	150	2	Q4YF83_PLABE	Q4yf83 plasmodium	385	39	43.8	430	2	Q7AR92_CAMJR	Q7ar92 campylobact
313	39	43.8	159	2	Q96Q80_HUMAN	Q96q80 homo sapien	386	39	43.8	434	2	Q5HUZ8_CAMJR	Q5huz8 campylobact
314	39	43.8	160	2	Q4VIV6_BACCC	Q4vive bacillus ce	387	39	43.8	440	2	Q9LGI4_ARATH	Q9lgi4 arabidopsis
315	39	43.8	171	2	Q651B5_ASF	Q651b5 ascaris swi	388	39	43.8	444	2	Q4HTB3_CAMCO	Q4htb3 campylobact
316	39	43.8	172	2	Q5GMR8_XANOR	Q5gmr8 xanthomonas	389	39	43.8	461	2	Q5AZI4_EMENT	Q5azi4 aspergillus
317	39	43.8	178	2	Q7SEB7_ASHGO	Q7seb7 ashbya goss	390	39	43.8	463	2	Q8LAN7_ARATH	Q8lan7 arabidopsis
318	39	43.8	179	2	Q9Q8W3_9POXY	Q9q8w3 rabbit fibr	391	39	43.8	463	2	Q9FTD2_ARATH	Q9ftd2 arabidopsis
319	39	43.8	181	2	Q57TN2_SALCH	Q57tn2 salmonella	392	39	43.8	466	2	Q8MRTO_DROME	Q8mrto drosophila
320	39	43.8	181	2	Q5PDJ8_SALPA	Q5pdj8 salmonella	393	39	43.8	469	2	Q9FLD6_ARATH	Q9fld6 arabidopsis
321	39	43.8	181	2	Q8Z9P9_SALTI	Q8z9p9 salmonella	394	39	43.8	488	2	Q8DS19_VIBVU	Q8ds19 vibrio vuln
322	39	43.8	181	2	Q9X607_SALTY	Q9x607 salmonella	395	39	43.8	488	2	Q7MBV2_VIBVU	Q7mbv2 vibrio vuln
323	39	43.8	188	2	Q83655_9POXY	Q83655 myxoma viru	396	39	43.8	489	2	Q6S114_9BACT	Q6s114 uncultured

835	37	41.6	274	2	O50FY8_CAMJUE	O50FY8_campylobact	908	37	41.6	428	2	O8TLJ2_METAC	O8TLJ2_methanosarc
836	37	41.6	276	2	O5UF08_9PROT	O5UF08_uncultured	909	37	41.6	428	2	O8TWC5_METAC	O8TWC5_methanosarc
837	37	41.6	278	1	ATG5_CANAL	O5YV1_candida alb	910	37	41.6	428	2	O8TMS5_METAC	O8TMS5_methanosarc
838	37	41.6	279	1	EFPS_BORCA	O6E2P0_borrelia ga	911	37	41.6	428	2	O8TNA0_METAC	O8TNA0_methanosarc
839	37	41.6	279	1	O96990_MANSE	O96990_manduca sex	912	37	41.6	428	2	O8TNP1_METAC	O8TNP1_methanosarc
840	37	41.6	279	2	O96991_MANSE	O96991_manduca sex	913	37	41.6	428	2	O8TTP7_METAC	O8TTP7_methanosarc
841	37	41.6	291	2	O97DJ3_CIOAB	O97DJ3_clostridium	914	37	41.6	428	2	O8TUH2_METAC	O8TUH2_methanosarc
842	37	41.6	293	2	O9AQO4_9PSED	O9AQO4_pseudomonas	915	37	41.6	432	1	YADA_YERPS	O43A2_CIOIN
843	37	41.6	295	2	O5NTR8_9BACT	O5NTR8_uncultured	916	37	41.6	439	2	O4H3A2_CIOIN	O97A18_THEVO
844	37	41.6	296	2	O4TRR8_98PHN	O4TRR8_erythrobact	917	37	41.6	444	2	O533R6_DICD1	O533R6_dicyosteli
845	37	41.6	299	2	O67AX9_STRAG	O67AX9_streptococc	918	37	41.6	444	2	O67580_AOUAE	O67580_aquilex aeo
846	37	41.6	299	2	O6GGI8_STRAR	O6GGI8_staphylococ	919	37	41.6	444	2	O6L0G7_PIC10	O6L0G7_picrophilus
847	37	41.6	305	2	O5DCK4_SCHJA	O5DCK4_schistosoma	920	37	41.6	450	2	O4Y251_PLACH	O4Y251_anopheles g
848	37	41.6	305	2	O7YXB1_SCHJA	O7YXB1_schistosoma	921	37	41.6	452	2	O700V4_AMOGA	O700V4_anopheles g
849	37	41.6	308	2	O5CTIO_CRYPV	O5CTIO_cryptospori	922	37	41.6	461	2	O783B9_VYIRU	O783B9_bacterioph
850	37	41.6	308	2	O5CKI3_CRYHO	O5CKI3_cryptospori	923	37	41.6	461	2	O9MBV9_VYIRU	O9MBV9_bacterioph
851	37	41.6	309	2	O6D0F7_ERWCT	O6D0F7_erwinia car	924	37	41.6	461	2	O9KGQ7_VIBPA	O9KGQ7_vibrioto para
852	37	41.6	319	1	PA1_SERLI	PA1952_serratia li	925	37	41.6	461	2	O4H873_9DEIO	O4H873_deinococcus
853	37	41.6	320	2	O700G4_USTMA	O700G4_ustilago ma	926	37	41.6	462	2	O4Z2P4_PLABE	O4Z2P4_plasmodium
854	37	41.6	320	2	O700G6_USTMA	O700G6_ustilago ma	927	37	41.6	469	2	O5FVP3_RAT	O5FVP3_rattus norv
855	37	41.6	320	2	O700G8_USTMA	O700G8_ustilago ma	928	37	41.6	475	2	O528I3_ORYGA	O528I3_oryza sativ
856	37	41.6	320	2	O700I5_USTMA	O700I5_ustilago ma	929	37	41.6	484	2	SYC_HELHP	SYC_HELHP
857	37	41.6	320	2	O700K7_USTMA	O700K7_ustilago ma	930	37	41.6	488	1	O5FIF6_LACAC	O5FIF6_lactobacilli
858	37	41.6	320	2	O8RKT9_SERMA	O8RKT9_serratia ma	931	37	41.6	493	2	O61XP3_CAEBR	O61XP3_caenorhabdi
859	37	41.6	320	2	O9X9D8_9ENTR	O9X9D8_serratia sp	932	37	41.6	495	2	O6BUV5_DEBHA	O6BUV5_debaryomyce
860	37	41.6	323	2	O6BNF1_DEBHA	O6BNF1_debaryomyce	933	37	41.6	498	2	O700D7_ARATH	O700D7_arabidopsis
861	37	41.6	326	2	O7JN08_FASHE	O7JN08_fasciola he	934	37	41.6	499	2	O5JDX0_PYRRO	O5JDX0_pyrococcus
862	37	41.6	328	2	O5B451_EMENT	O5B451_aspergillus	935	37	41.6	502	2	O4FNP2_PRIKC	O4FNP2_penicillati
863	37	41.6	328	2	O5ZP63_VYIRU	O5ZP63_cotesia con	936	37	41.6	508	2	O7X5W0_9BACL	O7X5W0_9bacill
864	37	41.6	334	2	O40686_ORYSA	O40686_oryza sativ	937	37	41.6	518	2	O9S0U9_ARATH	O9S0U9_arabidopsis
865	37	41.6	335	1	EBA2_FLAME	PA3612_flavobacter	938	37	41.6	520	2	O4Z0Y7_PLABE	O4Z0Y7_plasmodium
866	37	41.6	335	1	O8U2L6_PYRFU	O8U2L6_pyrococcus	939	37	41.6	524	2	O5LFP2_BACPN	O5LFP2_bacteroides
867	37	41.6	335	2	O9WX57_THEMA	O9WX57_thermotoga	940	37	41.6	524	2	O8A7M4_BACPN	O8A7M4_bacteroides
868	37	41.6	341	2	O4XGR2_PLACH	O4XGR2_plasmodium	941	37	41.6	524	2	O64W24_BACPN	O64W24_bacteroides
869	37	41.6	343	2	O6H1Y5_BACHK	O6H1Y5_bacillus th	942	37	41.6	524	2	O5HUD5_CAMDR	O5HUD5_campylobact
870	37	41.6	352	2	O51WAS_MAGGR	O51WAS_magnaporthe	943	37	41.6	529	2	O64Y51_BACPN	O64Y51_bacteroides
871	37	41.6	353	1	ADH1_NEUCR	O9P6C6_neurospora	944	37	41.6	533	2	O9BI47_CAEBL	O9BI47_caenorhabdi
872	37	41.6	353	1	O9TE69_9ESTRA	O9TE69_fragilari	945	37	41.6	534	2	O61B03_CAEBL	O61B03_caenorhabdi
873	37	41.6	354	1	AROC_DESVH	O7D5D5_dentulfovibr	946	37	41.6	534	2	O6A5D8_PROAC	O6A5D8_propionibac
874	37	41.6	354	2	O59257_9BACT	O59257_bacillus sp	947	37	41.6	548	2	O517H5_ENTH1	O517H5_entamoeba h
875	37	41.6	354	2	O9RC94_9BACT	O9RC94_bacillus sp	948	37	41.6	548	2	O4RWL6_TETNG	O4RWL6_tetradodon n
876	37	41.6	355	2	O8U7L7_AGRST	O8U7L7_agrobacteri	949	37	41.6	551	2	O620G9_CAEBR	O620G9_caenorhabdi
877	37	41.6	376	2	O5AT21_EMENT	O5AT21_aspergillus	950	37	41.6	552	2	O54S86_DICD1	O54S86_dicyosteli
878	37	41.6	380	1	NUP43_MOUSE	P59235_mus musculu	951	37	41.6	552	2	O4HVJ1_GIBBE	O4HVJ1_glibberella
879	37	41.6	386	2	O825P2_STRAW	O825P2_streptococc	952	37	41.6	553	2	O6CYA4_KLULA	O6CYA4_kluyveromyc
880	37	41.6	387	2	O86S90_9CELL	O86S90_epiditium c	953	37	41.6	560	2	O5FRD3_GLUDK	O5FRD3_gluconobact
881	37	41.6	391	2	O6CKW0_KLULA	O6CKW0_kluyveromyc	954	37	41.6	560	2	O88N04_PSEBK	O88N04_pseudomonas
882	37	41.6	391	2	O4L332_STAHJ	O4L332_staphylococ	955	37	41.6	562	2	O67IY3_ORYGA	O67IY3_oryza sativ
883	37	41.6	392	2	O97M90_CIOAB	O97M90_clostridium	956	37	41.6	564	2	O51BAS_ENTH1	O51BAS_entamoeba h
884	37	41.6	393	2	O4I749_GIBZE	O4I749_gibberella	957	37	41.6	564	2	O8R203_MOUSE	O8R203_mus musculu
885	37	41.6	393	2	O9C8M6_ARATH	O9C8M6_arabidopsis	958	37	41.6	566	2	O75Z05_HALVA	O75Z05_haloarcula
886	37	41.6	396	2	O8TH43_METAC	O8TH43_methanosarc	959	37	41.6	568	2	O7PDW4_PLAYO	O7PDW4_plasmodium
887	37	41.6	404	2	O99118_USTMA	O99118_ustilago ma	960	37	41.6	568	2	O5CDV6_MOUSE	O5CDV6_mus musculu
888	37	41.6	406	2	O51B78_ENTH1	O51B78_entamoeba h	961	37	41.6	568	2	O90491_BRAPR	O90491_brachydanio
889	37	41.6	408	2	O6CWO1_KLULA	O6CWO1_kluyveromyc	962	37	41.6	583	2	O73UC5_MYCPA	O73UC5_mycoabacteri
890	37	41.6	415	2	O6EHz6_TRIVA	O6EHz6_trichomonas	963	37	41.6	584	2	O6FAR3_ACINAD	O6FAR3_acinetobact
891	37	41.6	415	2	O8EAP8_SHEON	O8EAP8_sheanella	964	37	41.6	590	2	O7RZR3_NEUCR	O7RZR3_neurospora
892	37	41.6	416	1	HISX_STAM	P63952_staphylococ	965	37	41.6	590	2	O53370_MYCBO	O53370_m_probable
893	37	41.6	416	1	HISX_STAM	P63953_staphylococ	966	37	41.6	601	2	O510D4_ENTH1	O510D4_entamoeba h
894	37	41.6	416	1	HISX_STAM	P63954_staphylococ	967	37	41.6	602	2	O8LSZ5_PHYPA	O8LSZ5_physcomitire
895	37	41.6	416	1	HISX_STAM	O6G956_staphylococ	968	37	41.6	615	2	O6F259_MESP	O6F259_mesoplasma
896	37	41.6	418	1	HISX_STAM	O6G527_staphylococ	969	37	41.6	616	2	O6FAR3_ACINAD	O6FAR3_acinetobact
897	37	41.6	418	1	OSHC19_STRAC	O5HC19_staphylococ	970	37	41.6	627	2	O6C136_YARUT	O6C136_yarrowia li
898	37	41.6	418	2	O7RGER_PLAYO	O7RGER_plasmodium	971	37	41.6	640	2	O5M4P5_STR12	O5M4P5_strptococc
899	37	41.6	421	2	O74N30_NANEQ	O74N30_nanoarchaeu	972	37	41.6	642	1	YBBD_BACSU	YBBD_bacillus su
900	37	41.6	423	2	O6LNZ1_PHOPR	O6LNZ1_photobacter	973	37	41.6	642	1	O5M030_STR11	O5M030_streptococc
901	37	41.6	424	2	O6D4P1_ERWCT	O6D4P1_erwinia car	974	37	41.6	646	2	O61WM6_CAEBR	O61WM6_caenorhabdi
902	37	41.6	428	2	O4J908_SULAC	O4J908_sulfolobus	975	37	41.6	663	2	O6BPE9_DEBHA	O6BPE9_debaryomyce
903	37	41.6	428	2	O8TH34_METAC	O8TH34_methanosarc	976	37	41.6	667	2	BPL1_YEAST	BPL1_yeast
904	37	41.6	428	2	O8TH34_METAC	O8TH34_methanosarc	977	37	41.6	690	1	O92CT4_LISTIN	O92CT4_listeria in
905	37	41.6	428	2	O8TH35_METAC	O8TH35_methanosarc	978	37	41.6	696	2	O6LNT9_PHOPR	O6LNT9_photobacter
906	37	41.6	428	2	O8TH50_METAC	O8TH50_methanosarc	979	37	41.6	701	2	O5AZK9_EMENT	O5AZK9_ement
907	37	41.6	428	2	O8TIL4_METAC	O8TIL4_methanosarc	980	37	41.6				

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981 37 41.6 709 2 Q4HZP6_GIBZE
982 37 41.6 715 1 PTA_BUCBP
983 37 41.6 718 2 Q5LGP0_BACFN
984 37 41.6 739 2 Q64X15_BACFR
985 37 41.6 754 2 Q04332_ARATH
986 37 41.6 758 1 YP58_YEAST
987 37 41.6 769 2 Q59R40_CANAL
988 37 41.6 769 2 Q4QIX5_LEIMA
989 37 41.6 777 2 Q5TD33_HUMAN
990 37 41.6 787 2 Q43162_HUMAN
991 37 41.6 792 2 Q8TEP4_HUMAN
992 37 41.6 792 2 Q7NNR7_GLOVI
993 37 41.6 803 2 Q82VTR6_NITRU
994 37 41.6 805 2 Q4WBR3_ASPPU
995 37 41.6 807 2 Q8PVS7_METMA
996 37 41.6 816 2 Q6P3R3_HUMAN
997 37 41.6 817 2 Q7YY28_CRYPV
998 37 41.6 820 2 Q9SXB4_ARATH
999 37 41.6 820 2 Q9SXB5_ARATH
1000 37 41.6 852 2 Q6KZM2_PICCTO

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ALIGNMENTS

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RESULT 1
05F211_MOUSE PRELIMINARY; PRT; 120 AA.
ID 05F211_MOUSE PRELIMINARY;
AC 05F211;
DT 10-MAY-2005 (TREMBlrel. 30, Created)
DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)
DE Gamma heavy chain variable region (Fragment).
GN Name=IgG1 anti-TSI VH;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Erlanson A.; Holm P., Ullen A., Stigbrand T., Sundstrom B.E.;
RT "Studies of the interactions between the anticytokeratin 8 monoclonal
antibody TSI, its antigen and its anti-idiotypic antibody alphaTS1.";
RL J. Mol. Recognit. 16:157-163(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Erlanson A.;
RT Submitted (FAB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ884574; CA156336.1; -, mRNA.
DR InterPro; IPR003599; Ig_v.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG LIKE; 1.
FT NON_TER 1
FT NON_TER 120
SQ SEQUENCE 120 AA; 13087 MW; 4A6013141AB87BE2 CRC64;
Query Match 80.9%; Score 72; DB 2; Length 120;
Best Local Similarity 81.2%; Pred. No. 0.00037;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 IYGNDDISYNQKFXG 17
Db 51 IYGNDDISYNQKFXG 66

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AC 065ZL2;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE FV/M4.
GN Name=M4-IFN- $\epsilon$ tau>;
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96272580; Pubmed=8688499;
RA Qi Y., Xiang J.;
RT "A genetically engineered single-gene-encoded anti-TRG2 chimeric
antibody secreted from myeloma cells."
RL Hum. Antibodies Hybridomas 6:161-166(1995).
DR EMBL; S82493; AAB37424.2; -, mRNA.
DR GO; GO:0003823; F:antigen binding; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGC1; 2.
DR SMART; SM00408; IGC2; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PSS0835; IG LIKE; 4.
DR PROSITE; PSS00290; IG_MHC; 1.
SQ SEQUENCE 487 AA; 53578 MW; C7BAB69F30555504 CRC64;

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Query Match 76.4%; Score 68; DB 2; Length 487;
Best Local Similarity 75.0%; Pred. No. 0.0089;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 2 IYGNDDISYNQKFXG 17
Db 70 IYGNDDISYNQKFXG 85

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RESULT 3

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05B022_RAT PRELIMINARY; PRT; 458 AA.
ID 05B022_RAT PRELIMINARY;
AC 05B022;
DT 10-MAY-2005 (TREMBlrel. 30, Created)
DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)
DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)
DE LOC367586 protein.
GN Name=LOC367586;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Thymus;
RX MEDLINE=22388257; Pubmed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Heien F.,
RA Diatchenko L., Matrusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.U., McKernan K.J., Malek J.A., Gunnarane P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Hultk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

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RA Fahay J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield J.S.N., Krzywinski M.I., Skalska U., Stailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Maira M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Thymus;
RG NIH GGC Project;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Beta-2-microglobulin is the beta-chain of major
CC histocompatibility complex class I molecules (by similarity).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
DR EMBL; BC091272; AA091272.1; -; mRNA.
DR SMR; Q5B722; 21-454.
DR InterPro; IPR003599; 19.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGcl; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
KW Immunoglobulin domain; Repeat.
SQ SEQUENCE 458 AA; 50161 MW; A0A61DCDD2CA433E CRC64;

Query Match 70.8%; Score 63; DB 2; Length 458;
Best Local Similarity 68.8%; Pred. No. 0.06;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 2 IYPGNDISYNQKFXG 17
Db 70 IYPGNGTKYKQKFG 85
|||||:|||||
| | | | |

RESULT 4
O921C4_MOUSE PRELIMINARY; PRT; 118 AA.
ID O921C4_MOUSE PRELIMINARY; PRT; 118 AA.
AC O921C4;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anti-porcine VCAM mAb 3F4 heavy chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Balb/c;
RX MEDLINE=97450619; PubMed=9307060; DOI=10.1016/S0161-5890(97)00042-4;
RA Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
RA Matris L.A., Evans M.J.,
RT "Humanized porcine VCAM-specific monoclonal antibodies with chimeric
RT IgG2/G4 constant regions block human leukocyte binding to porcine
RT endothelial cells.";
RL Mol. Immunol. 34:441-452(1997).
DR EMBL; U78801; AAD00293.1; -; mRNA.
DR HSSP; P01751; INOB.
DR SMR; O921C4; 1-118.
DR Ensembl; ENSMUSG0000021155; Mus musculus.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1 1
FT 118 118

SQ SEQUENCE 118 AA; 13036 MW; 90EECE59D31EC4FC CRC64;

Query Match 68.5%; Score 61; DB 2; Length 118;
Best Local Similarity 68.8%; Pred. No. 0.026;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 2 IYPGNDISYNQKFXG 17
Db 51 IYPGNDISYNQKFXG 66
|||||:|||||
| | | | |

RESULT 5
O9D9B8_MOUSE PRELIMINARY; PRT; 111 AA.
ID O9D9B8_MOUSE PRELIMINARY; PRT; 111 AA.
AC O9D9B8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mus musculus adult male testis cDNA, RIKEN full-length enriched
DE library, clone:1700110L11 product:immunoglobulin heavy chain 6 (heavy
DE chain of IGM), full insert sequence.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.,
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
[2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aizawa T., Hara A., Fukunishi Y., Kondo H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Cavaant T.,
RA Fleschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Maceno Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Strubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Kono H., Baldarelli R., Barsh G.,
RA Blake J., Botfield D., Boujona N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombere P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Saeki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsank S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
[4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez R.A., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6NCR; TISSUE=Hematopoietic Stem Cell;
 RG NIH WGC Project;
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC092271; AA092271.1; -; mRNA.
 DR SMR; MG196443; Igh-1a.
 DR GO; GO:0003823; F:antigen binding; IEA.
 DR InterPro; IPR003599; IG_1.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003597; IG_C1.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF07654; C1-set; 3.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGc1; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 KM Hypothetical protein.
 SQ SEQUENCE 468 AA; 51666 MW; 5BF6E527329F8461 CRC64;
 Query Match 62.9%; Score 56; DB 2; Length 468;
 Best Local Similarity 62.5%; Pred. No. 0.98;
 Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 QY 2 IYPGNDISTYNOXFXG 17
 Db 70 IYFGNGYTYENKFXG 85
 RESULT 8
 Q7MT6 MOUSE PRELIMINARY; PRT; 614 AA.
 ID Q7MT6 MOUSE PRELIMINARY; PRT; 614 AA.
 AC Q7MT6;
 DT 01-OCT-2003 (Tremblrel. 25, Created)
 DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
 DE MG60843 protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6NCR; TISSUE=Hematopoietic Stem Cell;
 RG MEDLINE=32388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Tishiyuki S., Carrano R.D., Mullaly S.J.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez R.A., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6NCR; TISSUE=Hematopoietic Stem Cell;
 RG Strausberg R.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC053409; AA053409.1; -; mRNA.
 DR HSSP; P01820; IGJ.
 DR Ensembl; ENSMUSG0000054328; Mus musculus.
 DR GO; GO:0003823; F:antigen binding; IEA.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003597; IG_C1.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF07654; C1-set; 4.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 5.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
 KM Immunoglobulin domain.
 SQ SEQUENCE 614 AA; 67747 MW; 839BAF3B8D124F89 CRC64;
 Query Match 62.9%; Score 56; DB 2; Length 614;
 Best Local Similarity 56.2%; Pred. No. 1.3;
 Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 2 IYPGNDISTYNOXFXG 17
 Db 70 IYFGDGDGTNYNGKFXG 85
 RESULT 9
 Q7PE3 MOUSE PRELIMINARY; PRT; 136 AA.
 ID Q7PE3 MOUSE PRELIMINARY; PRT; 136 AA.
 AC Q7PE3;
 DT 01-OCT-2003 (Tremblrel. 25, Created)
 DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
 DE V23-D-J-IgG1 protein (Fragment).
 GN Name=V23-D-J-IgG1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6;
 RA Kozono Y., Kozono H., Azuma T.,
 RA "The higher density hapten Ag stimulates strong signal to B cells.";
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB069864; BAC54573.1; -; mRNA.
 DR HSSP; P01751; IAGV.
 DR SMR; Q7PE3; 1-136.
 DR Ensembl; ENSMUSG00000021155; Mus musculus.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003596; IG_V.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 136 AA; 14682 MW; 99392B1A31F663AF CRC64;
 Query Match 61.8%; Score 55; DB 2; Length 136;
 Best Local Similarity 64.3%; Pred. No. 0.36;

Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IYPGNDISYNOKR 15
 Db 48 IYPSNGDTYNEKRF 61

RESULT 10
 Q91WT1_MOUSE PRELIMINARY; PRT; 481 AA.
 ID Q91WT1_MOUSE PRELIMINARY; PRT; 481 AA.
 AC Q91WT1;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Igh-VJ558 protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 (1)
 NCLEOTIDE SEQUENCE.
 RC STRAIN=FVB/N; TISSUE=Colon;
 RX MEDLINE=2338257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshlyuk S., Carrincci P., Prange C.,
 RA Raha S.S., Loguigliano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Pheby J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.C., Krzywinski M.I., Skalska U., Smalls D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP NCLEOTIDE SEQUENCE.
 RC STRAIN=FVB/N; TISSUE=Colon;
 RA Strauberg R.;
 RL Submitted (SBP-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL; BC013490; AAH13490.1; -, mRNA.
 DR HSP; P01751; IAGW.
 DR Ensemble; ENSMUSG00000021155; Mus musculus.
 DR GO; GO:0003823; F:antigen binding; IEA.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG-CL.
 DR InterPro; IPR003006; IG-MHC.
 DR InterPro; IPR003596; IG-V.
 DR InterPro; IPR003596; IG-V.
 DR Pfam; PF07654; CI-sec; 2.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 4.
 DR PROSITE; PS00290; IG-MHC; UNKNOWN_2.
 KW Immunoglobulin domain.
 SQ SEQUENCE 481 AA; 52105 MW; 97DF68D159463F65 CRC64;

Query Match 61.8%; Score 55; DB 2; Length 481;
 Best Local Similarity 56.2%; Pred. No. 1.5;
 Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 IYPGNDISYNOKRFXG 17
 Db 70 IYPGDGNTRKYNKFXG 85

RESULT 11
 Q9JL83_MOUSE PRELIMINARY; PRT; 110 AA.
 ID Q9JL83_MOUSE PRELIMINARY; PRT; 110 AA.
 AC Q9JL83;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 25, Last annotation update)
 DE Anti-myosin immunoglobulin heavy chain variable region
 DE (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 (1)
 NCLEOTIDE SEQUENCE.
 RC STRAIN=BALB/c;
 RX MEDLINE=20448942; PubMed=10992488;
 RX DOI=10.1128/JAI.68.10.5803-5808.2000;
 RA Malkiel S., Liao L., Cunningham M.W., Diamond B.,
 RT "T-cell-dependent antibody response to the dominant epitope of
 RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
 RT with cardiac myosin.";
 RL Infect. Immun. 68:5803-5808 (2000).
 DR EMBL; AF206023; AAF69321.1; -, mRNA.
 DR HSP; P01751; INOB.
 DR SMR; Q9JL83; 1-110.
 DR Ensemble; ENSMUSG00000063520; Mus musculus.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG-V.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 110 AA; 12052 MW; 84E672AD219AF95E CRC64;

Query Match 60.7%; Score 54; DB 2; Length 110;
 Best Local Similarity 62.5%; Pred. No. 0.42;
 Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 IYPGNDISYNOKRFXG 17
 Db 43 IYPGDGDVAYYNGKFXG 58

RESULT 12
 HV06_MOUSE STANDARD; PRT; 117 AA.
 ID HV06_MOUSE STANDARD; PRT; 117 AA.
 AC P01750;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Ig heavy chain V region 102 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 (1)
 NCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6;
 RX MEDLINE=81234548; PubMed=6788376; DOI=10.1016/0092-8674(81)90089-1;
 RA Botwell A.L.M., Paekkind M., Reth M., Imanishi-Kari T., Rajewsky K.,
 RA Baltimore D.,
 RT "Heavy chain variable region contribution to the Npb family of
 RT antibodies: somatic mutation evident in a gamma 2a variable region.";
 RL Cell 24:625-637 (1981).
 CC -I- MISCRLANEOUS: This germline gene belongs to a set of closely
 CC related genes that could encode V regions of Npb antibodies.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its

CC use as long as its content is in no way modified and this statement is not
 CC removed.

DR PIR; A02032; HWM502.

DR PDB; 1QNZ; NMR; H=21-117.

DR Ensemble; ENSMUSG0000062849; Mus musculus.

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003596; IG_v.

DR SMART; SM00406; IG_v.1.

DR PROSITE; PS50835; IG-LIKE; 1.

KM 3D-structure; Immunoglobulin domain; Immunoglobulin V region; Signal.

FT SIGNAL 1 19

FT CHAIN 20 117 Ig heavy chain V region 102.

FT REGION 20 49 Framework-1.

FT REGION 50 54 Complementarity-determining-1.

FT REGION 55 68 Framework-2.

FT REGION 69 85 Complementarity-determining-2.

FT REGION 86 117 Framework-3.

FT DISULFID 41 115 By similarity.

FT NON TER 117 117

SEQ SEQUENCE 117 AA; 12867 MW; 740A65DD851FCAC8 CRC64;

Query Match 60.7%; Score 54; DB 1; Length 117;

Best Local Similarity 56.2%; Pred. No. 0.45;

Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 IYRGDDISYKQKFXG 17

Db 70 IHPDSDTNYPKFKG 85

RESULT 13

HV52_MOUSE

ID HV52_MOUSE STANDARD; PRT; 117 AA.

AC P06327;

DT 01-JAN-1988 (Rel. 06, Created)

DT 01-JAN-1988 (Rel. 06, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Ig heavy chain V region VH558 A1/A4 precursor.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Muridae; Murinae; Mus.

NCBI_Taxid=10090;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=85099340; PubMed=2578321; DOI=10.1016/0092-8674(85)90141-2;

RA Yancopoulos G.D., Alt F.W.;

RT "Developmentally controlled and tissue-specific expression of

RT unarranged VH gene segments.";

RL Cell 40:271-281(1985).

CC -----

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use as long as its content is in no way modified and this statement is not

CC removed.

CC -----

DR EMBL; M13787; AAA38499.1; -; mRNA.

DR PIR; A02029; HWM5A1.

DR HSSP; P01820; 1G7J.

DR SMR; P06327; 20-117.

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003596; IG_v.

DR SMART; SM00406; IG_v.1.

DR PROSITE; PS50835; IG-LIKE; 1.

KM Immunoglobulin domain; Immunoglobulin V region; Signal.

FT SIGNAL 1 19

FT CHAIN 20 117 Ig heavy chain V region VH558 A1/A4.

FT REGION 20 49 Framework-1.

FT REGION 50 54 Complementarity-determining-1.

FT REGION 55 68 Framework-2.

FT REGION 69 85 Complementarity-determining-2.

FT REGION 86 117 Framework-3.

FT DISULFID 41 115 By similarity.

FT NON TER 117 117

SEQ SEQUENCE 117 AA; 12971 MW; 8B0BC13856FC9D CRC64;

Query Match 60.7%; Score 54; DB 1; Length 117;

Best Local Similarity 56.2%; Pred. No. 0.45;

Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 IYRGDDISYKQKFXG 17

Db 70 IYPGDGSYKXKFKG 85

RESULT 14

Q9DCD9_MOUSE

ID Q9DCD9_MOUSE PRELIMINARY; PRT; 426 AA.

AC Q9DCD9;

DT 01-JUN-2001 (TREMBLrel. 17, Created)

DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)

DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

DE Mus musculus adult male kidney cDNA, RIKEN full-length enriched

DE library, clone:061004A01 product:Immunoglobulin heavy chain 6 (heavy

DE chain of IgM), full insert sequence.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Muridae; Murinae; Mus.

NCBI_Taxid=10090;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RX STRAIN=C57BL/6J; TISSUE=Kidney; DOI=10.1016/S0076-6879(99)03004-9;

RA MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;

RA Carninci P., Hayashizaki Y.;

RT "High-efficiency full-length cDNA cloning.";

RL Mech. Enzymol. 303:19-44(1999).

CC [2]

CC NUCLEOTIDE SEQUENCE.

RX STRAIN=C57BL/6J; TISSUE=Kidney; DOI=10.1038/35055500;

RA MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

RA Kawai T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Aikawa T., Hara A., Fukunishi Y., Komoto H., Adachi T., Fukuda S.,

RA Aikawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K. I.,

RA Saito T., Okazaki Y., Gotohori T., Bond H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H. A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido T., Pesole G., Quackenbush J.,

RA Schirral L. M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Blake J., Boffelli D., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Brownstein M. J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Guentrich S., Hill D., Hofmann M., Hume D. A., Kaniya M., Lee N. H.,

RA Lyons P., Marchionni L., Mashima Y., Mazzaletti U., Mombaerts P.,

RA Nodone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyooka K., Wang K. H., Weitz C., Whitaker C., Wilting L.,

RA Wyszewski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,

RA Hayashizaki Y.;

RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

CC [3]

CC NUCLEOTIDE SEQUENCE.

RX STRAIN=C57BL/6J; TISSUE=Kidney;

RA The PANTOM Consortium,

RA "The RIKEN Genome Exploration Research Group Phase I & II Team;

RT "Analysis of the mouse transcriptome based on functional annotation of

RL Nature 420:563-573(2002).

CC [4]

CC NUCLEOTIDE SEQUENCE.

RX STRAIN=C57BL/6J; TISSUE=Kidney;

RA MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;

RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,

RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subpartition of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630 (2000).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Kidney; DOI=10.1101/gr.152600;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Kitamura T., Tashiro H., Itoh M.,
 RA Sumi N., Ishi Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanuki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771 (2000).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Kidney;
 RA Aachai J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
 RA Aakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
 RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Horii F.,
 RA Imotani K., Ishi Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
 RA Kawai J., Kojima Y., Kono H., Konda M., Koya S., Kurihara C.,
 RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ono M.,
 RA Okazaki Y., Okido T., Owa C., Saito H., Saito K., Sakai C., Sakai K.,
 RA Sano H., Sasaki D., Shibata K., Shibata Y., Shingawa A., Shiraki T.,
 RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
 RA Teijima Y., Taya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
 RA Muramatsu M., Hayashizaki Y.;
 RT Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=2499887;
 RA Baccala R., Quang T.V., Gilbert M., Ternynck T., Avrameas S.;
 RT "Two murine natural polyreactive autoantibodies are encoded by
 RT nonmutated germ-line genes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628 (1989).
 CC -1- FUNCTION Beta-2-microglobulin is the beta-chain of major
 CC histocompatibility complex class I molecules (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
 DR EMBL: AK002875; BAB22422.1; -, mRNA.
 DR HSP; F33932; F33932.
 DR HSP; P01810; 2PBJ.
 DR GO: GO:0003843; F:antigen binding; IEA.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003597; IG_c1.
 DR InterPro: IPR003006; IG_MHC.
 DR Pfam: PF07654; CI-set; 3.
 DR SMART: SM00407; IGH1; 2.
 DR PROSITE: PS50835; IG_LIKE; 3.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN 2.
 KM Immune response; Immunoglobulin domain; MHC I.
 SQ SEQUENCE 426 AA; 45820 MW; 56E1275BA48FE6FB CRC64;

Query Match 60.7%; Score 54; DB 2; Length 426;
 Best Local Similarity 76.9%; Pred. No. 1.9;
 Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 5 GNDISYNQKFXG 17
 |||||
 Db 16 GNGDTSYNQKFXG 28

RESULT 15
 HV02 MOUSE
 ID HV02 MOUSE STANDARD; PRT; 140 AA.
 AC P01746;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Ig heavy chain V region 93G7 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=A/J;
 RX MEDLINE=2152818; PubMed=6801765;
 RA Sims J., Rabitts T.H., Bates P., Slaughter C., Tucker P.W.,
 RA Capra J.D.;
 RT "Somatic mutation in genes for the variable portion of the
 RT immunoglobulin heavy chain.";
 RL Science 216:309-311 (1982).
 CC -1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL: J00493; AAA38128.1; -, mRNA.
 DR HSP; P01747; 1JFQ.
 DR HSP; P01746; 20-140.
 DR SMR; P01746; 20-140.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003596; IG_v.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 KM Hybridoma; Immunoglobulin domain; Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 140 Ig heavy chain V region 93G7.
 FT DOMAIN 20 139 Ig-like.
 FT NON_TER 140 140
 SQ SEQUENCE 140 AA; 15514 MW; 25A4CBBE21DA5C8 CRC64;

Query Match 59.6%; Score 53; DB 1; Length 140;
 Best Local Similarity 62.5%; Pred. No. 0.81;
 Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 2 IYGNDDISYNQKFXG 17
 |||||
 Db 70 INPNGYINYNQKFXG 85

RESULT 16
 O6PUA7 MOUSE PRELIMINARY; PRT; 472 AA.
 ID O6PUA7; AC O6PUA7;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 GN Name=Igh-1a;
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 CC Muridae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Czech II;
 RC TISSUE=Mammary tumor metastatized to lung, MMTV-LTR/Mnt1 model.
 RC Expression driven by an MMTV-LTR enhancer; DOI=10.1073/pnas.242603899;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heileh F.,
 RA Dietchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant J.L., Scheetz T.E.,
 RA Brownstein M.J., Uedlin T.B., Yoshizaki S., Carninci P., Prange C.,


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RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Buterfield V.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=CZECH II;
RC TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.
RC Expression driven by an MMTV-LTR enhancer.;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018535; AAH18535.1; -; mRNA.
DR HSSP; P01865; IKB5.
DR MGI; MGI:36443; Igh-1a.
DR GO; GO:0003823; F:antigen binding; IDA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003597; IG-CL.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; CI-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGCL; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KM Hypothetical protein.
SQ SEQUENCE 472 AA; 52299 MW; 165169C2D5D54AB CRC64;

Query Match 59.6%; Score 53; DB 2; Length 472;
Best Local Similarity 62.5%; Pred. No. 3.2;
Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 IYPGNDISYNQKFXG 17
Db 70 IYPNNGGNGYNQKFXG 85

RESULT 17
Q58B56 MOUSE PRELIMINARY; PRT; 477 AA.
ID Q58B56;
AC Q58B56;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE Igh-1a protein.
GN Name=Igh-1a;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CZECH II;
RC TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.
RC Expression driven by an MMTV-LTR enhancer.;
RX MEDLINE=22388257; PubMed=124797932; DOI=10.1073/pnas.242603899;
RA Strausberg R., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Buterfield V.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=CZECH II;
RC TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.
RC Expression driven by an MMTV-LTR enhancer.;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018535; AAH18535.1; -; mRNA.
DR HSSP; P01865; IKB5.
DR MGI; MGI:36443; Igh-1a.
DR GO; GO:0003823; F:antigen binding; IDA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003597; IG-CL.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; CI-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGCL; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 477 AA; 52222 MW; 519211B55EA12364 CRC64;

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RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Buterfield V.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=CZECH II;
RC TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.
RC Expression driven by an MMTV-LTR enhancer.;
RA NIH MGC Project;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC092061; AAH92061.1; -; mRNA.
DR MGI; MGI:36443; Igh-1a.
DR GO; GO:0042571; C:immunoglobulin complex, circulating; IDA.
DR GO; GO:0005771; C:multivesicular body; IDA.
DR GO; GO:0003823; F:antigen binding; IDA.
DR GO; GO:0001788; P:antibody-dependent cellular cytotoxicity; IDA.
DR GO; GO:0006958; P:complement activation, classical pathway; IDA.
DR GO; GO:0045022; P:early endosome to late endosome transport; IDA.
DR GO; GO:0006911; P:phagocytosis, engulfment; IDA.
DR GO; GO:0006910; P:phagocytosis, recognition; IDA.
DR GO; GO:0050871; P:positive regulation of B cell activation; IDA.
DR GO; GO:0050778; P:positive regulation of immune response; IDA.
DR GO; GO:0050766; P:positive regulation of phagocytosis; IDA.
DR GO; GO:0001812; P:positive regulation of type I hypersensitivity; IDA.
DR GO; GO:0001798; P:positive regulation of type I hypersensit. . .; IDA.
DR GO; GO:0001622; P:regulation of proteolysis and peptidolysis; IDA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003597; IG-CL.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; CI-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGCL; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 477 AA; 52222 MW; 519211B55EA12364 CRC64;

Query Match 59.6%; Score 53; DB 2; Length 477;
Best Local Similarity 62.5%; Pred. No. 3.3;
Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 IYPGNDISYNQKFXG 17
Db 70 IYPNNGGNGYNQKFXG 85

RESULT 18
Q4VAB6 MOUSE PRELIMINARY; PRT; 483 AA.
ID Q4VAB6;
AC Q4VAB6;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.

```

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OX  NCBI_TaxID=10090;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=FVB/N; TISSUE=Colon;
RX  MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA  Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA  Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA  Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA  Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA  Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA  Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA  Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA  Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA  Bosak S.A., McKernan K.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA  Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA  Villalón D.K., Muzny D.M., Sodergren E.J., Green E.D., Dickson M.C.,
RA  Blakesley R.W., Touchman J.W., Green E.D., Jones S.J.M., Matra M.A.,
RA  Buttefield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA  Schermer A., Schein J.E., Jones S.J.M., Matra M.A.,
RT  "Generation and initial analysis of more than 15,000 full-length human
RT  and mouse cDNA sequences."
RL  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN  [2]
RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=FVB/N; TISSUE=Colon;
RG  NIH MGC Project;
RL  Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR  EMBL; BC096462; AA096462.1; -, mRNA.
KW  Hypothetical protein.
SQ  SEQUENCE 483 AA; 52436 MW; 368F7BEB56D99F CRC64;

Query Match      59.6%; Score 53; DB 2; Length 483;
Best Local Similarity 62.5%; Pred. No. 3.3;
Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY  2  TYPGNDISYNOKFXG 17
DB  70  TYPNSGATSYNOKFXG 85

RESULT 19
O4V9V8_MOUSE PRELIMINARY; PRT; 590 AA.
AC  O4V9V8;
DT  13-SEP-2005 (TREMBlrel. 31, Created)
DT  13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT  13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE  Hypothetical protein.
GN  Name=Igh-6;
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC  Muridea; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RC  TISSUE=Mammary gland;
RX  MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA  Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA  Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA  Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA  Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA  Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA  Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA  Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA  Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA  Bosak S.A., McKernan K.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA  Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA  Villalón D.K., Muzny D.M., Sodergren E.J., Green E.D., Dickson M.C.,
RA  Blakesley R.W., Touchman J.W., Green E.D., Jones S.J.M., Matra M.A.,
RA  Buttefield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA  Schermer A., Schein J.E., Jones S.J.M., Matra M.A.,
RT  "Generation and initial analysis of more than 15,000 full-length human
RT  and mouse cDNA sequences."
RL  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN  [2]
RP  NUCLEOTIDE SEQUENCE.
RC  TISSUE=Mammary gland;
RG  NIH MGC Project;
RL  Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR  EMBL; BC096667; AA096667.1; -, mRNA.
KW  MGI; 96448; Igh-6.
DR  InterPro; IPR003599; Ig.
DR  InterPro; IPR007110; Ig-like.
DR  InterPro; IPR003597; Ig_c1.
DR  InterPro; IPR003066; Ig_MHC.
DR  InterPro; IPR003596; Ig_v.
DR  Pfam; PF07654; C1-set; 4.
DR  SMART; SM00409; Ig; 2.
DR  SMART; SM00407; Igcl; 4.
DR  SMART; SM00406; IgV; 1.
DR  PROSITE; PS00835; IG_LIKE; 5.
DR  PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW  Hypothetical protein.
SQ  SEQUENCE 590 AA; 64892 MW; D425318F9A188B14 CRC64;

Query Match      59.6%; Score 53; DB 2; Length 590;
Best Local Similarity 56.2%; Pred. No. 4.2;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY  2  TYPGNDISYNOKFXG 17
DB  70  TYPNSGATSYNOKFXG 85

RESULT 20
O6FP95_MOUSE PRELIMINARY; PRT; 464 AA.
AC  O6FP95;
DT  05-JUL-2004 (TREMBlrel. 27, Created)
DT  05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT  05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE  Hypothetical protein.
GN  Name=Igh-1a;
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC  Muridea; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=C57BL/6J;
RC  TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/mt1 model.
RC  Expression driven by an MMTV-LTR enhancer;
RX  MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA  Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA  Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA  Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA  Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA  Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA  Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA  Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA  Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA  Bosak S.A., McKernan K.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA  Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA  Villalón D.K., Muzny D.M., Sodergren E.J., Green E.D., Dickson M.C.,
RA  Blakesley R.W., Touchman J.W., Green E.D., Jones S.J.M., Matra M.A.,
RA  Buttefield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA  Schermer A., Schein J.E., Jones S.J.M., Matra M.A.,
RT  "Generation and initial analysis of more than 15,000 full-length human
RT  and mouse cDNA sequences."
RL  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN  [2]
RP  NUCLEOTIDE SEQUENCE.
RC  TISSUE=Mammary gland;
RG  NIH MGC Project;
RL  Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR  EMBL; BC096667; AA096667.1; -, mRNA.
KW  MGI; 96448; Igh-6.
DR  InterPro; IPR003599; Ig.
DR  InterPro; IPR007110; Ig-like.
DR  InterPro; IPR003597; Ig_c1.
DR  InterPro; IPR003066; Ig_MHC.
DR  InterPro; IPR003596; Ig_v.
DR  Pfam; PF07654; C1-set; 4.
DR  SMART; SM00409; Ig; 2.
DR  SMART; SM00407; Igcl; 4.
DR  SMART; SM00406; IgV; 1.
DR  PROSITE; PS00835; IG_LIKE; 5.
DR  PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW  Hypothetical protein.
SQ  SEQUENCE 590 AA; 64892 MW; D425318F9A188B14 CRC64;
```

RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schain J.E., Jones S.J.M., Maira M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=CZECH 11;
 RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.
 RC Expression driven by an MMTV-LTR enhancer.;
 RA Strausberg R.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBSJ databases.
 DR EMBL; BC057672; AAH57672.1; -; mRNA.
 DR HSSP; P01865; 1XB5.
 DR MGI; MGI:96443; Igh-1a.
 DR GO; GO:0003823; F:antigen binding; IEA.
 DR InterPro; IPR003599; Ig_
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig-cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig V.
 DR Pfam; PF07654; C1-set; 3.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGC1; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 464 AA; 51096 MW; 5B837464D85A1888 CRC64;
 QY Query Match 57.3%; Score 51; DB 2; Length 464;
 Best Local Similarity 56.2%; Pred. No. 7;
 Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
 Db 2 IYPGNDISYNOKFXG 17
 70 IYPGSGTYNEKFXG 85
 RESULT 21
 HV12_MOUSE STANDARD; PRT; 117 AA.
 AC P01756;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Ig heavy chain V region MOPC 104E.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 CC Muridea; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP PROTEIN SEQUENCE AND CARBOHYDRATE-LINKAGE SITE ASN-55.
 RX MEDLINE=83075344; PubMed=6816276;
 RA Keniry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
 RA Hood L.E.;
 RT "Complete amino acid sequence of a mouse mu chain: homology among
 RT heavy chain constant region domains."; Biochemistry 21:5415-5424(1982).
 RL Biochemistry 21:5415-5424(1982).
 CC -I- MISCELLANEOUS: The sequence of the light chain of this Igm myeloma
 CC protein has also been determined.
 CC -I- MISCELLANEOUS: This protein binds dextran.
 CC -I- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC PIR; A02039; MHMS4E.
 DR HSSP; P01751; INOB.

DR SMR; P01756; 1-117.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Direct protein sequencing; Glycoprotein; Immunoglobulin domain;
 KW Immunoglobulin V region.
 FT DOMAIN 1 116 Ig-like.
 FT CARBOHYD 55 55 N-linked (GLCNAc. . .) (complex).
 FT DISULFID 22 96 By similarity.
 FT NON TER 117 117
 SQ SEQUENCE 117 AA; 12983 MW; 3CFBACE4BE447E41 CRC64;
 QY Query Match 56.2%; Score 50; DB 1; Length 117;
 Best Local Similarity 62.5%; Pred. No. 2.2;
 Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 Db 2 IYPGNDISYNOKFXG 17
 51 INPNNGTSYNOKFXG 66
 RESULT 22
 HV13_MOUSE STANDARD; PRT; 117 AA.
 AC P01757;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Ig heavy chain V region J558.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 CC Muridea; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=80078170; PubMed=6765983;
 RA Schilling J., Cleveland B., Davie J.M., Hood L.;
 RT "Amino acid sequence of homogeneous antibodies to dextran and DNA
 RT rearrangements in heavy chain V-region gene segments."; Nature 283:35-40(1980).
 RL Nature 283:35-40(1980).
 CC -I- MISCELLANEOUS: The sequences of 10 hybridoma proteins that also
 CC bind dextran differ from that shown at 1-7 positions, many of
 CC which occur in the D and J segments.
 CC -I- MISCELLANEOUS: This protein binds dextran.
 CC -I- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC PIR; A26242; MHMSJ5.
 DR HSSP; P01751; INOB.
 DR SMR; P01757; 1-117.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Direct protein sequencing; Immunoglobulin domain;
 KW Immunoglobulin V region.
 FT DOMAIN 1 116 Ig-like.
 FT DISULFID 22 96 By similarity.
 FT NON TER 117 117
 SQ SEQUENCE 117 AA; 13025 MW; 292E2AF4BE447E41 CRC64;
 QY Query Match 56.2%; Score 50; DB 1; Length 117;
 Best Local Similarity 62.5%; Pred. No. 2.2;
 Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 Db 2 IYPGNDISYNOKFXG 17

Db 51 INPNNGGTSTYNOKFXG 66

RESULT 23

Q90XE9 MOUSE PRELIMINARY; PRT; 117 AA.

ID Q90XE9

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE Immunoglobulin heavy chain V-D-J region (Fragment).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RP NUCLEOTIDE SEQUENCE.

RA Clemens A., Rademakers A., Specht C., Koelsch E.;

RL Submitted (DEC-1997) to the EMBL/Genbank/DBJ databases.

RN [2]

RP NUCLEOTIDE SEQUENCE.

RA Baccala R., Quang T.V., Gilbert M., Ternynck T., Avrameas S.;

RT "Two murine natural polyclonal autoantibodies are encoded by

RT nonmutated germ-line genes."

RL Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628 (1989).

DR EMBL; AJ225174; CAB65237.1; -, mRNA.

DR PIR; F33932; F33932.

DR HSSP; P01751; INOB.

DR SMR; O90XE9; 1-117.

DR InterPro; IPR007110; IG-like.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG-LIKE; 1.

FT NON_TER 1

FT NON_TER 117

SQ SEQUENCE 117 AA; 13000 MW; CDDE2AF84D499734 CRC64;

Query Match 56.2%; Score 50; DB 2; Length 117;

Best Local Similarity 62.5%; Pred. No. 2.2;

Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 2 IYPGNDISTYNOKFXG 17

Db 51 INPNNGGTSTYNOKFXG 66

RESULT 24

Q90XF0 MOUSE PRELIMINARY; PRT; 117 AA.

ID Q90XF0

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

DE Immunoglobulin heavy chain V-D-J region (Fragment).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RP NUCLEOTIDE SEQUENCE.

RA Clemens A., Rademakers A., Specht C., Koelsch E.;

RL Submitted (DEC-1997) to the EMBL/Genbank/DBJ databases.

RN [2]

RP NUCLEOTIDE SEQUENCE.

RA MEDLINE=92381444; PubMed=1512540; DOI=10.1084/jem.176.3.761;

RA Tullman D.M., Jou N.T., Hill R.J., Marion T.N.;

RT "Both IgM and IgG anti-DNA antibodies are the products of clonally

RT selective B cell stimulation in (NZB x NZW) F1 mice."

J. Exp. Med. 176:761-779 (1992).

DR EMBL; AJ225171; CAB65236.1; -, mRNA.

DR PIR; PH0973; PH0973.

DR HSSP; P01751; INOB.

DR SMR; Q90XF0; 1-117.

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003596; IG_V.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG-LIKE; 1.

FT NON_TER 1

FT NON_TER 117

SQ SEQUENCE 117 AA; 13060 MW; D816AD0858A47E4C CRC64;

Query Match 56.2%; Score 50; DB 2; Length 117;

Best Local Similarity 62.5%; Pred. No. 2.2;

Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 2 IYPGNDISTYNOKFXG 17

Db 51 INPNNGGTSTYNOKFXG 66

RESULT 25

HVS1_MOUSE STANDARD; PRT; 118 AA.

ID HVS1_MOUSE

AC P06330;

DT 01-JAN-1988 (Rel. 06, Created)

DT 01-JAN-1988 (Rel. 06, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Ig heavy chain V region AC38 205.12.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RP NUCLEOTIDE SEQUENCE.

RA MEDLINE=84182519; PubMed=6201362;

RT "A V region determinant (idiotope) expressed at high frequency in B

RT lymphocytes is encoded by a large set of antibody structural genes."

RL EMBL J. 3:517-523 (1984).

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation

CC at the European Bioinformatics Institute. There are no restrictions on its

CC use as long as its content is in no way modified and this statement is not

CC removed.

CC PIR; A02040; MEMS38.

DR HSSP; P01751; INOB.

DR SMR; P06330; 1-118.

DR InterPro; IPR007110; IG-like.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG-LIKE; 1.

KW Direct protein sequencing; Immunoglobulin domain;

KW Immunoglobulin V region.

FT REGION 1 98 V segment.

FT REGION 99 104 D segment.

FT REGION 105 118 J segment.

FT DISULFID 22 96 By similarity.

FT NON_TER 118

SQ SEQUENCE 118 AA; 12934 MW; 94F7BEE4C762A018 CRC64;

Query Match 56.2%; Score 50; DB 1; Length 118;

Best Local Similarity 62.5%; Pred. No. 2.2;

Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 2 IYPGNDISTYNOKFXG 17

Db 51 INPNNGGTSTYNOKFXG 66

RESULT 26
Q65ZR6 MOUSE PRELIMINARY; PRT; 134 AA.
AC Q65ZR6;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Ab 126.33 heavy chain variable and joining regions (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=91237115; PubMed=1709665;
RA Rueff-Juy D., Marche P.N., Drapier A.-M., Cazenave P.-A.;
RT "Functional diversity of H and L chains allows the coexpression of two
mutually exclusive idiotopes (Id1104 and Id1558).";
RL J. Immunol. 146:4024-4030(1991).
DR EMBL; M74139; AAA37776.1; -; mRNA.
DR SMR; Q65ZR6; 18-134.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-1-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
SQ SEQUENCE 134 AA; 14908 MW; 1852D86D26FC7567 CRC64;

Query Match 56.2%; Score 50; DB 2; Length 134;
Best Local Similarity 62.5%; Pred. No. 2.5;
Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 IYPGNDISYNOKFXG 17
Db 68 INPNNGTSTYNEKFXG 83

RESULT 27
Q924Q0 MOUSE PRELIMINARY; PRT; 143 AA.
AC Q924Q0;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE V165-D-J-C mu protein (Fragment).
GN Name=V165-D-J-C mu;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB069915; BAB63931.1; -; mRNA.
DR PIR; PH1159; PH1159.
DR HSSP; P01751; 1A6W.
DR SMR; Q924Q0; 1-134.
DR Ensemble; ENSMUSG0000002115; Mus musculus.
DR InterPro; IPR007110; IG-1-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
SQ SEQUENCE 143 AA; 15704 MW; C99D2433F2BAD8A0 CRC64;

Query Match 56.2%; Score 50; DB 2; Length 143;

Best Local Similarity 57.1%; Pred. No. 2.7;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Qy 2 IYPGNDISYNOKFXG 15
Db 51 IYPGSGSTYNEKFXG 64

RESULT 28
Q925S3 MOUSE PRELIMINARY; PRT; 147 AA.
AC Q925S3;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE MRJ3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BA1B/c;
RX PubMed=11819679;
RA Cui D.X., Zeng G.Y., Wang F., Xu J.R., Ren D.Q., Guo Y.H., Tian F.R.,
Yan X.J., Hou Y., Su C.Z.;
RT "Mechanism of exogenous nucleic acids and their precursors improving
the repair of intestinal epithelium after gamma-irradiation in mice";
RL World J. Gastroenterol. 6:709-717(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BA1B/c;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium
of the irradiated mice by treatment with the intestinal RNA of mice of
the same strain.";
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR EMBL; AF240166; AKA3731.1; -; mRNA.
DR HSSP; P01751; 1A6W.
DR SMR; Q925S3; 3-139.
DR InterPro; IPR007110; IG-1-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain
SQ SEQUENCE 147 AA; 16274 MW; 800594A12B97191F CRC64;

Query Match 55.1%; Score 49; DB 2; Length 147;
Best Local Similarity 50.0%; Pred. No. 4.2;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 2 IYPGNDISYNOKFXG 17
Db 53 IYPGSGSTYNEKFXG 68

RESULT 29
Q7VB33 PROMA PRELIMINARY; PRT; 293 AA.
AC Q7VB33;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Predicted calcineurin family phosphatase.
GN OrderedLocustNames=Pro1267;
OS Prochlorococcus marinus.
OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;
OC Prochlorococcus.
NCBI_TaxID=1219;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SARG / CCMF 1375 / SS120;

```

DE      21-JUN-1986 (Rel. 01, Created)
DT      21-JUN-1986 (Rel. 01, Last sequence update)
DT      10-MAY-2005 (Rel. 47, Last annotation update)
DE      Ig heavy chain V region 3 precursor.
GN      Name=Igh-VJ558;
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC      Muridea; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=C57BL/6;
RX      MEDLINE=81234548; PubMed=6788376; DOI=10.1016/0092-8674(81)90089-1;
RA      Botwell A.L.M., Pakind M., Retz M., Imanishi-Kari T., Rajewsky K.,
RA      Baltimore D.;
RT      "Heavy chain variable region contribution to the NpB family of
RT      antibodies: somatic mutation evident in a gamma 2a variable region.";
RL      Cell 24:625-637(1981).
CC      -I- MISCELLANEOUS: This germline gene belongs to a set of closely
CC      related genes that could encode V regions of NPb antibodies.
CC      -----
CC      The Swiss-Prot entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use as long as its content is in no way modified and this statement is not
CC      removed.
CC      -----
CC      EMBL; J00536; AAA38605.1; -; Genomic_DNA.
CC      PIR; A02031; HVMS3.
DR      PDB; 1A14; X-ray; H=20-117.
DR      SMR; P01749; 20-117.
DR      Ensemble; ENSMUSG0000060210; Mus musculus.
DR      MGI; MGI:96486; Igh-VJ558.
DR      InterPro; IPR007110; Ig-like.
DR      InterPro; IPR003596; Ig_V.
DR      SMART; SMO0406; IG_V.
DR      PROSITE; PS50835; IG_LIKE; 1.
KW      3D-structure; Immunoglobulin domain; Immunoglobulin V region; Signal.
FT      SIGNAL
FT      1
FT      19
FT      CHAIN
FT      20 117
FT      REGION
FT      20 49
FT      REGION
FT      50 54
FT      REGION
FT      55 68
FT      REGION
FT      69 85
FT      REGION
FT      86 117
FT      DISULFID
FT      41 115
FT      NON TER
FT      117 117
SQ      SEQUENCE
SQ      117 AA; 13016 MW; 427C661C53975EDC CRC64;

Query Match      53.9%; Score 48; DB 1; Length 117;
Best Local Similarity 57.1%; Pred. No. 4.8;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      2 IYPGNDISTYNOKF 15
      ||| : : ||||
DB      70 IYPSDSETHYNOKF 83

RESULT 32
099LC4_MOUSE
ID      099LC4_MOUSE PRELIMINARY; PRT; 463 AA.
AC      099LC4;
DT      01-JUN-2001 (TREMBlrel. 17, Created)
DT      01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT      01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE      Igh-4 protein.
DE      Name=Igh-4;
OS      Mus musculus (Mouse).
OS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC      Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;

```

[1]
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=FVB/N;
 RC TISSUE=Mammary tumor. Metallochromien-TGF alpha model. 10 month old
 RC virgin mouse. Taken by biopsy.;
 RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg H., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan B., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Ditchenko L., Marinina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stepleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carlini P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Heiton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Schermer A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FVB/N;
 RC TISSUE=Mammary tumor. Metallochromien-TGF alpha model. 10 month old
 RC virgin mouse. Taken by biopsy.;
 RA Strauberg R.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC003435; AAH03435.1; -, mRNA.
 DR PIR; B45837; B45837.
 DR HSSP; P01869; ICL7.
 DR SMR; Q99LC4; 21-459.
 DR MGI; MGI:96446; Igh-4.
 DR GO; GO:0042571; C:immunoglobulin complex, circulating; IDA.
 DR GO; GO:0003823; P:antigen binding; IDA.
 DR GO; GO:0019783; P:antibacterial humoral response (sensu Verte. . .; IDA.
 DR GO; GO:0001788; P:antibody-dependent cellular cytotoxicity; IDA.
 DR GO; GO:0006988; P:complement activation, classical pathway; IDA.
 DR GO; GO:0042830; P:defense response to pathogenic bacteria; IDA.
 DR GO; GO:0006911; P:phagocytosis, engulfment; IDA.
 DR GO; GO:0050778; P:positive regulation of immune response; IDA.
 DR GO; GO:0050766; P:positive regulation of phagocytosis; IDA.
 DR GO; GO:0001812; P:positive regulation of type I hypersensitivity; IDA.
 DR GO; GO:0001798; P:positive regulation of type I hypersensit. . .; IDA.
 DR InterPro; IPR007110; Ig-1-like.
 DR InterPro; IPR003597; Ig-cl.
 DR InterPro; IPR003596; Ig-v.
 DR Pfam; PF07654; C1-set; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 KW Immunoglobulin domain.
 SQ SEQUENCE 463 AA; 51008 MW; EAA674C6BBC0763 CRC64;

Query Match 53.9%; Score 48; DB 2; Length 463;
 Best Local Similarity 50.0%; Pred. No. 23;
 Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 2 YPGNDISYNOKFXG 17
 DB 70 YPGSGNTYSEKPKG 85

RESULT 33
 OSNMND6 CAEBR
 ID OSNMND6 CAEBR PRELIMINARY; PRT; 483 AA.
 AC OSNMND6;
 DT 25-OCT-2004 (TREMBlrel. 28, Created)

DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Hypothetical protein CBG08050 (Fragment).
 GN Name=CBG08050;
 OS Caenorhabditis briggsae.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
 OC Rhabditidae; Pterodermidae; Caenorhabditis.
 OX NCBI_Taxid=6238;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RG The C. briggsae Sequencing Consortium;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; CA001000033; CAE63563.1; -, Genomic_DNA.
 DR InterPro; IPR000873; AMP-bind.
 DR Pfam; PF00501; AMP-binding; 2.
 KW Hypothetical protein.
 FT NON TER 483
 FT 483
 SQ SEQUENCE 483 AA; 54499 MW; DDB36B7AC9526A9 CRC64;

Query Match 53.9%; Score 48; DB 2; Length 483;
 Best Local Similarity 61.5%; Pred. No. 24;
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 3 YPGNDISYNOKF 15
 DB 463 YPGNDLNKNRKF 475

RESULT 34
 OSNMND6 MOUSE
 ID OSNMND6 MOUSE PRELIMINARY; PRT; 109 AA.
 AC OSNMND6;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Anti-myosin immunoglobulin heavy chain variable region
 DE (fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=BA1B/c;
 RX MEDLINE=20448942; PubMed=10992488;
 RX DOI=10.1128/JAI.68.10.5803-5808.2000;
 RA Melkiet S., Liao L., Cunningham M.W., Diamond B.;
 RA "T-cell-dependent antibody response to the dominant epitope of
 RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
 RT with cardiac myosin.";
 RL Infect. Immun. 68:5803-5808(2000).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=2457627;
 RA Elliot D., Webster D.M., Rees A.R.;
 RT "V region sequences of anti-DNA and anti-RNA autoantibodies from
 RT NZB/NZW F1 mice.";
 RL J. Immunol. 141:1745-1753(1988).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=82381444; PubMed=1512540; DOI=10.1084/jem.176.3.761;
 RA Tilieman D.M., Jou N.T., Hill R.J., Marston T.N.;
 RT "Both IgM and IgG anti-DNA antibodies are the products of clonally
 RT selective B cell stimulation in (NZB x NZW)F1 mice.";
 RL J. Exp. Med. 176:761-779(1992).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=91341421; PubMed=1908510; DOI=10.1084/jem.174.3.613;
 RA Stark S.E., Caton A.J.;

RT "Antibodies that are specific for a single amino acid interchange in a
RT protein epitope use structurally distinct variable regions.";
RL J. Exp. Med. 174:613-624(1991).
DR EMBL; AF206031; AAE69329.1; -; mRNA.
DR PIR; A30502; A30502.
DR PIR; PH0989; PH0989.
DR PIR; PH0990; PH0990.
DR PIR; PH0991; PH0991.
DR PIR; PH0992; PH0992.
DR PIR; PH0993; PH0993.
DR PIR; PH0994; PH0994.
DR PIR; PH0995; PH0995.
DR PIR; PH1094; PH1094.
DR PIR; PH1096; PH1096.
DR PIR; S26312; S26312.
DR PIR; S26313; S26313.
DR HSSP; P01751; 1NOB.
DR Ensembl; ENSMUSG0000021155; Mus musculus.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1 1
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 12118 MW; FE65E441BBF936A6 CRC64;
Query Match 52.8%; Score 47; DB 2; Length 109;
Best Local Similarity 56.2%; Pred. No. 6.5;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
Qy 2 IYPGNDISYNQKFXG 17
Db 42 INPYNDGTYNKEKFXG 57
RESULT 35
HVL4_MOUSE
ID HVL4_MOUSE STANDARD; PRT; 117 AA.
AC P01758;
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V region 108A precursor.
GN Name=Igh-VJ558;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=81245215; PubMed=6789211;
RA Givol D., Zakut R., Efron K., Rechavi G., Ram D., Cohen J.B.;
RT "Diversity of germ-line immunoglobulin VH genes.";
RL Nature 292:426-430(1981).
CC -! SIMILARITY: Contains 1 Ig-1like (immunoglobulin-like) domain.
CC -----
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CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; J00488; AAA38519.1; -; Genomic_DNA.
DR PIR; A02041; HWS8A.
DR HSSP; P01751; 1NOB.
DR SMR; P01758; 20-116.
DR MGI; MGI:96486; Igh-VJ558.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.

FT SIGNAL 1 19
FT CHAIN 20 117 Ig heavy chain V region 108A.
FT DOMAIN 20 >117 Ig-1like.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12972 MW; 428CB44DP25D1BC2 CRC64;
Query Match 52.8%; Score 47; DB 1; Length 117;
Best Local Similarity 64.3%; Pred. No. 7.1;
Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 2 IYPGNDISYNQKFX 15
Db 70 INPYNGGTGYNOKFX 83
RESULT 36
Q5R3X0_MOUSE
ID Q5R3X0_MOUSE PRELIMINARY; PRT; 118 AA.
AC Q5R3X0;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Poc. H26-1 variable region precursor (fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Balb-c;
RX MEDLINE=85230574; PubMed=3924600;
RA Schiff C., Millili M., Fougereau M.;
RT "Functional and pseudogenes are similarly organized and may equally
RT contribute to the extensive antibody diversity of the Ighv11 family.";
RL EMBL; X02462; CAA26299.1; -; Genomic_DNA.
DR SMR; Q5R3X0; 20-116.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT SIGNAL.
FT SIGNAL <1 19 Potential.
FT CHAIN 20 117 poc. H26-1 variable region.
FT NON_TER 1 1
FT NON_TER 118 118
SQ SEQUENCE 118 AA; 13276 MW; 938EFF8D35416188 CRC64;
Query Match 52.8%; Score 47; DB 2; Length 118;
Best Local Similarity 62.5%; Pred. No. 7.2;
Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 2 IYPGNDISYNQKFXG 17
Db 70 INPYNGGTGYNOKFXG 85
RESULT 37
HVO3_MOUSE
ID HVO3_MOUSE STANDARD; PRT; 120 AA.
AC P01747;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Ig heavy chain V region 36-65.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.


```

RX MEDLINE=83131846; PubMed=6186498;
RA Stieglitz M., Gelfer M.L., Brodeur P., Riblet R.,
RA Marchak-Rothstein A.;
RT "The genetic basis of antibody production: the dominant anti-arsenate
RT idotype response of the strain A mouse.";
RL Eur. J. Immunol. 12:1023-1032(1982).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 1-120.
RX MEDLINE=21528949; PubMed=11673524;
RA Parham-Seren B., Viswanathan M., Strong R.K., Margolies M.N.;
RT "Structural analysis of mutants of high-affinity and low-affinity P-
RT azophenylarsenate-specific antibodies generated by alanine scanning of
RT heavy chain complementarity-determining region 2.";
RL J. Immunol. 167:5129-5135(2001).
CC -1- MISCELLANEOUS: From analysis of the sizes of several other
CC differentiated genes that hybridize to this one, the authors
CC conclude that all of these V regions have rearranged to the same J
CC segment, JH2.
CC -1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR: A94264; HVMG7.
CC DR PDB: LFFO; X-ray; H=1-120.
CC DR Ensembl; ENSMUSG00000021155; Mus musculus.
CC DR InterPro; IPR007110; Ig-like.
CC DR InterPro; IPR003596; Ig_V.
CC DR SMART; SM00406; IGV; 1.
CC DR PROSITE; PS00835; Ig_Like; 1.
CC 3D-structure: Hybridoma; Immunoglobulin domain;
CC Immunoglobulin V region.
CC DOMAIN 1 111 Ig-like.
CC FT NON_TER 120 120
CC SQ SEQUENCE 120 AA; 13307 MW; FP04E4A167B654AF CRC64;

Query Match 52.8%; Score 47; DB 1; Length 120;
Best Local Similarity 56.2%; Pred. No. 73;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2 IYPGNDISYNQKFXG 17
Db 50 INPFGYTKNEKFKG 65

RESULT 38
O91WR1 MOUSE PRELIMINARY; PRT; 488 AA.
AC O91WR1_
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Igh-VJ558 protein.
GN Name=Igh-VJ558;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Kidney;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stjepienko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stjepienko M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

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RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013539; AAH13539.1; -, mRNA.
DR HSSP; P01751; 1A6W.
DR Ensembl; ENSMUSG00000021155; Mus musculus.
DR MGI; MGI:96486; Igh-VJ558.
DR GO; GO:0003823; F:antigen binding; IEA.
DR GO; GO:0003823; F:antigen binding; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; Ig_Like; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Immunoglobulin domain.
SQ SEQUENCE 488 AA; 52965 MW; F12068460B40089D CRC64;

Query Match 52.8%; Score 47; DB 2; Length 488;
Best Local Similarity 62.5%; Pred. No. 36;
Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 IYPGNDISYNQKFXG 17
Db 70 INPFGTSTYQKFKG 85

RESULT 39
O8VCX7 MOUSE PRELIMINARY; PRT; 613 AA.
AC O8VCX7_
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Igh-6 protein.
GN Name=Igh-6;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stjepienko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stjepienko M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

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RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RA Strauberg R.;
RN Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.
RP [3]
RX PubMed2464031.
RA Sikder S.K., Borden P., Gruneo F., Akoliar P.N., Bhattacharya S.B.,
RA Morrison S.L., Kabat E.A.;
RT "Amino acid substitutions in VH CDR2 change the idotype but not the
RT antigen-binding of monoclonal antibodies to alpha(1---6)dextran.";
RL J. Immunol. 142:888-893 (1989).
DR EMBL; BC018315; AAH18315.1; -; mRNA.
DR PIR; C30562; C30562.
DR HSSP; P01751; 1A6W.
DR Ensemble; ENSMUSG0000054328; Mus musculus.
DR MGI; MGI:96448; Igh-6.
DR GO; GO:0019815; C:B cell receptor complex; IDA.
DR GO; GO:0009897; C:external side of plasma membrane; IDA.
DR GO; GO:0042571; C:immunoglobulin complex; circulating; IDA.
DR GO; GO:0048471; C:perinuclear region; IDA.
DR GO; GO:0003823; F:antigen binding; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0004888; F:transmembrane receptor activity; IDA.
DR GO; GO:0000187; F:activation of MAPK activity; IDA.
DR GO; GO:0030333; P:antigen processing; IDA.
DR GO; GO:0050893; P:B cell receptor signaling pathway; IDA.
DR GO; GO:0045042; P:early endosome to late endosome transport; IDA.
DR GO; GO:0016064; P:humoral defense mechanism (sensu Vertebrata); IDA.
DR GO; GO:0030890; P:positive regulation of B cell proliferation; IDA.
DR GO; GO:0045807; P:positive regulation of endocytosis; IDA.
DR GO; GO:0050711; P:positive regulation of peptidyl-tyrosine ph. . .; IDA.
DR InterPro; IPR007110; IG-1-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG-MHC.
DR InterPro; IPR003596; IG-v.
DR Pfam; PF07654; CI-set; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
DR KW Immunoglobulin domain.
SQ SEQUENCE 613 AA; 67855 MW; 41A9384DD4C22862 CRC64;

Query Match 52.8%; Score 47; DB 2; Length 613;
Best Local Similarity 50.0%; Pred. No. 46;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Oy 2 IYPGNDISYNOKFXG 17
Db 70 ILPGSGSTINKEKFG 85

RESULT 40
OSPE17 SALPA PRELIMINARY; PRT; 881 AA.
AC OSPE17
DT 01-FEB-2005 (TRENBLREL. 29, Created)
DT 01-FEB-2005 (TRENBLREL. 29, Last sequence update)
DE Outer membrane usher protein.
GN Name=teb; OrderedlocusNames=SPA2813;
OS Salmonella paratyphi-a.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
```

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OX NCBI_TaxID=54388;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 9150 / SARB42;
RX PubMed15531882; DOI=10.1038/ng1470;
RA McClelland M., Sanderson K.E., Clifton S.W., Latreille P.,
RA Porwollik S., Sabo A., Meyer R., Bieri T., Ozersky P., McLellan M.,
RA Harkins C.R., Wang C., Nguyen C., Berghoff A., Elliott G.,
RA Kohlberg S., Strong C., Du F., Carter J., Kremizki C., Layman D.,
RA Leonard S., Sun H., Fulton L., Nash W., Miner T., Minx P.,
RA Deleauauy K., Fronick C., Magrini V., Nhan M., Warren W., Florea L.,
RA Spieth J., Wilson R.K.;
RT "Comparison of genome degradation in Paratyphi A and Typhi, human-
RT restricted serovars of Salmonella enterica that cause typhoid.";
RL Nat. Genet. 36:1268-1274 (2004).
DR EMBL; CP000026; AAV78663.1; -; Genomic_DNA.
DR GO; GO:0009289; C:fimbrium; IEA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019867; C:outer membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR000015; Fimb_usher.
DR Pfam; PF00577; Usher; 1.
DR PROSITE; PS01151; FIMBRIAL_USHER; 1.
DR KW Complete proteome; Fimbria; Membrane; Outer membrane; Transmembrane;
KW Transport.
SQ SEQUENCE 881 AA; 96703 MW; 9105D5AC2CAF3885 CRC64;

Query Match 52.8%; Score 47; DB 2; Length 881;
Best Local Similarity 69.2%; Pred. No. 70;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 5 GNDISYNOKFXG 17
Db 565 GNDISYNGTPTNG 577

RESULT 41
OS7KG6 SALCH PRELIMINARY; PRT; 889 AA.
AC OS7KG6
DT 10-MAY-2005 (TRENBLREL. 30, Created)
DT 10-MAY-2005 (TRENBLREL. 30, Last sequence update)
DE Outer membrane usher protein.
GN Name=teb; OrderedlocusNames=SC2890;
OS Salmonella choleraesuis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=591;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=SC-B67;
RX PubMed15781495; DOI=10.1093/nar/gki297;
RA Chu C.-H., Tang P., Chu C., Hu S., Bao Q., Yu J., Chou Y.-Y.,
RA Wang H.-S., Lee Y.-S.;
RT "The genome sequence of Salmonella enterica serovar Choleraesuis, a
RT highly invasive and resistant zoonotic pathogen.";
RL Nucleic Acids Res. 33:1690-1698 (2005).
DR EMBL; AE017220; AAX66796.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR KW Complete proteome; Fimbria; Membrane; Outer membrane; Transmembrane;
KW Transport.
SQ SEQUENCE 899 AA; 96677 MW; 485696FBB439EBD0 CRC64;

Query Match 52.8%; Score 47; DB 2; Length 899;
Best Local Similarity 69.2%; Pred. No. 72;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 5 GNDISYNOKFXG 17
Db 565 GNDISYNGTPTNG 577
```

Db 583 GNDSISYNGTFNG 595

RESULT 42

ID 083SX7_SALTI PRELIMINARY; PRT; 899 AA.

AC 083SX7;

DT 01-JUN-2003 (TREMBLrel. 24, Created)

DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE Outer membrane usher protein.

GN Name=steb; OrderedLocustNames=t2857;

OS Salmonella typhi.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Salmonella.

OX NCBI_TaxID=601;

RN NUCLEOTIDE SEQUENCE.

RP STRAIN=CT18;

RC STRAIN=Ty2 / ATCC 700931;

RX MEDLINE=22531367; PubMed=12644504;

RX DOI=10.1128/JB.185.7.2330-2337.2003;

RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,

RA Burland V., Kodyanski V., Schwartz D.C., Blattner F.R.,

RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18."

RL J. Bacteriol. 185:2330-2337(2003).

DR EMBL: AE016843; AAO70413.1; -: Genomic_DNA.

DR GO: GO:0009289; C:fimbrium; IEA.

DR GO: GO:0016021; C:integral to membrane; IEA.

DR GO: GO:0019867; C:outer membrane; IEA.

DR GO: GO:0005215; F:transporter activity; IEA.

DR GO: GO:0006810; P:transport; IEA.

DR InterPro: IPR000015; Fimb_usher.

DR Pfam: PF00577; Usher, 1.

DR PROSITE: PS01151; FIMBRIAL_USHER, 1.

DR Fimbrin; Membrane; Outer membrane; Transmembrane; Transport.

KW SEQUENCE 899 AA; 98673 MW; 8170A47C3981FA44 CRC64;

SQ

Query Match 52.8%; Score 47; DB 2; Length 899;

Best Local Similarity 69.2%; Pred. No. 72;

Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 GNDSISYNGTFNG 17

Db 583 GNDSISYNGTFNG 595

RESULT 43

ID 082455_SALTI PRELIMINARY; PRT; 899 AA.

AC 082455;

DT 01-MAR-2002 (TREMBLrel. 20, Created)

DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)

DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)

DE Outer membrane usher protein.

GN Name=steb; OrderedLocustNames=STY3086;

OS Salmonella typhi.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Salmonella.

OX NCBI_TaxID=601;

RN NUCLEOTIDE SEQUENCE.

RP STRAIN=CT18;

RC MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;

RX Parkhill J., Dougan G., James K.D., Thomson N.R., Pichard D., Main J.,

RX Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebatia M.,

RX Baker S., Baaham D., Brooks R., Chillingworth T., Connor P.,

RX Cronin A., Davis P., Davies K.M., Dowd L., White N., Farrar J.,

RX Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jajale K.,

RX Krogh A., Larsen T.S., Leach S., Moule S., O'Gaora P., Parry C.,

RX Quail M.A., Rutherford K.M., Simmonds W., Skelton J., Stevens K.,

RX Whitehead S., Barrett B.G.;

RT "Complete genome sequence of a multiple drug resistant Salmonella

RT enterica serovar Typhi CT18.";

RL Nature 413:848-852(2001).

DR EMBL: AL627276; CAP06062.1; -: Genomic_DNA.

DR GO: GO:0009289; C:fimbrium; IEA.

DR GO: GO:0016021; C:integral to membrane; IEA.

DR GO: GO:0019867; C:outer membrane; IEA.

DR GO: GO:0005215; F:transporter activity; IEA.

DR GO: GO:0006810; P:transport; IEA.

DR InterPro: IPR000015; Fimb_usher.

DR Pfam: PF00577; Usher, 1.

DR PROSITE: PS01151; FIMBRIAL_USHER, 1.

DR Complete proteome; Fimbria; Membrane; Outer membrane; Transmembrane; Transport.

KW SEQUENCE 899 AA; 98643 MW; 9464E17C229B48BF CRC64;

SQ

Query Match 52.8%; Score 47; DB 2; Length 899;

Best Local Similarity 69.2%; Pred. No. 72;

Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 GNDSISYNGTFNG 17

Db 583 GNDSISYNGTFNG 595

RESULT 44

ID 07RLX6_PLAYO PRELIMINARY; PRT; 1911 AA.

AC 07RLX6;

DT 01-MAR-2004 (TREMBLrel. 26, Created)

DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)

DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

DE Tubulin-tyrosine ligase family, putative.

GN Name=PY02412;

OS Plasmodium yoelii yoelii.

OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.

OX NCBI_TaxID=73239;

RN NUCLEOTIDE SEQUENCE.

RP STRAIN=17XNL.

RC MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;

RX Carlson J.W., Angiolini S.V., Sun B.B., Kooij T.W., Perlea M.,

RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,

RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Blawell S.L.,

RA Shalom S.J., van Aken S.E., Riedmuller S.B., Feldblum T.V.,

RA Cho J.K., Quackenbush J., Sedegah M., Shoabli A., Cummings L.M.,

RA Florens L., Yates J.R. II, Raine J.D., Sinden R.E., Harris M.A.,

RA Cunningham D.A., Preiser P.R., Bergman L.W., Valdy A.B.,

RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,

RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,

RA Carucci D.J.;

RT "Genome sequence and comparative analysis of the model rodent malaria parasite Plasmodium yoelii yoelii."

RL Nature 419:512-519(2002).

CC -!- CAUTION: The sequence shown here is derived from an EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is preliminary data.

CC EMBL: AAB0100662; EAA21855.1; -: Genomic_DNA.

DR GO: GO:0016874; F:ligase activity; IEA.

DR GO: GO:0004835; F:tubulin-tyrosine ligase activity; IEA.

DR GO: GO:0006464; P:protein modification; IEA.

DR InterPro: IPR011591; Botulinum.

DR InterPro: IPR004344; Tub_tyr_ligase.

DR Pfam: PF03133; TTL, 1.

DR ProDom: PD001963; Botulinum; 1.

KW Ligase.

SQ SEQUENCE 1911 AA; 221521 MW; A31ACM42B5A4A316 CRC64;

Query Match 52.8%; Score 47; DB 2; Length 1911;

Best Local Similarity 61.5%; Pred. No. 17e+02;

Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 GNDSISYNGTFNG 17

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Db      1333 GNDLEVNKKENG 1345

RESULT 45
ID      087A00_XYLFT PRELIMINARY; PRT; 146 AA.
AC      087A00:
DT      01-JUN-2003 (TReMBLrel. 24, Created)
DT      01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT      01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE      Stringent starvation protein B.
GN      Name=SPB; OrderedLocustNames=PD1773;
OS      Xylella fastidiosa (strain Temecual / ATCC 700964).
OC      Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC      Xanthomonadaceae; Xylella.
OX      NCBI_TaxID=183190;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RX      DOI=10.1128/7B.185.3.1018-1026.2003;
RA      Van Sluys M.A., de Oliveira M.C., Monteiro-Vitorello C.B.,
RA      Miyaki C.Y., Furlan L.R., Camargo L.E.A., da Silva A.C.R., Moon D.H.,
RA      Takita M.A., Lemos E.G.M., Machado M.A., Ferro M.I.T., da Silva F.R.,
RA      Goldman M.H.S., Goldman G.H., Lemos M.V.F., El-Dorriy H., Tsai S.M.,
RA      Carrier H., Carraro D.M., de Oliveira R.C., Nunes L.R., Siqueira W.J.,
RA      Coutinho L.L., Kimura E.T., Ferro E.S., Harakava R., Kuramae E.E.,
RA      Martino C.L., Gigliotti E., Abreu I.L., Alves L.M.C., do Amaral A.M.,
RA      Baia G.S., Blanco S.R., Brito M.S., Camaván F.S., Celestino A.V.,
RA      da Cunha A.F., Fenille R.C., Ferro J.A., Formighieri E.F., Kishi L.T.,
RA      Leoni S.G., Oliveira A.R., Rosa V.E. Jr., Sasaki F.T., Sena J.A.D.,
RA      de Souza E.L., Truffi D., Tsukumo F., Yanai G.M., Zeros L.G.,
RA      Civerio E.L., Simpson A.J.G., Almeida N.F. Jr., Setubal J.C.,
RA      Kitajima J.P.;
RT      "Comparative analyses of the complete genome sequences of Pierce's
RT      disease and citrus variegated chlorosis strains of Xylella
RT      fastidiosa.";
RL      J. Bacteriol. 185:1018-1026(2003).
DR      EMBL; AE012559; AAO29607.1; -, Genomic_DNA.
DR      HSSP; P25663; 10X8.
DR      InterPro; IPR007481; SGPB.
DR      Pfam; PF04386; SGPB; 1.
DR      PIRSF; PIRSF005276; SGPB; 1.
KW      Complete proteome.
SQ      SEQUENCE 146 AA; 15728 MW; 08D394A9569D407 CRC64;

Query Match      51.7%; Score 46; DB 2; Length 146;
Best Local Similarity 43.8%; Pred. No. 14;
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Cy      2 TYPGNDISTYNQKFXG 17
Db      66 LHIGNDGVSNARFG 81

RESULT 46
ID      09PEW6_XYLFA PRELIMINARY; PRT; 146 AA.
AC      09PEW6:
DT      01-OCT-2000 (TReMBLrel. 15, Created)
DT      01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT      01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE      Stringent starvation protein B.
GN      OrderedLocustNames=Xf0912;
OS      Xylella fastidiosa.
OC      Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC      Xanthomonadaceae; Xylella.
OX      NCBI_TaxID=2371;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RX      STRAIN=9a5c;
RX      MEDLINE=20365717; PubMed=10910347; DOI=10.1038/35018003;
RA      Simpson A.J.G., Reinach F.C., Abreu F.A., Acencio M.,
RA      Alvaranga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,

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RA      Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA      Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrier H.,
RA      Coutaro N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.H.,
RA      Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorriy H.,
RA      Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.R.,
RA      Fraga J.S., Franca S.C., Franco M.C., Fromme M., Furlan L.R.,
RA      Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA      Ho P.L., Hohisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA      Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA      Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA      Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA      Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA      Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA      Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA      Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA      de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA      Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA      Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA      de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA      da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA      de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsukumo M.H.,
RA      Valada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA      Zago M.A., Zatz M., Zeldanis J., Setubal J.C.;
RT      "The genome sequence of the plant pathogen Xylella fastidiosa.";
RL      Nature 406:151-159(2000).
DR      EMBL; AE003930; AAP83722.1; -, Genomic_DNA.
DR      PIR; D82748; D82748.
DR      HSSP; P25663; 10X8.
DR      InterPro; IPR007481; SGPB.
DR      Pfam; PF04386; SGPB; 1.
DR      PIRSF; PIRSF005276; SGPB; 1.
KW      Complete proteome.
SQ      SEQUENCE 146 AA; 15714 MW; 42C9394A957802DC CRC64;

Query Match      51.7%; Score 46; DB 2; Length 146;
Best Local Similarity 43.8%; Pred. No. 14;
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Cy      2 TYPGNDISTYNQKFXG 17
Db      66 LHIGNDGVSNARFG 81

RESULT 47
ID      08DEJ5_VIBVU PRELIMINARY; PRT; 158 AA.
AC      08DEJ5:
DT      01-MAR-2003 (TReMBLrel. 23, Created)
DT      01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT      01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE      Stringent starvation protein B.
GN      OrderedLocustNames=VV10593;
OS      Vibrio vulnificus.
OC      Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC      Vibrionaceae; Vibrio.
OX      NCBI_TaxID=672;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RX      STRAIN=CMCP6;
RX      Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
RX      Choy H.E.;
RT      "Complete genome sequence of Vibrio vulnificus CMCP6.";
RL      Submitted (DRC-2002) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AE016799; AA009109.1; -, Genomic_DNA.
DR      HSSP; P25663; 10X9.
DR      SMR; O8DEJ5; 5-110.
DR      InterPro; IPR007481; SGPB.
DR      Pfam; PF04386; SGPB; 1.
KW      Complete proteome.
SQ      SEQUENCE 158 AA; 17642 MW; 163905C5A9315431 CRC64;

Query Match      51.7%; Score 46; DB 2; Length 158;

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Best Local Similarity 61.5%; Pred. No. 15;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Qy 5 GNDDISYNOKFXG 17
Db 66 GNDTISFNARFG 78

RESULT 48

Q7MNM5 VIBVY

ID Q7MNM5 VIBVY PRELIMINARY; PRT; 158 AA.

AC 07MNM5-2004 (TREMBLrel. 26, Created)

DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)

DE Stringent starvation protein B.

GN OrderedLocNames=V00600;

OS Vibrio vulnificus (strain Y016).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;

OC Vibrionaceae; Vibrrio.

OX NCBI_TaxID=196600;

RP NUCLEOTIDE SEQUENCE.

RA PubMed=1456965; DOI=10.1101/gr.1295503;

RA Chen C.-Y., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C.,

RA Liao T.-L., Liu Y.-M., Shen A.B.-T., Li J.-C., Su T.-L.,

RA Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-F.;

RT "Comparative genome analysis of Vibrio vulnificus, a marine

pathogen."

RL Genome Res. 13:2577-2587 (2003).

DR EMBL; BA000037; BAC93364.1; -; Genomic_DNA.

DR HSSP; P25663; 10X9.

DR SMR; Q7MNM5; 5-110.

DR InterPro; IPR007481; SGPB.

DR Pfam; PF04386; SGPB; 1.

DR PIRSF; PIRSF005276; SGPB; 1.

KW Complete proteome.

SO SEQUENCE 158 AA; 17642 MW; 163905C5A9315431 CRC64;

Query Match 51.7%; Score 46; DB 2; Length 158;
Best Local Similarity 61.5%; Pred. No. 15;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 5 GNDDISYNOKFXG 17
Db 66 GNDTISFNARFG 78

RESULT 49
Q8R3H6 MOUSE PRELIMINARY; PRT; 474 AA.

AC Q8R3H6-2002 (TREMBLrel. 21, Created)

DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)

DE 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

DE 199g protein.

GN Name=199g; Synonyms=AU044919;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Muridae; Mus.

OX NCBI_TaxID=10090;

RP NUCLEOTIDE SEQUENCE.

RA STRAIN=CZECH IT;

RA TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;

RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Ditschenko L., Marinina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McEwan S.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzyzanski M.I., Skalska U., Smallos D.E.,

RA Schermer A., Schein J.E., Jones S.J.M., Marra M.A.,

RT "Generation and initial analysis of more than 15,000 full-length human

and mouse cDNA sequences."

RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=CZECH IT;

RC TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;

RA Director MGC Project;

RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC025447; AAH25447.1; -; mRNA.

DR HSSP; P01869; 1CL7.

DR SMR; Q8R3H6; 20-470.

DR MGI; MGI:2144967; AU044919.

DR MGI; MGI:2144967; 199g.

DR GO; GO:0003823; F:antigen binding; IEA.

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003597; IG C1.

DR InterPro; IPR003066; IG_MHC.

DR InterPro; IPR003596; IG_V.

DR Pfam; PF07654; C1-set; 3.

DR SMART; SMO0406; IG; 1.

DR PROSITE; PS00290; IG_LIKE; 4.

DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.

KW Immunoglobulin domain.

SO SEQUENCE 474 AA; 51749 MW; 8608B57C6CD2874A CRC64;

Query Match 51.7%; Score 46; DB 2; Length 474;
Best Local Similarity 50.0%; Pred. No. 52;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 2 TYRNDISYNOKFXG 17
Db 70 IFPGDGDTHYSKFG 85

RESULT 50
O94613 SCHPO PRELIMINARY; PRT; 558 AA.

AC O94613-1999 (TREMBLrel. 10, Created)

DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)

DE 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

DE SPAC1296.06 protein (BC 1.6.2.4).

GN ORENAMES=SPAC1296.06;

OS Schizosaccharomyces pombe (Fission Yeast).

OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

OC Schizosaccharomycetales; Schizosaccharomycetaceae;

OC Schizosaccharomycetes.

OX NCBI_TaxID=4896;

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RA STRAIN=972;

RA MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;

RA Wood V., Gwilliam R., Rajandream M.A., Lyne M.H., Lyne R., Stewart A.,

RA Sgouros J.G., Peat N., Hayles J., Baker S.G., Bauman S.,

RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,

RA Gentles S., Goble A., Hamlin N., Harris D.E., Hidalgo J., Hodgson G.,

RA Holtroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,

RA James K.D., Jones L., Jones M., Leather S., McDonald S., McLean J.,

RA Mooney P., Moule S., Mungall K.L., Murphy L.D., Niblett D., Odell C.,

RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitz E.,

RA Rutherford K.M., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M.N., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J.R., Volckaert G., Aert R., Robben J., Grymompiez B.,
 RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Duesterhoeft A., Filtz C., Holzer E., Moestl D.,
 RA Hilbert H., Borzym K., langer I., Beck A., Lehnach H., Reinhardt R.,
 RA Pohl T.M., Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Leleaux V., Mortier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shipakovski G.V., Usery D., Barrell B.G., Nurse P.,
 RT "The genome sequence of Schizosaccharomyces pombe.";
 RL Nature 415:871-880(2002).
 DR EMBL; AL035439; CAB36512.2; -; Genomic_DNA.
 DR PIR; T37567; T37567.
 DR HSSP; P00388; IAMO.
 DR Gened3_Spombe; SPAC1296.06; -;
 DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0010181; F:FMN binding; IEA.
 DR GO; GO:0003958; F:NADPH-hemoprotein reductase activity; IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR003097; FAD_binding.
 DR InterPro; IPR001094; Flavodoxin_like.
 DR InterPro; IPR008254; Flav_nitox_synth.
 DR InterPro; IPR001709; FPN_cyt_reductse.
 DR InterPro; IPR001433; Oxred_FAD/NAD(P).
 DR pfam; PF00667; FAD_binding_1; 1.
 DR pfam; PF00258; Flavodoxin_1; 1.
 DR pfam; PF00175; NAD_binding_1; 1.
 DR PRINTS; PR00369; FLAVODOXIN.
 DR PRINTS; PR00371; FPNCR.
 DR PROSITE; PS50902; FLAVODOXIN LIKE; 1.
 KW Complete proteome; Oxidoreductase.
 SQ SEQUENCE 558 AA; 64199 MW; 12D64991612E7E00 CRC64;

Query Match 51.7%; Score 46; DB 2; Length 558;
 Best Local Similarity 66.7%; Pred.No. 62;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VLYPNDISYN 12
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 Db 215 VLYPNDISYN 226

Search completed: May 4, 2006, 13:08:09
 Job time : 211.206 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 4, 2006, 13:09:53 ; Search time 38.3175 Seconds
(without alignments)
36.680 Million cell updates/sec

Title: US-10-700-632-2
Perfect score: 89
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Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued_Patents_AA:*

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- 2: /cgn2_6/ptodata/1/1aa/6_COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/H_COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/RE_COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/Backlist1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	73	82.0	17	2	US-08-479-089A-8
2	73	82.0	17	2	US-07-669-545B-8
3	73	82.0	106	1	US-08-793-490-9
4	73	82.0	117	2	US-08-479-089A-2
5	73	82.0	117	2	US-08-479-089A-3
6	73	82.0	117	2	US-07-669-545B-2
7	73	82.0	117	2	US-07-669-545B-3
8	72	80.9	140	1	US-08-476-275-6
9	72	80.9	140	2	US-08-475-815B-11
10	72	80.9	140	2	US-09-724-138-44
11	72	80.9	140	2	US-08-475-813-6
12	72	80.9	140	2	US-09-630-198-44
13	72	80.9	470	2	US-09-238-741-4
14	69	77.5	118	2	US-08-766-350B-48
15	68	76.4	117	2	US-09-091-071-7
16	68	76.4	114	2	US-09-344-587-10
17	68	76.4	115	2	US-09-232-290-33
18	68	76.4	120	1	US-09-091-071-2
19	68	76.4	133	1	US-08-822-028-6
20	68	76.4	133	1	US-08-822-028-6
21	68	76.4	133	1	US-08-822-028-6
22	68	76.4	133	2	US-08-479-285-6
23	68	76.4	133	2	US-08-479-285-10
24	68	76.4	133	2	US-08-961-309-48
25	68	76.4	133	2	US-09-503-653A-6
26	68	76.4	133	6	US-09-503-653A-30
27	68	76.4	134	1	US-08-822-028-10

28	68	76.4	134	2	US-08-479-285-10	Sequence 10, Appl
29	68	76.4	134	2	US-08-961-309-49	Sequence 49, Appl
30	68	76.4	134	2	US-09-503-653A-10	Sequence 10, Appl
31	68	76.4	150	1	US-08-400-115-2	Sequence 2, Appl
32	68	76.4	271	1	US-08-403-853-18	Sequence 4, Appl
33	66	74.2	273	1	US-08-403-853-18	Sequence 18, Appl
34	64	71.9	257	2	US-09-419-788-113	Sequence 113, App
35	63	70.8	17	1	US-08-318-970B-4	Sequence 4, Appl
36	62	69.7	153	2	US-09-096-244-4	Sequence 4, Appl
37	62	69.7	153	2	US-08-766-350B-4	Sequence 4, Appl
38	61	68.5	117	1	US-08-822-028-2	Sequence 2, Appl
39	61	68.5	117	2	US-08-479-285-2	Sequence 2, Appl
40	61	68.5	117	2	US-08-961-309-45	Sequence 45, Appl
41	61	68.5	117	2	US-09-503-653A-2	Sequence 2, Appl
42	61	68.5	132	2	US-09-386-658A-2	Sequence 2, Appl
43	60	67.4	355	2	US-08-875-811-57	Sequence 57, Appl
44	59	66.3	17	2	US-09-830-748B-5	Sequence 5, Appl
45	59	66.3	42	2	US-09-244-592-6	Sequence 6, Appl
46	59	66.3	46	2	US-09-244-592-3	Sequence 3, Appl
47	59	66.3	75	2	US-09-244-592-4	Sequence 4, Appl
48	59	66.3	90	2	US-09-244-592-5	Sequence 5, Appl
49	59	66.3	90	1	US-08-263-911-4	Sequence 2, Appl
50	59	66.3	115	1	US-08-819-033-2	Sequence 2, Appl
51	59	66.3	115	1	US-09-025-203-1	Sequence 1, Appl
52	59	66.3	115	2	US-09-025-203-3	Sequence 3, Appl
53	59	66.3	115	2	US-09-025-203-4	Sequence 4, Appl
54	59	66.3	115	2	US-09-025-203-5	Sequence 5, Appl
55	59	66.3	115	2	US-09-025-203-6	Sequence 6, Appl
56	59	66.3	115	2	US-09-025-203-10	Sequence 10, Appl
57	59	66.3	115	2	US-09-025-203-11	Sequence 11, Appl
58	59	66.3	115	2	US-08-961-309-14	Sequence 14, Appl
59	59	66.3	115	2	US-08-961-309-16	Sequence 16, Appl
60	59	66.3	115	2	US-08-961-309-16	Sequence 76, Appl
61	59	66.3	115	2	US-09-999-021-1	Sequence 1, Appl
62	59	66.3	115	2	US-09-999-021-3	Sequence 3, Appl
63	59	66.3	115	2	US-09-999-021-4	Sequence 4, Appl
64	59	66.3	115	2	US-09-999-021-5	Sequence 5, Appl
65	59	66.3	115	2	US-09-999-021-6	Sequence 6, Appl
66	59	66.3	115	2	US-09-999-021-10	Sequence 10, Appl
67	59	66.3	115	2	US-09-999-021-11	Sequence 11, Appl
68	59	66.3	115	2	US-09-999-025-1	Sequence 1, Appl
69	59	66.3	115	2	US-09-999-025-3	Sequence 3, Appl
70	59	66.3	115	2	US-09-999-025-4	Sequence 4, Appl
71	59	66.3	115	2	US-09-999-025-5	Sequence 5, Appl
72	59	66.3	115	2	US-09-999-025-6	Sequence 6, Appl
73	59	66.3	115	2	US-09-999-025-10	Sequence 10, Appl
74	59	66.3	115	2	US-09-999-025-11	Sequence 11, Appl
75	59	66.3	115	2	US-10-040-997-1	Sequence 1, Appl
76	59	66.3	115	2	US-10-040-997-3	Sequence 3, Appl
77	59	66.3	115	2	US-10-040-997-7	Sequence 7, Appl
78	59	66.3	115	2	US-10-040-997-5	Sequence 5, Appl
79	59	66.3	115	2	US-10-040-997-6	Sequence 6, Appl
80	59	66.3	115	2	US-10-040-997-10	Sequence 10, Appl
81	59	66.3	115	2	US-10-040-997-11	Sequence 11, Appl
82	59	66.3	115	2	US-09-999-040-1	Sequence 1, Appl
83	59	66.3	115	2	US-09-999-040-3	Sequence 3, Appl
84	59	66.3	115	2	US-09-999-040-4	Sequence 4, Appl
85	59	66.3	115	2	US-09-999-040-5	Sequence 5, Appl
86	59	66.3	115	2	US-09-999-040-6	Sequence 6, Appl
87	59	66.3	115	2	US-09-999-040-10	Sequence 10, Appl
88	59	66.3	115	2	US-09-999-040-11	Sequence 11, Appl
89	59	66.3	115	2	US-09-998-817-3	Sequence 3, Appl
90	59	66.3	115	2	US-09-998-817-4	Sequence 4, Appl
91	59	66.3	115	2	US-09-998-817-5	Sequence 5, Appl
92	59	66.3	115	2	US-09-998-817-6	Sequence 6, Appl
93	59	66.3	115	2	US-09-998-817-7	Sequence 7, Appl
94	59	66.3	115	2	US-09-998-817-10	Sequence 10, Appl
95	59	66.3	115	2	US-09-998-817-11	Sequence 11, Appl
96	59	66.3	115	2	US-09-830-748B-14	Sequence 14, Appl
97	59	66.3	116	2	US-09-244-592-1	Sequence 1, Appl
98	59	66.3	119	2	US-10-194-975-121	Sequence 121, App
99	59	66.3	134	1	US-08-822-028-4	Sequence 4, Appl
100	59	66.3	134	1	US-08-822-028-8	Sequence 8, Appl

101	59	66.3	134	1	US-08-822-028-29	Sequence 29, Appl	174	59	66.3	483	2	US-09-166-094-19	Sequence 19, Appl
102	59	66.3	134	2	US-08-479-285-4	Sequence 4, Appl	175	59	66.3	483	2	US-09-443-213-19	Sequence 19, Appl
103	59	66.3	134	2	US-08-479-285-8	Sequence 8, Appl	176	59	66.3	553	1	US-08-263-911-7	Sequence 7, Appl
104	59	66.3	134	2	US-08-479-285-29	Sequence 29, Appl	177	59	66.3	553	1	US-08-263-911-9	Sequence 9, Appl
105	59	66.3	134	2	US-08-961-309-46	Sequence 46, Appl	178	58	65.2	111	2	US-09-823-746-10	Sequence 10, Appl
106	59	66.3	134	2	US-08-961-309-47	Sequence 47, Appl	179	58	65.2	111	2	US-09-823-746-14	Sequence 14, Appl
107	59	66.3	134	2	US-09-503-653A-4	Sequence 4, Appl	180	58	65.2	119	1	US-08-458-516-10	Sequence 10, Appl
108	59	66.3	134	2	US-09-503-653A-8	Sequence 8, Appl	181	58	65.2	119	1	US-08-458-516-11	Sequence 11, Appl
109	59	66.3	134	2	US-09-503-653A-29	Sequence 29, Appl	182	58	65.2	138	1	US-08-458-516-7	Sequence 7, Appl
110	59	66.3	238	1	US-08-224-551-12	Sequence 12, Appl	183	58	65.2	141	1	US-08-459-567-4	Sequence 4, Appl
111	59	66.3	238	1	US-08-392-338A-21	Sequence 21, Appl	184	58	65.2	222	1	US-08-458-516-22	Sequence 22, Appl
112	59	66.3	238	1	US-08-926-789-12	Sequence 12, Appl	185	58	65.2	235	1	US-08-458-516-23	Sequence 23, Appl
113	59	66.3	238	2	US-09-166-750-21	Sequence 21, Appl	186	58	65.2	449	1	US-08-458-516-13	Sequence 13, Appl
114	59	66.3	238	2	US-09-166-093-21	Sequence 21, Appl	187	57	64.0	247	1	US-10-620-049-21	Sequence 21, Appl
115	59	66.3	238	2	US-09-172-019-21	Sequence 21, Appl	188	56	62.9	17	2	US-09-563-222C-57	Sequence 57, Appl
116	59	66.3	238	2	US-09-166-094-21	Sequence 21, Appl	189	56	62.9	121	2	US-08-579-378A-7	Sequence 7, Appl
117	59	66.3	238	2	US-09-443-213-21	Sequence 21, Appl	190	56	62.9	121	2	US-08-579-378A-8	Sequence 8, Appl
118	59	66.3	239	4	PCT-US93-11138-12	Sequence 12, Appl	191	56	62.9	121	4	PCT-US93-11612-7	Sequence 7, Appl
119	59	66.3	240	1	US-08-392-338A-11	Sequence 11, Appl	192	56	62.9	121	4	PCT-US93-11612-8	Sequence 8, Appl
120	59	66.3	240	2	US-09-166-750-11	Sequence 11, Appl	193	56	62.9	125	2	US-09-357-710A-20	Sequence 20, Appl
121	59	66.3	240	2	US-09-166-093-11	Sequence 11, Appl	194	56	62.9	125	2	US-09-357-707-20	Sequence 20, Appl
122	59	66.3	240	2	US-09-172-019-11	Sequence 11, Appl	195	56	62.9	125	2	US-09-357-708-20	Sequence 20, Appl
123	59	66.3	240	2	US-09-166-094-11	Sequence 11, Appl	196	56	62.9	128	1	US-08-202-047-21	Sequence 21, Appl
124	59	66.3	240	2	US-09-443-213-11	Sequence 11, Appl	197	56	62.9	128	2	US-08-964-690-21	Sequence 21, Appl
125	59	66.3	241	2	US-09-791-540-6	Sequence 6, Appl	198	56	62.9	135	1	US-08-860-174A-4	Sequence 4, Appl
126	59	66.3	241	2	US-09-791-578-6	Sequence 6, Appl	199	56	62.9	140	2	US-08-579-378A-4	Sequence 4, Appl
127	59	66.3	244	2	US-09-244-369B-1	Sequence 1, Appl	200	56	62.9	140	2	US-08-579-378A-12	Sequence 12, Appl
128	59	66.3	244	2	US-09-940-391-1	Sequence 1, Appl	201	56	62.9	140	4	PCT-US93-11612-4	Sequence 4, Appl
129	59	66.3	246	2	US-09-791-540-2	Sequence 2, Appl	202	56	62.9	140	4	PCT-US93-11612-12	Sequence 12, Appl
130	59	66.3	246	2	US-09-791-578-2	Sequence 2, Appl	203	56	62.9	247	2	US-10-620-049-23	Sequence 23, Appl
131	59	66.3	248	1	US-08-323-445A-6	Sequence 6, Appl	204	56	62.9	247	2	US-10-620-049-25	Sequence 25, Appl
132	59	66.3	248	1	US-08-515-903A-6	Sequence 6, Appl	205	56	62.9	249	1	US-08-797-689-18	Sequence 18, Appl
133	59	66.3	248	4	PCT-US95-12840-6	Sequence 6, Appl	206	56	62.9	249	1	US-09-984-186-18	Sequence 18, Appl
134	59	66.3	249	2	US-09-069-821-2	Sequence 2, Appl	207	56	62.9	274	1	US-08-860-174A-12	Sequence 12, Appl
135	59	66.3	249	2	US-09-986-086-2	Sequence 2, Appl	208	55	61.8	17	2	US-09-508-413A-4	Sequence 4, Appl
136	59	66.3	257	2	US-09-956-087-2	Sequence 2, Appl	209	55	61.8	113	2	US-09-508-413A-14	Sequence 14, Appl
137	59	66.3	257	2	US-09-420-592A-2	Sequence 2, Appl	210	55	61.8	231	1	US-08-681-432-1	Sequence 1, Appl
138	59	66.3	257	2	US-09-985-442-2	Sequence 2, Appl	211	54	60.7	216	1	US-08-888-366-2	Sequence 2, Appl
139	59	66.3	257	2	US-09-983-580-2	Sequence 2, Appl	212	54	60.7	219	2	US-09-254-180C-131	Sequence 131, App
140	59	66.3	257	2	US-09-791-540-4	Sequence 4, Appl	213	54	60.7	219	2	US-09-254-180C-181	Sequence 181, App
141	59	66.3	257	2	US-09-791-578-4	Sequence 4, Appl	214	53	59.6	17	1	US-08-318-970B-7	Sequence 7, Appl
142	59	66.3	260	2	US-08-463-903-2	Sequence 2, Appl	215	53	59.6	17	2	US-09-269-921-7	Sequence 7, Appl
143	59	66.3	260	2	US-07-935-695-2	Sequence 2, Appl	216	53	59.6	98	2	US-08-881-037-64	Sequence 64, Appl
144	59	66.3	260	2	US-08-961-309-64	Sequence 64, Appl	217	53	59.6	116	2	US-09-065-059-9	Sequence 9, Appl
145	59	66.3	262	1	US-08-323-445A-4	Sequence 4, Appl	218	53	59.6	116	2	US-08-913-555-9	Sequence 9, Appl
146	59	66.3	262	1	US-08-515-903A-4	Sequence 4, Appl	219	53	59.6	117	2	US-08-913-555-27	Sequence 27, Appl
147	59	66.3	262	4	PCT-US95-12840-4	Sequence 4, Appl	220	53	59.6	124	1	US-08-657-012-16	Sequence 16, Appl
148	59	66.3	264	1	US-08-323-445A-8	Sequence 8, Appl	221	53	59.6	124	1	US-08-657-012-17	Sequence 17, Appl
149	59	66.3	264	1	US-08-515-903A-8	Sequence 8, Appl	222	53	59.6	124	1	US-08-657-012-18	Sequence 18, Appl
150	59	66.3	264	4	PCT-US95-12840-8	Sequence 8, Appl	223	53	59.6	124	1	US-08-657-012-19	Sequence 19, Appl
151	59	66.3	269	2	US-09-420-592A-4	Sequence 4, Appl	224	53	59.6	124	1	US-08-657-012-23	Sequence 23, Appl
152	59	66.3	269	2	US-09-985-442-4	Sequence 4, Appl	225	53	59.6	124	2	US-09-013-872-16	Sequence 16, Appl
153	59	66.3	269	2	US-09-983-580-4	Sequence 4, Appl	226	53	59.6	124	2	US-09-013-872-17	Sequence 17, Appl
154	59	66.3	274	2	US-08-961-309-66	Sequence 66, Appl	227	53	59.6	124	2	US-09-013-872-18	Sequence 18, Appl
155	59	66.3	275	2	US-08-463-903-6	Sequence 6, Appl	228	53	59.6	124	2	US-09-013-872-19	Sequence 19, Appl
156	59	66.3	275	2	US-08-463-903-8	Sequence 8, Appl	229	53	59.6	124	2	US-09-013-872-23	Sequence 23, Appl
157	59	66.3	275	2	US-08-463-903-17	Sequence 17, Appl	230	53	59.6	124	2	US-09-184-198-16	Sequence 16, Appl
158	59	66.3	275	2	US-07-935-695-6	Sequence 6, Appl	231	53	59.6	124	2	US-09-184-198-17	Sequence 17, Appl
159	59	66.3	275	2	US-07-935-695-8	Sequence 8, Appl	232	53	59.6	124	2	US-09-184-198-18	Sequence 18, Appl
160	59	66.3	280	2	US-07-935-695-17	Sequence 17, Appl	233	53	59.6	124	2	US-09-184-198-19	Sequence 19, Appl
161	59	66.3	280	2	US-08-463-903-10	Sequence 10, Appl	234	53	59.6	124	2	US-09-184-198-23	Sequence 23, Appl
162	59	66.3	280	2	US-07-935-695-10	Sequence 10, Appl	235	53	59.6	124	2	US-09-633-653-16	Sequence 16, Appl
163	59	66.3	282	2	US-08-463-903-12	Sequence 12, Appl	236	53	59.6	124	2	US-09-633-653-17	Sequence 17, Appl
164	59	66.3	282	2	US-08-463-903-15	Sequence 15, Appl	237	53	59.6	124	2	US-09-633-653-18	Sequence 18, Appl
165	59	66.3	282	2	US-07-935-695-12	Sequence 12, Appl	238	53	59.6	124	2	US-09-633-653-19	Sequence 19, Appl
166	59	66.3	282	2	US-07-935-695-15	Sequence 15, Appl	239	53	59.6	124	2	US-09-633-653-23	Sequence 23, Appl
167	59	66.3	284	2	US-08-961-309-70	Sequence 70, Appl	240	53	59.6	139	2	US-09-355-925-7	Sequence 7, Appl
168	59	66.3	285	2	US-08-463-903-22	Sequence 22, Appl	241	53	59.6	139	2	US-09-355-925-8	Sequence 8, Appl
169	59	66.3	285	2	US-07-935-695-22	Sequence 22, Appl	242	53	59.6	139	2	US-09-269-921-105	Sequence 105, App
170	59	66.3	483	1	US-08-392-338A-19	Sequence 19, Appl	243	53	59.6	139	2	US-09-269-921-108	Sequence 108, App
171	59	66.3	483	2	US-09-166-750-19	Sequence 19, Appl	244	53	59.6	139	2	US-09-269-921-109	Sequence 109, App
172	59	66.3	483	2	US-09-166-093-19	Sequence 19, Appl	245	53	59.6	139	2	US-09-269-921-110	Sequence 110, App
173	59	66.3	483	2	US-09-172-019-19	Sequence 19, Appl	246	53	59.6	139	2	US-09-269-921-111	Sequence 111, App

247	53	59.6	139	2	US-09-269-921-112	Sequence 112, App	320	50	56.2	120	2	US-09-490-153-40	Sequence 40, Appl
248	53	59.6	139	2	US-09-269-921-113	Sequence 113, App	321	50	56.2	120	2	US-09-490-153-40	Sequence 67, Appl
249	53	59.6	139	2	US-09-269-921-114	Sequence 114, App	322	50	56.2	120	2	US-09-490-153-40	Sequence 40, Appl
250	53	59.6	139	2	US-09-269-921-115	Sequence 115, App	323	50	56.2	120	2	US-09-490-153-40	Sequence 67, Appl
251	53	59.6	139	2	US-09-269-921-116	Sequence 116, App	324	50	56.2	122	2	US-08-767-128-4	Sequence 4, Appl
252	53	59.6	139	2	US-09-269-921-117	Sequence 117, App	325	50	56.2	137	1	US-08-116-778E-3	Sequence 3, Appl
253	53	59.6	139	2	US-09-269-921-118	Sequence 118, App	326	50	56.2	137	1	US-08-438-562-3	Sequence 93, Appl
254	53	59.6	139	2	US-09-269-921-119	Sequence 119, App	327	50	56.2	137	1	US-08-483-528B-93	Sequence 44, Appl
255	53	59.6	139	2	US-09-269-921-120	Sequence 120, App	328	50	56.2	138	2	US-08-513-968-4	Sequence 11, Appl
256	53	59.6	139	2	US-09-269-921-121	Sequence 121, App	329	50	56.2	139	1	US-08-116-778E-1	Sequence 1, Appl
257	53	59.6	139	2	US-09-269-921-122	Sequence 122, App	330	50	56.2	139	1	US-08-438-562-1	Sequence 1, Appl
258	53	59.6	139	2	US-09-269-921-123	Sequence 123, App	331	50	56.2	139	1	US-08-483-528B-91	Sequence 36, Appl
259	53	59.6	139	2	US-09-269-921-124	Sequence 124, App	332	50	56.2	144	1	US-08-116-778E-36	Sequence 100, App
260	53	59.6	139	2	US-09-269-921-125	Sequence 125, App	333	50	56.2	144	1	US-08-438-562-46	Sequence 112, App
261	53	59.6	139	2	US-09-269-921-126	Sequence 126, App	334	50	56.2	144	1	US-08-483-528B-100	Sequence 6, Appl
262	53	59.6	139	2	US-09-269-921-127	Sequence 127, App	335	50	56.2	144	2	US-09-393-185B-112	Sequence 112, App
263	53	59.6	139	2	US-09-269-921-128	Sequence 128, App	336	50	56.2	144	2	US-10-135-752-112	Sequence 6, Appl
264	53	59.6	200	6	US-09-905-243-12	Sequence 12, App	337	50	56.2	222	2	US-08-737-129A-6	Sequence 25, Appl
265	52	58.4	96	2	US-09-905-243-13	Sequence 13, App	338	50	56.2	264	2	US-10-114-716A-46	Sequence 46, Appl
266	52	58.4	119	2	US-09-344-587-11	Sequence 11, App	339	50	56.2	301	1	US-08-656-906-25	Sequence 25, Appl
267	52	58.4	120	2	US-09-513-999C-7802	Sequence 7802, App	340	50	56.2	301	2	US-09-217-847-25	Sequence 13, Appl
268	52	58.4	237	1	US-08-468-252-5	Sequence 5, Appl	341	49	55.1	17	2	US-10-146-305-13	Sequence 1, Appl
269	52	58.4	237	1	US-08-668-706B-5	Sequence 5, Appl	342	49	55.1	102	1	US-08-793-490-1	Sequence 1, Appl
270	52	58.4	237	4	PCT-US95-10740-5	Sequence 5, Appl	343	49	55.1	117	2	US-09-027-449-48	Sequence 48, Appl
271	52	58.4	17	1	US-08-482-228-40	Sequence 40, Appl	344	49	55.1	117	2	US-09-027-449-49	Sequence 49, Appl
272	51	57.3	17	2	US-08-482-528-40	Sequence 40, Appl	345	49	55.1	117	2	US-08-804-444A-48	Sequence 48, Appl
273	51	57.3	31	2	US-08-525-539A-34	Sequence 34, Appl	346	49	55.1	117	2	US-08-804-444A-49	Sequence 49, Appl
274	51	57.3	98	2	US-09-905-243-47	Sequence 47, Appl	347	49	55.1	117	2	US-09-026-985-48	Sequence 48, Appl
275	51	57.3	112	1	US-07-942-245-23	Sequence 23, Appl	348	49	55.1	117	2	US-09-026-985-49	Sequence 49, Appl
276	51	57.3	115	1	US-08-672-345C-16	Sequence 16, Appl	349	49	55.1	117	2	US-09-121-952A-48	Sequence 48, Appl
277	51	57.3	115	2	US-09-214-095D-16	Sequence 16, Appl	350	49	55.1	117	2	US-09-121-952A-49	Sequence 49, Appl
278	51	57.3	115	2	US-09-940-727B-16	Sequence 16, Appl	351	49	55.1	117	2	US-09-234-340A-48	Sequence 48, Appl
279	51	57.3	118	1	US-08-491-845-6	Sequence 6, Appl	352	49	55.1	117	2	US-09-234-340A-49	Sequence 49, Appl
280	51	57.3	118	1	US-08-491-845-14	Sequence 14, Appl	353	49	55.1	117	2	US-09-355-014-48	Sequence 48, Appl
281	51	57.3	121	2	US-09-232-290-59	Sequence 59, Appl	354	49	55.1	117	2	US-09-355-014-49	Sequence 49, Appl
282	51	57.3	137	2	US-08-513-968-38	Sequence 38, Appl	355	49	55.1	119	2	US-08-767-128-10	Sequence 10, Appl
283	51	57.3	138	2	US-08-589-939-1	Sequence 9, Appl	356	49	55.1	119	2	US-09-556-605-1	Sequence 1, Appl
284	51	57.3	140	2	US-09-069-628-28	Sequence 28, Appl	357	49	55.1	120	2	US-08-875-706C-1	Sequence 1, Appl
285	51	57.3	17	1	US-08-116-778E-7	Sequence 7, Appl	358	49	55.1	122	2	US-08-983-607-30	Sequence 30, Appl
286	50	56.2	17	1	US-08-438-562-7	Sequence 7, Appl	359	49	55.1	125	1	US-08-665-302-44	Sequence 44, Appl
287	50	56.2	17	1	US-08-483-528B-95	Sequence 95, Appl	360	49	55.1	125	1	US-08-665-302-45	Sequence 45, Appl
288	50	56.2	17	1	US-08-672-345C-65	Sequence 65, Appl	361	49	55.1	125	1	US-08-665-302-46	Sequence 46, Appl
289	50	56.2	17	2	US-09-214-095D-65	Sequence 65, Appl	362	49	55.1	125	1	US-08-665-302-47	Sequence 47, Appl
290	50	56.2	17	2	US-09-393-385B-106	Sequence 106, App	363	49	55.1	125	1	US-08-665-302-48	Sequence 48, Appl
291	50	56.2	17	2	US-09-724-409-9	Sequence 9, Appl	364	49	55.1	125	1	US-08-665-302-49	Sequence 49, Appl
292	50	56.2	17	2	US-10-195-752-106	Sequence 106, App	365	49	55.1	125	1	US-08-665-302-50	Sequence 50, Appl
293	50	56.2	17	2	US-09-940-727B-65	Sequence 65, Appl	366	49	55.1	125	1	US-08-665-302-51	Sequence 51, Appl
294	50	56.2	17	2	US-08-478-039-81	Sequence 81, Appl	367	49	55.1	125	1	US-08-665-302-52	Sequence 52, Appl
295	50	56.2	17	2	US-08-665-202-33	Sequence 33, Appl	368	49	55.1	125	1	US-08-665-302-53	Sequence 53, Appl
296	50	56.2	17	2	US-09-315-574-33	Sequence 33, Appl	369	49	55.1	125	1	US-09-315-574-34	Sequence 34, Appl
297	50	56.2	17	2	US-09-315-574-45	Sequence 45, Appl	370	49	55.1	125	1	US-09-315-574-46	Sequence 46, Appl
298	50	56.2	17	2	US-09-315-574-45	Sequence 45, Appl	371	49	55.1	125	1	US-09-315-574-47	Sequence 47, Appl
299	50	56.2	17	2	US-09-315-574-45	Sequence 45, Appl	372	49	55.1	125	1	US-09-315-574-48	Sequence 48, Appl
300	50	56.2	17	2	US-09-315-574-45	Sequence 45, Appl	373	49	55.1	125	1	US-09-315-574-49	Sequence 49, Appl
301	50	56.2	17	2	US-09-315-574-45	Sequence 45, Appl	374	49	55.1	125	1	US-09-315-574-50	Sequence 50, Appl
302	50	56.2	17	2	US-09-315-574-45	Sequence 45, Appl	375	49	55.1	125	1	US-09-315-574-51	Sequence 51, Appl
303	50	56.2	17	2	US-09-315-574-45	Sequence 45, Appl	376	49	55.1	125	1	US-09-315-574-52	Sequence 52, Appl
304	50	56.2	17	2	US-09-315-574-45	Sequence 45, Appl	377	49	55.1	125	1	US-09-315-574-53	Sequence 53, Appl
305	50	56.2	17	2	US-09-315-574-45	Sequence 45, Appl	378	49	55.1	125	1	US-09-315-574-54	Sequence 54, Appl
306	50	56.2	17	2	US-09-315-574-45	Sequence 45, Appl	379	49	55.1	125	1	US-09-315-574-55	Sequence 55, Appl
307	50	56.2	17	2	US-09-315-574-45	Sequence 45, Appl	380	49	55.1	125	1	US-09-315-574-56	Sequence 56, Appl
308	50	56.2	17	2	US-09-315-574-45	Sequence 45, Appl	381	49	55.1	125	1	US-09-315-574-57	Sequence 57, Appl
309	50	56.2	17	2	US-09-315-574-45	Sequence 45, Appl	382	49	55.1	125	1	US-09-315-574-58	Sequence 58, Appl
310	50	56.2	17	2	US-09-315-574-45	Sequence 45, Appl	383	49	55.1	125	1	US-09-315-574-59	Sequence 59, Appl
311	50	56.2	17	2	US-09-315-574-45	Sequence 45, Appl	384	49	55.1	125	1	US-09-315-574-60	Sequence 60, Appl
312	50	56.2	17	2	US-09-315-574-45	Sequence 45, Appl	385	49	55.1	125	1	US-09-315-574-61	Sequence 61, Appl
313	50	56.2	17	2	US-09-315-574-45	Sequence 45, Appl	386	49	55.1	125	1	US-09-315-574-62	Sequence 62, Appl
314	50	56.2	17	2	US-09-315-574-45	Sequence 45, Appl	387	49	55.1	125	1	US-09-315-574-63	Sequence 63, Appl
315	50	56.2	17	2	US-09-315-574-45	Sequence 45, Appl	388	49	55.1	125	1	US-09-315-574-64	Sequence 64, Appl
316	50	56.2	17	2	US-09-315-574-45	Sequence 45, Appl	389	49	55.1	125	1	US-09-315-574-65	Sequence 65, Appl
317	50	56.2	17	2	US-09-315-574-45	Sequence 45, Appl	390	49	55.1	125	1	US-09-315-574-66	Sequence 66, Appl
318	50	56.2	17	2	US-09-315-574-45	Sequence 45, Appl	391	49	55.1	125	1	US-09-315-574-67	Sequence 67, Appl
319	50	56.2	17	2	US-09-315-574-45	Sequence 45, Appl	392	49	55.1	125	1	US-09-315-574-68	Sequence 68, Appl

393	49	55.1	135	2	US-09-027-449-37	Sequence 37, Appl	466	48	53.9	119	1	US-08-474-040-65	Sequence 65, Appl
394	49	55.1	135	2	US-08-804-444A-37	Sequence 37, Appl	467	48	53.9	119	1	US-08-474-040-89	Sequence 89, Appl
395	49	55.1	135	2	US-09-026-985-37	Sequence 37, Appl	468	48	53.9	119	1	US-08-487-200-64	Sequence 64, Appl
396	49	55.1	135	2	US-09-121-952A-37	Sequence 37, Appl	469	48	53.9	119	1	US-08-487-200-65	Sequence 65, Appl
397	49	55.1	135	2	US-09-234-340A-37	Sequence 37, Appl	470	48	53.9	119	1	US-08-487-200-89	Sequence 89, Appl
398	49	55.1	135	2	US-09-355-014-37	Sequence 37, Appl	471	48	53.9	119	2	US-08-484-537-64	Sequence 64, Appl
399	49	55.1	138	2	US-10-146-305-8	Sequence 8, Appl	472	48	53.9	119	2	US-08-484-537-65	Sequence 65, Appl
400	49	55.1	239	2	US-10-093-246-33	Sequence 33, Appl	473	48	53.9	119	2	US-08-484-537-89	Sequence 89, Appl
401	49	55.1	239	2	US-10-086-266A-33	Sequence 33, Appl	474	48	53.9	119	2	US-09-438-954-4	Sequence 4, Appl
402	49	55.1	253	1	US-08-398-613A-58	Sequence 58, Appl	475	48	53.9	119	2	US-10-194-975-122	Sequence 122, App
403	49	55.1	253	1	US-08-398-613A-58	Sequence 58, Appl	476	48	53.9	124	2	US-09-232-990-51	Sequence 51, Appl
404	49	55.1	253	1	US-08-398-612A-58	Sequence 58, Appl	477	48	53.9	138	1	US-07-634-278-85	Sequence 85, Appl
405	49	55.1	253	1	US-08-398-611A-58	Sequence 58, Appl	478	48	53.9	138	1	US-08-477-728-85	Sequence 85, Appl
406	49	55.1	253	2	US-08-491-334A-58	Sequence 58, Appl	479	48	53.9	138	1	US-08-474-040-85	Sequence 85, Appl
407	49	55.1	253	2	US-09-027-449-44	Sequence 44, Appl	480	48	53.9	138	1	US-08-487-200-85	Sequence 85, Appl
408	49	55.1	253	2	US-09-027-449-52	Sequence 52, Appl	481	48	53.9	138	2	US-08-484-537-85	Sequence 85, Appl
409	49	55.1	253	2	US-09-027-449-55	Sequence 55, Appl	482	48	53.9	163	2	US-09-318-786-27	Sequence 27, Appl
410	49	55.1	253	2	US-08-804-444A-44	Sequence 44, Appl	483	48	53.9	287	2	US-09-318-786-37	Sequence 37, Appl
411	49	55.1	253	2	US-08-804-444A-52	Sequence 52, Appl	484	47	52.8	17	2	US-07-987-264-2	Sequence 2, Appl
412	49	55.1	253	2	US-09-026-985-44	Sequence 44, Appl	485	47	52.8	22	2	US-08-918-148-4	Sequence 4, Appl
413	49	55.1	253	2	US-09-026-985-52	Sequence 52, Appl	486	47	52.8	22	2	US-09-138-091A-4	Sequence 4, Appl
414	49	55.1	253	2	US-09-026-985-55	Sequence 55, Appl	487	47	52.8	108	1	US-08-273-146-57	Sequence 57, Appl
415	49	55.1	253	2	US-09-121-952A-44	Sequence 44, Appl	488	47	52.8	108	2	US-09-486-814A-4	Sequence 4, Appl
416	49	55.1	253	2	US-09-121-952A-55	Sequence 55, Appl	489	47	52.8	109	2	US-09-497-997C-29	Sequence 29, Appl
417	49	55.1	253	2	US-09-121-952A-55	Sequence 55, Appl	490	47	52.8	116	1	US-07-634-278-56	Sequence 56, Appl
418	49	55.1	253	2	US-09-234-340A-44	Sequence 44, Appl	491	47	52.8	116	1	US-07-634-278-57	Sequence 57, Appl
419	49	55.1	253	2	US-09-234-340A-52	Sequence 52, Appl	492	47	52.8	116	1	US-07-634-278-73	Sequence 73, Appl
420	49	55.1	253	2	US-09-234-340A-55	Sequence 55, Appl	493	47	52.8	116	1	US-08-477-728-56	Sequence 56, Appl
421	49	55.1	253	2	US-09-355-014-44	Sequence 44, Appl	494	47	52.8	116	1	US-08-477-728-57	Sequence 57, Appl
422	49	55.1	253	2	US-09-355-014-52	Sequence 52, Appl	495	47	52.8	116	1	US-08-477-728-73	Sequence 73, Appl
423	49	55.1	253	2	US-09-355-014-55	Sequence 55, Appl	496	47	52.8	116	1	US-08-474-040-56	Sequence 56, Appl
424	49	55.1	256	2	US-09-027-449-70	Sequence 70, Appl	497	47	52.8	116	1	US-08-474-040-57	Sequence 57, Appl
425	49	55.1	256	2	US-09-026-985-70	Sequence 70, Appl	498	47	52.8	116	1	US-08-474-040-73	Sequence 73, Appl
426	49	55.1	256	2	US-09-121-952A-70	Sequence 70, Appl	499	47	52.8	116	1	US-08-487-200-56	Sequence 56, Appl
427	49	55.1	256	2	US-09-234-340A-70	Sequence 70, Appl	500	47	52.8	116	1	US-08-487-200-57	Sequence 57, Appl
428	49	55.1	256	2	US-09-355-014-70	Sequence 70, Appl	501	47	52.8	116	1	US-08-487-200-73	Sequence 73, Appl
429	49	55.1	256	2	US-08-665-202-5	Sequence 5, Appl	502	47	52.8	116	2	US-08-484-537-56	Sequence 56, Appl
430	49	55.1	258	2	US-09-315-574-5	Sequence 5, Appl	503	47	52.8	116	2	US-08-484-537-57	Sequence 57, Appl
431	49	55.1	262	2	US-09-069-882-4	Sequence 4, Appl	504	47	52.8	116	2	US-08-484-537-73	Sequence 73, Appl
432	49	55.1	262	2	US-09-956-086-4	Sequence 4, Appl	505	47	52.8	117	2	US-10-194-975-117	Sequence 117, App
433	49	55.1	262	2	US-09-956-087-4	Sequence 4, Appl	506	47	52.8	118	1	US-08-428-257A-74	Sequence 74, Appl
434	49	55.1	282	2	US-09-420-592A-7	Sequence 7, Appl	507	47	52.8	118	1	US-08-428-257A-78	Sequence 78, Appl
435	49	55.1	282	2	US-09-985-442-7	Sequence 7, Appl	508	47	52.8	118	2	US-07-987-264-14	Sequence 14, Appl
436	49	55.1	282	2	US-09-985-580-7	Sequence 7, Appl	509	47	52.8	118	2	US-07-987-264-60	Sequence 60, Appl
437	49	55.1	298	2	US-09-027-449-60	Sequence 60, Appl	510	47	52.8	119	2	US-08-767-128-20	Sequence 20, Appl
438	49	55.1	298	2	US-08-804-444A-60	Sequence 60, Appl	511	47	52.8	120	1	US-08-111-080-25	Sequence 25, Appl
439	49	55.1	298	2	US-09-026-985-60	Sequence 60, Appl	512	47	52.8	120	1	US-08-211-980-25	Sequence 25, Appl
440	49	55.1	298	2	US-09-121-952A-60	Sequence 60, Appl	513	47	52.8	120	2	US-09-065-089-1	Sequence 1, Appl
441	49	55.1	298	2	US-09-234-340A-60	Sequence 60, Appl	514	47	52.8	120	2	US-08-913-585-1	Sequence 1, Appl
442	49	55.1	298	2	US-09-355-014-60	Sequence 60, Appl	515	47	52.8	120	4	PCT-US93-07967-25	Sequence 25, Appl
443	49	55.1	452	2	US-09-027-449-71	Sequence 71, Appl	516	47	52.8	121	1	US-08-388-672A-23	Sequence 23, Appl
444	49	55.1	452	2	US-09-026-985-71	Sequence 71, Appl	517	47	52.8	121	1	US-08-388-672A-23	Sequence 23, Appl
445	49	55.1	452	2	US-09-121-952A-71	Sequence 71, Appl	518	47	52.8	121	2	US-09-080-584-23	Sequence 23, Appl
446	49	55.1	452	2	US-09-234-340A-71	Sequence 71, Appl	519	47	52.8	121	2	US-08-913-585-19	Sequence 19, Appl
447	49	55.1	452	2	US-09-355-014-71	Sequence 71, Appl	520	47	52.8	126	2	US-09-080-584-20	Sequence 20, Appl
448	49	53.9	17	2	US-08-672-345C-59	Sequence 59, Appl	521	47	52.8	129	2	US-09-471-276-664	Sequence 864, App
449	48	53.9	17	2	US-09-214-095D-59	Sequence 59, Appl	522	47	52.8	132	2	US-08-434-000A-14	Sequence 14, Appl
450	48	53.9	17	2	US-09-940-727B-59	Sequence 59, Appl	523	47	52.8	132	2	US-09-312-157-14	Sequence 14, Appl
451	48	53.9	31	2	US-08-525-539A-32	Sequence 32, Appl	524	47	52.8	132	2	US-09-717-888-14	Sequence 14, Appl
452	48	53.9	110	1	US-08-672-345C-104	Sequence 104, App	525	47	52.8	134	1	US-08-137-117D-39	Sequence 39, Appl
453	48	53.9	110	2	US-09-214-095D-94	Sequence 94, Appl	526	47	52.8	134	1	US-08-436-717-39	Sequence 39, Appl
454	48	53.9	110	2	US-09-940-727B-94	Sequence 94, Appl	527	47	52.8	135	1	US-07-634-278-59	Sequence 69, Appl
455	48	53.9	115	2	US-07-942-245-22	Sequence 22, Appl	528	47	52.8	135	1	US-08-477-728-69	Sequence 69, Appl
456	48	53.9	116	1	US-08-672-345C-14	Sequence 14, Appl	529	47	52.8	135	1	US-08-474-040-69	Sequence 69, Appl
457	48	53.9	116	2	US-09-214-095D-14	Sequence 14, Appl	530	47	52.8	135	2	US-08-487-200-69	Sequence 69, Appl
458	48	53.9	116	2	US-09-940-727B-14	Sequence 14, Appl	531	47	52.8	135	2	US-08-487-200-69	Sequence 69, Appl
459	48	53.9	119	1	US-07-634-278-64	Sequence 64, Appl	532	47	52.8	137	1	US-08-379-057-18	Sequence 18, Appl
460	48	53.9	119	1	US-07-634-278-65	Sequence 65, Appl	533	47	52.8	141	1	US-08-461-284-4	Sequence 4, Appl
461	48	53.9	119	1	US-07-634-278-89	Sequence 89, Appl	534	47	52.8	141	1	US-08-462-939-4	Sequence 4, Appl
462	48	53.9	119	1	US-08-477-728-64	Sequence 64, Appl	535	47	52.8	141	1	US-08-253-877C-4	Sequence 4, Appl
463	48	53.9	119	1	US-08-477-728-65	Sequence 65, Appl	536	47	52.8	141	1	US-08-452-164A-4	Sequence 4, Appl
464	48	53.9	119	1	US-08-477-728-89	Sequence 89, Appl	537	47	52.8	249	2	US-08-918-148-74	Sequence 74, Appl
465	48	53.9	119	1	US-08-474-040-64	Sequence 64, Appl	538	47	52.8	249	2	US-09-138-091A-72	Sequence 72, Appl

539	47	52.8	297	2	US-09-486-814A-2	Sequence 2, Appli	612	44	49.4	17	2	US-09-795-798-11	Sequence 11, Appli
540	46	51.7	17	1	US-08-137-117D-144	Sequence 144, App	613	44	49.4	84	2	US-08-928-433B-16	Sequence 16, Appli
541	46	51.7	17	1	US-08-436-717-144	Sequence 144, App	614	44	49.4	111	2	US-08-881-037-21	Sequence 21, Appli
542	46	51.7	17	1	US-08-672-345C-62	Sequence 62, Appli	615	44	49.4	117	2	US-10-092-246-8	Sequence 8, Appli
543	46	51.7	17	2	US-09-214-095D-62	Sequence 62, Appli	616	44	49.4	117	2	US-10-092-246-8	Sequence 8, Appli
544	46	51.7	17	2	US-09-254-180C-15	Sequence 2, Appli	617	44	49.4	121	2	US-08-974-899-5	Sequence 5, Appli
545	46	51.7	17	2	US-09-940-727B-62	Sequence 62, Appli	618	44	49.4	121	2	US-09-795-798-5	Sequence 5, Appli
546	46	51.7	108	2	US-08-477-347-7	Sequence 7, Appli	619	44	49.4	140	2	US-08-836-561-17	Sequence 27, Appli
547	46	51.7	108	2	US-09-800-908-7	Sequence 7, Appli	620	44	49.4	140	2	US-08-836-561-17	Sequence 27, Appli
548	46	51.7	116	1	US-08-561-521-41	Sequence 41, Appli	621	44	49.4	140	2	US-08-836-561-17	Sequence 27, Appli
549	46	51.7	116	1	US-08-672-345C-15	Sequence 15, Appli	622	44	49.4	140	2	US-08-836-561-17	Sequence 27, Appli
550	46	51.7	116	1	US-08-672-345C-105	Sequence 105, App	623	44	49.4	140	2	US-08-836-561-17	Sequence 27, Appli
551	46	51.7	116	2	US-09-214-095D-15	Sequence 15, Appli	624	44	49.4	140	2	US-09-434-122-7	Sequence 74, Appli
552	46	51.7	116	2	US-09-214-095D-90	Sequence 90, Appli	625	44	49.4	140	2	US-09-434-122-7	Sequence 74, Appli
553	46	51.7	116	2	US-09-940-727B-15	Sequence 15, Appli	626	44	49.4	140	2	US-09-434-122-7	Sequence 74, Appli
554	46	51.7	116	2	US-09-940-727B-90	Sequence 90, Appli	627	44	49.4	140	2	US-09-434-122-7	Sequence 74, Appli
555	46	51.7	116	2	PCT-US95-01219-41	Sequence 41, Appli	628	44	49.4	140	2	US-09-434-122-7	Sequence 74, Appli
556	46	51.7	117	4	US-10-194-975-118	Sequence 118, App	629	44	49.4	239	2	US-10-092-246-12	Sequence 83, Appli
557	46	51.7	118	2	US-09-065-059-5	Sequence 5, Appli	630	44	49.4	239	2	US-10-092-246-12	Sequence 83, Appli
558	46	51.7	118	2	US-09-802-083-5	Sequence 5, Appli	631	44	49.4	240	2	US-10-096-246A-32	Sequence 32, Appli
559	46	51.7	118	2	US-08-913-555-5	Sequence 5, Appli	632	44	49.4	240	2	US-10-092-246-14	Sequence 35, Appli
560	46	51.7	119	2	US-09-254-180C-16	Sequence 16, Appli	633	44	49.4	240	2	US-10-092-246-14	Sequence 35, Appli
561	46	51.7	119	2	US-09-254-180C-18	Sequence 18, Appli	634	44	49.4	240	2	US-10-092-246-14	Sequence 35, Appli
562	46	51.7	119	2	US-09-254-180C-19	Sequence 19, Appli	635	44	49.4	240	2	US-10-096-246A-34	Sequence 34, Appli
563	46	51.7	119	2	US-09-254-180C-149	Sequence 149, App	636	44	49.4	240	2	US-10-096-246A-35	Sequence 35, Appli
564	46	51.7	119	2	US-08-913-555-23	Sequence 23, Appli	637	44	49.4	240	2	US-10-096-246A-35	Sequence 35, Appli
565	46	51.7	121	2	US-08-487-761-11	Sequence 11, Appli	638	44	49.4	240	2	US-10-096-246A-37	Sequence 37, Appli
566	46	51.7	121	2	US-09-698-705-8	Sequence 8, Appli	639	44	49.4	245	2	US-09-248-796A-19387	Sequence 19387, A
567	46	51.7	122	2	US-08-957-001B-26	Sequence 26, Appli	640	44	49.4	257	2	US-10-092-246-2	Sequence 2, Appli
568	46	51.7	122	2	US-09-496-301-26	Sequence 26, Appli	641	44	49.4	257	2	US-10-096-246A-2	Sequence 2, Appli
569	46	51.7	135	1	US-08-137-117D-27	Sequence 27, Appli	642	44	49.4	18	2	US-09-563-222C-45	Sequence 45, Appli
570	46	51.7	135	1	US-08-137-117D-102	Sequence 102, App	643	44	49.4	88	2	US-09-726-219A-172	Sequence 172, App
571	46	51.7	135	1	US-08-137-117D-102	Sequence 102, App	644	44	49.4	88	2	US-09-196-522-172	Sequence 172, App
572	46	51.7	135	1	US-08-137-117D-112	Sequence 112, App	645	44	49.4	95	2	US-09-905-343-15	Sequence 15, Appli
573	46	51.7	135	1	US-08-436-717-27	Sequence 27, Appli	646	44	49.4	108	1	US-08-888-366-6	Sequence 6, Appli
574	46	51.7	135	1	US-08-436-717-100	Sequence 100, App	647	44	49.4	115	1	US-08-308-494A-17	Sequence 17, Appli
575	46	51.7	135	1	US-08-436-717-102	Sequence 102, App	648	44	49.4	115	1	US-08-477-347-5	Sequence 5, Appli
576	46	51.7	135	1	US-08-436-717-112	Sequence 112, App	649	44	49.4	115	2	US-09-800-308-5	Sequence 5, Appli
577	46	51.7	138	2	US-09-254-180C-143	Sequence 143, App	650	44	49.4	116	2	US-08-881-037-19	Sequence 19, Appli
578	46	51.7	139	1	US-08-137-117D-35	Sequence 35, Appli	651	44	49.4	116	2	US-08-545-009A-104	Sequence 104, App
579	46	51.7	219	1	US-08-436-717-35	Sequence 35, Appli	652	44	49.4	116	2	US-09-726-219A-217	Sequence 217, App
580	46	51.7	219	1	US-09-254-180C-180	Sequence 180, App	653	44	49.4	116	2	US-09-196-522-17	Sequence 17, App
581	46	51.7	222	2	US-09-698-705-13	Sequence 13, Appli	654	44	49.4	116	2	US-09-515-697-104	Sequence 104, App
582	46	51.7	241	2	US-09-581-345-5	Sequence 5, Appli	655	44	49.4	118	2	US-08-513-968-80	Sequence 80, Appli
583	45	50.6	20	2	US-09-556-605-9	Sequence 9, Appli	656	44	49.4	124	2	US-09-301-593-10	Sequence 8, Appli
584	45	50.6	113	2	US-08-881-037-18	Sequence 18, Appli	657	44	49.4	124	2	US-09-301-593-12	Sequence 12, Appli
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587	45	50.6	119	2	US-09-438-954-2	Sequence 2, Appli	660	44	49.4	124	2	US-09-301-593-38	Sequence 38, Appli
588	45	50.6	121	2	US-09-438-954-39	Sequence 39, Appli	661	44	49.4	124	2	US-09-301-593-39	Sequence 39, Appli
589	45	50.6	121	2	US-08-881-037-65	Sequence 65, Appli	662	44	49.4	124	2	US-09-301-593-40	Sequence 40, Appli
590	45	50.6	127	2	US-09-561-500-7	Sequence 7, Appli	663	44	49.4	124	2	US-09-301-593-41	Sequence 41, Appli
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592	45	50.6	127	2	US-09-561-526-7	Sequence 7, Appli	665	44	49.4	124	2	US-09-301-593-108	Sequence 108, App
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594	45	50.6	127	2	US-09-998-831-7	Sequence 7, Appli	667	44	49.4	128	1	US-08-964-690-22	Sequence 22, Appli
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596	45	50.6	127	2	US-09-562-245-7	Sequence 7, Appli	669	44	49.4	129	1	US-08-525-539A-77	Sequence 77, Appli
597	45	50.6	138	2	US-08-603-024-2	Sequence 2, Appli	670	44	49.4	129	4	PCT-US95-01219-45	Sequence 45, Appli
598	45	50.6	139	1	US-08-253-877C-8	Sequence 8, Appli	671	44	49.4	133	1	US-09-301-593-3	Sequence 3, Appli
599	45	50.6	139	1	US-08-253-877C-19	Sequence 19, Appli	672	44	49.4	133	1	US-08-579-940-4	Sequence 4, Appli
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601	45	50.6	139	1	US-08-452-164A-19	Sequence 19, Appli	674	44	49.4	151	2	US-08-513-968-34	Sequence 34, Appli
602	45	50.6	139	2	US-08-603-024-18	Sequence 18, Appli	675	44	49.4	239	2	US-09-830-954A-6	Sequence 6, Appli
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604	45	50.6	141	2	US-09-063-628-29	Sequence 29, Appli	677	44	49.4	472	2	US-09-301-593-30	Sequence 30, Appli
605	45	50.6	244	1	US-08-230-843-2	Sequence 2, Appli	678	44	49.4	472	2	US-09-301-593-43	Sequence 43, Appli
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607	45	50.6	794	2	US-09-417-485D-6	Sequence 6, Appli	680	42.5	47.8	580	1	US-09-657-252-2	Sequence 2, Appli
608	45	50.6	2184	2	US-09-417-485D-6	Sequence 6, Appli	681	42	47.2	17	2	US-08-672-345C-77	Sequence 77, Appli
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611	44	49.4	17	2	US-09-434-122-41	Sequence 41, Appli	684	42	47.2	104	1	US-07-942-245-13	Sequence 13, Appli

685	42	47.2	114	2	US-09-344-587-9	Sequence 9, Appli	758	40	44.9	91	2	US-09-943-9b6-78	Sequence 78, Appl
686	42	47.2	114	2	US-09-726-219A-222	Sequence 222, App	759	40	44.9	91	2	US-10-435-6b2-70	Sequence 70, Appl
687	42	47.2	114	2	US-09-196-322-222	Sequence 82, App	760	40	44.9	91	2	US-10-435-6b2-78	Sequence 78, Appl
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691	42	47.2	115	2	US-09-357-707-8	Sequence 8, Appli	764	40	44.9	92	2	US-09-036-579-85	Sequence 85, Appl
692	42	47.2	115	2	US-09-357-708-8	Sequence 8, Appli	765	40	44.9	92	2	US-09-550-374-79	Sequence 79, Appl
693	42	47.2	115	2	US-09-726-219A-216	Sequence 216, App	766	40	44.9	92	2	US-09-550-374-85	Sequence 85, Appl
694	42	47.2	115	2	US-09-196-522-216	Sequence 16, App	767	40	44.9	92	2	US-09-943-906-79	Sequence 79, Appl
695	42	47.2	118	1	US-08-553-497A-16	Sequence 16, Appl	768	40	44.9	92	2	US-09-943-906-85	Sequence 85, Appl
696	42	47.2	118	1	US-08-888-366-4	Sequence 4, Appli	769	40	44.9	92	2	US-10-435-602-79	Sequence 79, Appl
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699	42	47.2	130	2	US-08-895-914-4	Sequence 4, Appli	772	40	44.9	95	1	US-08-713-939A-86	Sequence 86, Appl
700	42	47.2	130	2	US-09-357-710A-4	Sequence 4, Appli	773	40	44.9	95	2	US-09-036-579-86	Sequence 86, Appl
701	42	47.2	130	2	US-09-357-707-4	Sequence 4, Appli	774	40	44.9	95	2	US-09-550-374-86	Sequence 86, Appl
702	42	47.2	130	2	US-09-357-708-4	Sequence 4, Appli	775	40	44.9	95	2	US-09-943-906-86	Sequence 86, Appl
703	42	47.2	137	1	US-08-392-419-2	Sequence 2, Appli	776	40	44.9	95	2	US-10-435-602-86	Sequence 86, Appl
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705	42	47.2	467	1	US-07-916-098A-45	Sequence 45, Appli	778	40	44.9	97	4	PCT-US95-10053-13	Sequence 13, Appl
706	42	47.2	661	1	US-09-248-796A-18678	Sequence 216, A	779	40	44.9	97	2	PCT-US96-09448-16	Sequence 16, Appl
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708	41.5	46.6	661	2	US-08-394-326-2	Sequence 2, Appli	781	40	44.9	101	1	US-08-713-939A-82	Sequence 82, Appl
709	41.5	46.6	1151	2	US-09-082-306-2	Sequence 2, Appli	782	40	44.9	101	2	US-09-036-579-82	Sequence 82, Appl
710	41.5	46.6	2391	1	US-09-252-991A-23596	Sequence 23596, A	783	40	44.9	101	2	US-09-550-374-82	Sequence 82, Appl
711	41.5	46.6	2391	1	US-08-446-855A-2	Sequence 2, Appli	784	40	44.9	101	2	US-09-943-906-82	Sequence 82, Appl
712	41	46.1	17	2	US-09-156-741-2	Sequence 2, Appli	785	40	44.9	101	2	US-10-435-602-82	Sequence 82, Appl
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714	41	46.1	17	2	US-09-627-896B-12	Sequence 12, Appl	787	40	44.9	103	1	US-09-036-579-84	Sequence 84, Appl
715	41	46.1	50	4	PCT-US91-02942-51	Sequence 51, Appl	788	40	44.9	103	2	US-09-550-374-84	Sequence 84, Appl
716	41	46.1	50	4	PCT-US91-02942-52	Sequence 52, Appl	789	40	44.9	103	2	US-09-943-906-84	Sequence 84, Appl
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726	41	46.1	119	1	US-08-561-521-13	Sequence 13, Appl	799	40	44.9	114	1	US-08-713-939A-77	Sequence 77, Appl
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728	41	46.1	119	4	PCT-US95-01219-10	Sequence 10, Appl	801	40	44.9	114	2	US-09-036-579-68	Sequence 68, Appl
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732	41	46.1	125	2	US-09-315-574-56	Sequence 56, Appl	805	40	44.9	114	2	US-09-550-374-76	Sequence 76, Appl
733	41	46.1	135	2	US-09-627-896B-2	Sequence 2, Appli	806	40	44.9	114	2	US-09-550-374-77	Sequence 77, Appl
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738	41	46.1	462	2	US-09-627-896B-24	Sequence 24, Appl	811	40	44.9	114	2	US-10-435-602-76	Sequence 76, Appl
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740	40.5	45.5	560	2	US-09-643-597-225	Sequence 225, App	813	40	44.9	116	1	US-08-273-146-55	Sequence 55, Appl
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742	40.5	45.5	560	2	US-09-542-615A-225	Sequence 225, App	815	40	44.9	117	2	US-08-545-809A-128	Sequence 128, App
743	40.5	45.5	560	2	US-09-606-421B-225	Sequence 225, App	816	40	44.9	117	2	US-09-535-697-128	Sequence 128, App
744	40.5	45.5	560	2	US-09-476-496A-225	Sequence 225, App	817	40	44.9	118	2	US-09-199-149-2	Sequence 2, Appli
745	40.5	45.5	560	2	US-09-630-940B-225	Sequence 225, App	818	40	44.9	118	2	US-09-199-149-5	Sequence 5, Appli
746	40.5	45.5	560	2	US-09-943-075A-6	Sequence 6, Appli	819	40	44.9	118	2	US-09-647-468-139	Sequence 139, App
747	40.5	45.5	560	2	US-10-039-272A-2	Sequence 2, Appli	820	40	44.9	118	2	US-09-647-468-140	Sequence 140, App
748	40.5	45.5	560	2	US-10-007-700-225	Sequence 225, App	821	40	44.9	118	2	US-09-905-243-74	Sequence 74, Appl
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750	40.5	45.5	560	5	US-09-977-371-90	Sequence 90, Appl	823	40	44.9	119	1	US-08-478-399A-65	Sequence 65, Appl
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752	40	44.9	91	1	US-08-713-939A-78	Sequence 78, Appl	825	40	44.9	119	1	US-08-553-497A-12	Sequence 12, Appl
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754	40	44.9	91	2	US-09-036-579-78	Sequence 78, Appl	827	40	44.9	130	2	US-09-556-605-3	Sequence 3, Appli
755	40	44.9	91	2	US-09-550-374-70	Sequence 70, Appl	828	40	44.9	137	2	US-09-647-468-153	Sequence 153, App
756	40	44.9	91	2	US-09-550-374-78	Sequence 78, Appl	829	40	44.9	137	2	US-09-647-468-154	Sequence 154, App
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833	40	44.9	139	1	US-08-202-047-11	Sequence 11, Appli	906	39	43.8	328	2	US-09-615-192A-274	Sequence 274, Appl
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838	40	44.9	141	2	US-08-957-001B-7	Sequence 7, Appli	911	39	43.8	592	2	US-09-765-471-222	Sequence 222, App
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847	40	44.9	419	2	US-09-134-001C-4658	Sequence 4658, Ap	920	38	42.7	17	2	US-08-974-899-23	Sequence 23, Appli
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852	39.5	44.4	396	1	US-08-227-540-4	Sequence 4, Appli	925	38	42.7	44	2	US-09-205-258-257	Sequence 257, App
853	39.5	44.4	396	1	US-08-430-787A-4	Sequence 4, Appli	926	38	42.7	81	2	US-09-513-599C-4118	Sequence 257, App
854	39	43.8	16	2	US-09-269-332-63	Sequence 63, Appli	927	38	42.7	111	2	US-08-881-037-15	Sequence 15, Appl
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856	39	43.8	106	1	US-07-942-245-15	Sequence 15, Appl	929	38	42.7	116	1	US-08-477-484B-168	Sequence 168, App
857	39	43.8	114	2	US-09-726-219A-221	Sequence 221, App	930	38	42.7	116	1	US-08-107-669D-54	Sequence 54, Appli
858	39	43.8	114	2	US-09-156-532-221	Sequence 221, App	931	38	42.7	116	1	US-08-472-788A-54	Sequence 54, Appli
859	39	43.8	115	2	US-09-233-250-54	Sequence 54, Appli	932	38	42.7	116	1	US-08-477-511B-54	Sequence 54, Appli
860	39	43.8	115	1	US-08-690-102A-4	Sequence 4, Appli	933	38	42.7	116	1	US-08-646-360-168	Sequence 168, App
861	39	43.8	116	1	US-08-690-102A-8	Sequence 8, Appli	934	38	42.7	116	1	US-08-082-842A-54	Sequence 54, Appli
862	39	43.8	116	1	US-08-690-102A-9	Sequence 9, Appli	935	38	42.7	116	1	US-08-839-765-168	Sequence 168, App
863	39	43.8	116	2	US-09-127-902-4	Sequence 4, Appli	936	38	42.7	116	2	US-09-136-389-168	Sequence 168, App
864	39	43.8	116	2	US-09-127-902-8	Sequence 8, Appli	937	38	42.7	116	2	US-09-610-838-168	Sequence 168, App
865	39	43.8	116	2	US-09-127-902-9	Sequence 9, Appli	938	38	42.7	116	2	US-09-711-485-168	Sequence 168, App
866	39	43.8	116	2	US-09-155-107-4	Sequence 4, Appli	939	38	42.7	119	1	US-08-467-393-2	Sequence 2, Appli
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900	39	43.8	235	2	US-08-444-644-28	Sequence 28, Appli	973	37	41.6	113	1	US-08-211-202-115	Sequence 115, App
901	39	43.8	235	2	US-08-444-644-42	Sequence 42, Appli	974	37	41.6	117	2	US-08-525-539A-76	Sequence 76, Appli
902	39	43.8	235	2	US-08-232-246A-19	Sequence 19, Appli	975	37	41.6	117	2	US-08-525-539A-78	Sequence 78, Appli
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979 37 41.6 120 1 US-08-211-202-1 Sequence 1, Appl
980 37 41.6 120 2 US-10-092-246-12 Sequence 12, Appl
981 37 41.6 120 2 US-10-096-246A-12 Sequence 12, Appl
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987 37 41.6 123 1 US-08-476-176B-2 Sequence 2, Appl
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989 37 41.6 123 2 US-08-714-017-86 Sequence 86, Appl
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991 37 41.6 123 2 US-08-485-246A-2 Sequence 2, Appl
992 37 41.6 123 2 US-08-475-680-86 Sequence 86, Appl
993 37 41.6 136 2 US-08-525-539A-47 Sequence 47, Appl
994 37 41.6 136 2 US-08-525-539A-63 Sequence 63, Appl
995 37 41.6 138 1 US-08-482-882-78 Sequence 78, Appl
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997 37 41.6 138 1 US-08-487-113D-78 Sequence 78, Appl
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ALIGNMENTS

RESULT 1
US-08-479-089A-8
Sequence 8, Application US/08479089A
Patent No. 6383487
GENERAL INFORMATION:
APPLICANT: Amlot, Peter L.
APPLICANT: Akbar, Arne N.
APPLICANT: Heinrich, Gunther
APPLICANT: Cammisuli, Salvatore
TITLE OF INVENTION: CD25 Binding Molecules
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6383487artis Corporation
STREET: 564 Morris Avenue
CITY: Summit
STATE: NJ
COUNTRY: USA
ZIP: 07901-1027
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479, 089A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/669,545
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9019323
FILING DATE: 05-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Furman, Diane E.
REGISTRATION NUMBER: 31,104
REFERENCE/DOCKET NUMBER: 100-7617
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 522-6924
TELEFAX: (908) 522-6955
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-479-089A-8

Query Match 82.0%; Score 73; DB 2; Length 17;
Best Local Similarity 81.2%; Pred. No. 3.7e-05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGNDISYNQKFXG 17
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Db 2 IYPGNDISYNQKFXG 17

RESULT 2
US-07-669-545B-8
Sequence 8, Application US/07669545B
Patent No. 6521230
GENERAL INFORMATION:
APPLICANT: Amlot, Peter L.
APPLICANT: Akbar, Arne N.
APPLICANT: Heinrich, Gunther
APPLICANT: Cammisuli, Salvatore
TITLE OF INVENTION: CD25 Binding Molecules
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6521230artis Corporation
STREET: 564 Morris Avenue
CITY: Summit
STATE: NJ
COUNTRY: USA
ZIP: 07901-1027
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/669,545B
FILING DATE: 14-MAR-1991
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9005962
FILING DATE: 16-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9019323
FILING DATE: 05-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Furman, Diane E.
REGISTRATION NUMBER: 31,104
REFERENCE/DOCKET NUMBER: 100-7617
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 522-6924
TELEFAX: (908) 522-6955
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-07-669-545B-8

Query Match 82.0%; Score 73; DB 2; Length 17;
Best Local Similarity 81.2%; Pred. No. 3.7e-05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 2 IYPGNSDTSYNOKFEG 17

RESULT 3

US-08-793-490-9
; Sequence 9, Application US/08793490
; Patent No. 5968824
; GENERAL INFORMATION:
; APPLICANT: Spruce, Barbara A
; APPLICANT: Prescott, Alan
; APPLICANT: Botlinger, Angelika
; APPLICANT: Dewar, Deborah A
; TITLE OF INVENTION: Agents for Inducing Apoptosis and Applications of Said
; TITLE OF INVENTION: Agents in Therapy
; FILE REFERENCE: ME A9701
; CURRENT APPLICATION NUMBER: US/08/793,490
; CURRENT FILING DATE: 1997-04-28
; EARLIER APPLICATION NUMBER: GB 9419285.3
; EARLIER FILING DATE: 1994-09-23
; EARLIER APPLICATION NUMBER: GB 9417444.8
; EARLIER FILING DATE: 1994-08-30
; EARLIER APPLICATION NUMBER: PCT/GB95/02037
; EARLIER FILING DATE: 1995-08-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 9
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sequence
; OTHER INFORMATION: encoded by anti-proenkephalin immunoglobulin heavy
; OTHER INFORMATION: chain variable domain genes
US-08-793-490-9

Query Match 82.0%; Score 73; DB 1; Length 106;
Best Local Similarity 81.2%; Pred. No. 0.00028;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IYPGNDISYNOKFXG 17
Db 50 IYPGNSDTSYNOKFEG 65

RESULT 4

US-08-479-089A-2
; Sequence 2, Application US/08479089A
; Patent No. 6383487
; GENERAL INFORMATION:
; APPLICANT: Amloc, Peter L.
; APPLICANT: Akbar, Arne N.
; APPLICANT: Heinrich, Gunther
; APPLICANT: Cammsuli, Salvatore
; TITLE OF INVENTION: CD25 Binding Molecules
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6383487artis Corporation
; STREET: 564 Morris Avenue
; CITY: Summit
; STATE: NJ
; COUNTRY: USA
; ZIP: 07901-1027
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,089A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/669,545

FILING DATE:

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: GB 9019323
;; FILING DATE: 05-SEP-1990
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Furman, Diane E.
;; REGISTRATION NUMBER: 31,104
;; REFERENCE/DOCKET NUMBER: 100-7617
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (908) 522-6924
;; TELEFAX: (908) 522-6955
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 117 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-479-089A-2

Query Match 82.0%; Score 73; DB 2; Length 117;
Best Local Similarity 81.2%; Pred. No. 0.00031;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IYPGNDISYNOKFXG 17
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; Sequence 3, Application US/08479089A
; Patent No. 6383487
; GENERAL INFORMATION:
; APPLICANT: Amloc, Peter L.
; APPLICANT: Akbar, Arne N.
; APPLICANT: Heinrich, Gunther
; APPLICANT: Cammsuli, Salvatore
; TITLE OF INVENTION: CD25 Binding Molecules
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6383487artis Corporation
; STREET: 564 Morris Avenue
; CITY: Summit
; STATE: NJ
; COUNTRY: USA
; ZIP: 07901-1027
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,089A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/669,545
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9019323
; FILING DATE: 05-SEP-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Furman, Diane E.
; REGISTRATION NUMBER: 31,104
; REFERENCE/DOCKET NUMBER: 100-7617
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 522-6955
; TELEFAX: (908) 522-6924
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

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MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: Region
LOCATION: 1..30
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OTHER INFORMATION: /note= "Framework Region 1"
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US-08-479-089A-3

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Best Local Similarity 81.2%; Pred. No. 0.00031;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2  IYPGNDISYNOKFXG 17
Db      51  IYPGNSDTSYNOKFEG 66

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US-07-669-545B-2
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; Patent No. 652130
; GENERAL INFORMATION:
; APPLICANT: Amlot, Peter L.
; APPLICANT: Akbar, Arne N.
; APPLICANT: Heinrich, Gunther
; APPLICANT: Cammisuli, Salvatore
; TITLE OF INVENTION: CD25 Binding Molecules
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: No. 652130artis Corporation
; STREET: 564 Morris Avenue
; CITY: Summit
; STATE: NJ
; COUNTRY: USA
; ZIP: 07901-1027
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; SOFTWARE: Patentin Release #1.0, Version #1.25
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APPLICATION NUMBER: US/07/669,545B
FILING DATE: 14-MAR-1991
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9005962
FILING DATE: 16-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9019323
FILING DATE: 05-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Furman, Diane E.
REGISTRATION NUMBER: 31,104
REFERENCE/DOCKET NUMBER: 100-7617
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 522-6924
TELEFAX: (908) 522-6955
;
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-669-545B-2

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Best Local Similarity 81.2%; Pred. No. 0.00031;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2  IYPGNDISYNOKFXG 17
Db      51  IYPGNSDTSYNOKFEG 66

RESULT 7
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; Patent No. 6521230
; GENERAL INFORMATION:
; APPLICANT: Amlot, Peter L.
; APPLICANT: Akbar, Arne N.
; APPLICANT: Heinrich, Gunther
; APPLICANT: Cammisuli, Salvatore
; TITLE OF INVENTION: CD25 Binding Molecules
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: No. 6521230artis Corporation
; STREET: 564 Morris Avenue
; CITY: Summit
; STATE: NJ
; COUNTRY: USA
; ZIP: 07901-1027
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/669,545B
; FILING DATE: 14-MAR-1991
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9005962
; FILING DATE: 16-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9019323
; FILING DATE: 05-SEP-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Furman, Diane E.
; REGISTRATION NUMBER: 31,104
; REFERENCE/DOCKET NUMBER: 100-7617
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 522-6924
; TELEFAX: (908) 522-6955
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; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..30
; OTHER INFORMATION: /label= FR1
; OTHER INFORMATION: /note= "Framework Region 1"
; FEATURE:
; NAME/KEY: Binding-site
; LOCATION: 31..35
; OTHER INFORMATION: /label= CDR1
; OTHER INFORMATION: /note= "Complementarity Determining Region 1"
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; LOCATION: 36..49
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; LOCATION: 50..66
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; FEATURE:
; NAME/KEY: Region
; LOCATION: 67..98
; OTHER INFORMATION: /label= FR3
; OTHER INFORMATION: /note= "Framework Region 3"
; FEATURE:
; NAME/KEY: Binding-site
; LOCATION: 99..106
; OTHER INFORMATION: /label= CDR3
; OTHER INFORMATION: /note= "Complementarity Determining Region 3"
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; OTHER INFORMATION: /note= "Framework Region 4"
; US-07-669-545B-3
;
Query Match 82.0%; Score 73; DB 2; Length 117;
Best Local Similarity 81.2%; Pred. No. 0.00031;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
;
OY 2 IYGNDDISYNOKFXG 17
DB 51 IYGNDDISYNOKFXG 66
;
RESULT 8
US-08-476-275-6
; Sequence 6, Application US/08476275
; Patent No. 5776456
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; APPLICANT: Hanna, Nabli
; APPLICANT: Leonard, John E.
; APPLICANT: Newman, Roland A.
; APPLICANT: Reff, Mitchell E.
; APPLICANT: Rastetter, William H.
; TITLE OF INVENTION: Therapeutic Application of Chimeric and
; TITLE OF INVENTION: Radiolabeled Antibodies to Human B Lymphocyte Restricted
; TITLE OF INVENTION: Differentiation Antigen for the Treatment of B-Cell
; TITLE OF INVENTION: Lymphoma
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SNECKER & MATHIS
; STREET: 699 Prince St.

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; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,275
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/149,099
; FILING DATE: 03-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/978,891
; FILING DATE: 13-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-2021
; TELEFAX: 703-836-6620
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-476-275-6
;
Query Match 80.9%; Score 72; DB 1; Length 140;
Best Local Similarity 81.2%; Pred. No. 0.00054;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
;
OY 2 IYGNDDISYNOKFXG 17
DB 70 IYGNDDISYNOKFXG 85
;
RESULT 9
US-08-475-815B-11
; Sequence 11, Application US/08475815B
; Patent No. 6399061
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, DARRELL R.
; APPLICANT: HANNA, NABLI
; APPLICANT: LEONARD, JOHN E.
; APPLICANT: NEWMAN, ROLAND A.
; APPLICANT: REFF, MITCHELL E.
; APPLICANT: RASTETTER, WILLIAM H.
; TITLE OF INVENTION: THERAPEUTIC APPLICATION OF CHIMERIC AND
; TITLE OF INVENTION: RADIOLABELLED ANTIBODIES TO HUMAN B LYMPHOCYTE RESTRICTED
; TITLE OF INVENTION: DIFFERENTIATION ANTIGEN FOR THE TREATMENT OF B CELL
; TITLE OF INVENTION: LYMPHOMA
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY WINTHROP
; STREET: 1100 New York Avenue, N.W., Ninth FL.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,815B

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; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/149,099
; FILING DATE: 03-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/978,891
; FILING DATE: 13-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 23522-0157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-475-815B-11

Query Match      80.9%; Score 72; DB 2; Length 140;
Best Local Similarity 81.2%; Pred. No. 0.00054;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY      2 IYPGNDISYNOKFXG 17
      ||||| |||||
Db      70 IYPGNGDTSYNOKFXG 85

RESULT 10
US-09-724-138-44
; Sequence 44, Application US/09724138
; Patent No. 6652852
; GENERAL INFORMATION:
; APPLICANT: Robinson, Randy
; APPLICANT: Liu, Alvin
; APPLICANT: Ledbetter, Jeffrey
; TITLE OF INVENTION: Chimeric Antibody with Specificity to Human B Cell Surface Anti-
; FILE REFERENCE: PPL-001CN2
; CURRENT APPLICATION NUMBER: US/09/724,138
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/630198
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: US 09/021934
; PRIOR FILING DATE: 1998-02-12
; PRIOR APPLICATION NUMBER: US 08/471984
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 07/665939
; PRIOR FILING DATE: 1991-03-05
; PRIOR APPLICATION NUMBER: US 07/195961
; PRIOR FILING DATE: 1988-05-13
; PRIOR APPLICATION NUMBER: US 07/016202
; PRIOR FILING DATE: 1987-01-08
; PRIOR APPLICATION NUMBER: PCT/US86/02269
; PRIOR FILING DATE: 1986-10-27
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 44
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-724-138-44

Query Match      80.9%; Score 72; DB 2; Length 140;
Best Local Similarity 81.2%; Pred. No. 0.00054;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY      2 IYPGNDISYNOKFXG 17
      ||||| |||||
Db      70 IYPGNGDTSYNOKFXG 85
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; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/149,099
; FILING DATE: 03-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/978,891
; FILING DATE: 13-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-158
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-475-813-6

Query Match      80.9%; Score 72; DB 2; Length 140;
Best Local Similarity 81.2%; Pred. No. 0.00054;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY      2 IYPGNDISYNOKFXG 17
      ||||| |||||
Db      70 IYPGNGDTSYNOKFXG 85

RESULT 12
US-09-630-198-44
; Sequence 44, Application US/09630198
; Patent No. 6893625
; GENERAL INFORMATION:
; APPLICANT: Robinson, Randy
; APPLICANT: Liu, Alvin
; APPLICANT: Ledbetter, Jeffrey
; TITLE OF INVENTION: Chimeric Antibody with Specificity to Human B Cell Surface Anti-
; FILE REFERENCE: PPL-001CN

; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/149,099
; FILING DATE: 03-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/978,891
; FILING DATE: 13-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-158
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-475-813-6

Query Match      80.9%; Score 72; DB 2; Length 140;
Best Local Similarity 81.2%; Pred. No. 0.00054;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY      2 IYPGNDISYNOKFXG 17
      ||||| |||||
Db      70 IYPGNGDTSYNOKFXG 85

RESULT 11
US-08-475-813-6
; Sequence 6, Application US/08475813
; Patent No. 6682734
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; APPLICANT: Hanna, Nabil
; APPLICANT: Leonard, John E.
; APPLICANT: Newman, Roland A.
; APPLICANT: Reiff, Mitchell E.
; APPLICANT: Rastetter, William H.
; TITLE OF INVENTION: Therapeutic Application of Chimeric and
; TITLE OF INVENTION: Radiolabeled Antibodies to Human B Lymphocyte Restricted
; TITLE OF INVENTION: Differentiation Antigen for the Treatment of B-Cell Lymphoma
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,813
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/149,099
; FILING DATE: 03-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/978,891
; FILING DATE: 13-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-158
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-475-813-6

Query Match      80.9%; Score 72; DB 2; Length 140;
Best Local Similarity 81.2%; Pred. No. 0.00054;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY      2 IYPGNDISYNOKFXG 17
      ||||| |||||
Db      70 IYPGNGDTSYNOKFXG 85
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;; CURRENT APPLICATION NUMBER: US/09/630,198
;; CURRENT FILING DATE: 2000-08-01
;; PRIOR APPLICATION NUMBER: US 09/021934
;; PRIOR FILING DATE: 1998-02-12
;; PRIOR APPLICATION NUMBER: US 08/471984
;; PRIOR FILING DATE: 1995-06-06
;; PRIOR APPLICATION NUMBER: US 07/665939
;; PRIOR FILING DATE: 1991-03-05
;; PRIOR APPLICATION NUMBER: US 07/195961
;; PRIOR FILING DATE: 1988-05-13
;; PRIOR APPLICATION NUMBER: US 07/016202
;; PRIOR FILING DATE: 1987-01-08
;; PRIOR APPLICATION NUMBER: PCT/US86/02269
;; PRIOR FILING DATE: 1986-10-27
;; NUMBER OF SEQ ID NOS: 50
;; SOFTWARE: Patentin version 3.0
;; SEQ ID NO 44
;; LENGTH: 140
;; TYPE: PRT
;; ORGANISM: Mus musculus
US-09-630-198-44

Query Match 80.9%; Score 72; DB 2; Length 140;
Best Local Similarity 81.2%; Pred. No. 0.00054;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGNDISYNOKFXG 17
Db 70 IYPGNDISYNOKFXG 85

RESULT 13
US-09-238-741-4
;; Sequence 4, Application US/09238741
;; Patent No. 6897044
;; GENERAL INFORMATION:
;; APPLICANT: BRASLAWSKY, GARY R.
;; APPLICANT: HANNA, NABIL
;; APPLICANT: HARIHARAN, KANDASAMY
;; APPLICANT: LABAREE, MICHAEL J.
;; APPLICANT: HUTNH, TRI B.
;; TITLE OF INVENTION: PRODUCTION OF TETRAVALENT ANTIBODIES
;; FILE REFERENCE: 23522.0584
;; CURRENT APPLICATION NUMBER: US/09/238,741
;; CURRENT FILING DATE: 1999-01-28
;; NUMBER OF SEQ ID NOS: 4
;; SOFTWARE: Patentin Ver. 2.1
;; SEQ ID NO 4
;; LENGTH: 470
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence:
;; OTHER INFORMATION: "Dimeric" Anti-CD20 Heavy Chain (Version 1)
US-09-238-741-4

Query Match 80.9%; Score 72; DB 2; Length 470;
Best Local Similarity 81.2%; Pred. No. 0.002;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGNDISYNOKFXG 17
Db 70 IYPGNDISYNOKFXG 85

RESULT 14
US-08-766-3508-48
;; Sequence 48, Application US/087663508
;; Patent No. 6949244
;; GENERAL INFORMATION:
;; APPLICANT: Chatterjee, Malaya
;; Foon, Kenneth A.
;; Chatterjee, Sunil K.

;; TITLE OF INVENTION: MURINE MONOCLONAL ANTI-IDIOTYPE ANTIBODY
;; 11D10 AND METHODS OF USE THEREOF
;; NUMBER OF SEQUENCES: 58
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: MORRISON & FOERSTER
;; STREET: 755 PAGE MILL ROAD
;; CITY: PALO ALTO
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 94304-1018
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/766,3508
;; FILING DATE: 13-Dec-1996
;; CLASSIFICATION: <Unknown>
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Polizzi, Catherine M.
;; REGISTRATION NUMBER: 40,130
;; REFERENCE/DOCKET NUMBER: 30414-20003.21
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 813-5600
;; TELEFAX: (415) 494-0792
;; TELE: 706141
;; INFORMATION FOR SEQ ID NO: 48:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 118 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-08-766-3508-48

Query Match 77.5%; Score 69; DB 2; Length 118;
Best Local Similarity 75.0%; Pred. No. 0.0013;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGNDISYNOKFXG 17
Db 51 IYPGNDISYNOKFXG 66

RESULT 15
US-09-091-071-7
;; Sequence 7, Application US/09091071
;; Patent No. 6610500
;; GENERAL INFORMATION:
;; APPLICANT:
;; TITLE OF INVENTION: DESIGN OF HORMONE-LIKE ANTIBODIES WITH
;; NUMBER OF SEQUENCES: 9
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/091,071
;; FILING DATE:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/CA96/00815
;; FILING DATE: 06-DEC-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: GB 9525180.7
;; FILING DATE: 08-DEC-1995
;; INFORMATION FOR SEQ ID NO: 7:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 17 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:

TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-091-071-7

Query Match 76.4%; Score 68; DB 2; Length 17;
Best Local Similarity 75.0%; Pred. No. 0.00023;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGNDISYNOKFXG 17
Db 2 IYPGSDSYNOKFXG 17

RESULT 16
US-09-344-587-10

Sequence 10, Application US/09344587
Patent No. 6331402
GENERAL INFORMATION:
APPLICANT: Praast, Gerald
APPLICANT: Nusbaum, Sabine
APPLICANT: Moesner, Ellen
APPLICANT: Lenz, Helmut
TITLE OF INVENTION: REDUCTION OF INTERFERENCE OF IMMUNOASSAYS BY SUBSTANCES
FILE REFERENCE: BMID 9928 4897/00/US-Im
CURRENT FILING DATE: 1999-06-25
EARLIER APPLICATION NUMBER: US/09/344,587
EARLIER FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 10
LENGTH: 114
TYPE: PRT
ORGANISM: Mus musculus
US-09-344-587-10

Query Match 76.4%; Score 68; DB 2; Length 114;
Best Local Similarity 75.0%; Pred. No. 0.0019;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGNDISYNOKFXG 17
Db 51 IYPGNDISYNOKFXG 66

RESULT 17
US-09-232-290-33

Sequence 33, Application US/09232290A
Patent No. 6815540
GENERAL INFORMATION:
APPLICANT: PLUCKTHORN, ANDREAS
APPLICANT: NIEBA, LARS
APPLICANT: HONEGGER, ANNEMARIE
TITLE OF INVENTION: IMMUNOLOGICAL SUPER FAMILY DOMAINS AND FRAGMENTS WITH
FILE REFERENCE: MORPHO/7
CURRENT FILING DATE: 1999-01-15
EARLIER APPLICATION NUMBER: PCT/EP96/02230
EARLIER FILING DATE: 1996-05-23
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 33
LENGTH: 115
TYPE: PRT
ORGANISM: Murine
US-09-232-290-33

Query Match 76.4%; Score 68; DB 2; Length 115;
Best Local Similarity 75.0%; Pred. No. 0.0019;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGNDISYNOKFXG 17
Db 50 IYPGSDSYNOKFXG 65

RESULT 18
US-09-091-071-2

Sequence 2, Application US/09091071
Patent No. 6610500
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: DESIGN OF HORMONE-LIKE ANTIBODIES WITH
NUMBER OF SEQUENCES: 9
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/091,071
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/CA96/00815
FILING DATE: 06-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9525180.7
FILING DATE: 08-DEC-1995
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-091-071-2

Query Match 76.4%; Score 68; DB 2; Length 120;
Best Local Similarity 75.0%; Pred. No. 0.002;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGNDISYNOKFXG 17
Db 50 IYPGSDSYNOKFXG 65

RESULT 19
US-08-822-028-6

Sequence 6, Application US/08822028
Patent No. 5993813
GENERAL INFORMATION:
APPLICANT: MEZES, PETER S
APPLICANT: GOURLIE, BRIAN B
APPLICANT: RIXON, MARK W
APPLICANT: ANDERSON, WH KERR
APPLICANT: KAPLAN, DONALD A
APPLICANT: SCHOLIM, JEFFREY
TITLE OF INVENTION: A NOVEL FAMILY OF HIGH AFFINITY,
MODIFIED ANTIBODIES FOR CANCER TREATMENT
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: DUANE C ULMER
STREET: P.O. BOX 1967
CITY: MIDLAND
STATE: MICHIGAN
COUNTRY: USA
ZIP: 48641-1967
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/822,028
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/040,687
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: ULMER, DUANE C
REGISTRATION NUMBER: 34,941
REFERENCE/DOCKET NUMBER: C-37,075C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 636-8104
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 133 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-822-028-6

Query Match 76.4%; Score 68; DB 1; Length 133;
Best Local Similarity 75.0%; Pred. No. 0.0022;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IYFGNDISTYNQKFXG 17
| | | | | | | | | | | | | | | | | | | | | |
Db 70 ISFGNDIKYNEKFXG 85

RESULT 20
US-08-822-028-30
Sequence 30, Application US/08822028
Patent No. 5993813
GENERAL INFORMATION:

APPLICANT: MEZES, PETER S
APPLICANT: GOURLIE, BRIAN B
APPLICANT: RIXON, MARK W
APPLICANT: ANDERSON, WH KERR
APPLICANT: KAPLAN, DONALD A
APPLICANT: SCHOLOM, JEFFREY
TITLE OF INVENTION: A NOVEL FAMILY OF HIGH AFFINITY,
TITLE OF INVENTION: MODIFIED ANTIBODIES FOR CANCER TREATMENT
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSER: DUANE C ULMER
STREET: P. O. BOX 1967
CITY: MIDLAND
STATE: MICHIGAN
COUNTRY: USA
ZIP: 48641-1967
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,028
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/040,687
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: ULMER, DUANE C
REGISTRATION NUMBER: 34,941
REFERENCE/DOCKET NUMBER: C-37,075C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 636-8104
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 133 amino acids
TYPE: amino acid
STRANDEDNESS: double

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-822-028-30

Query Match 76.4%; Score 68; DB 1; Length 133;
Best Local Similarity 75.0%; Pred. No. 0.0022;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IYFGNDISTYNQKFXG 17
| | | | | | | | | | | | | | | | | | | | | |
Db 70 ISFGNDIKYNEKFXG 85

RESULT 21
US-08-479-285-6
Sequence 6, Application US/08479285
Patent No. 6207815
GENERAL INFORMATION:

APPLICANT: MEZES, PETER S
APPLICANT: GOURLIE, BRIAN B
APPLICANT: RIXON, MARK W
APPLICANT: ANDERSON, WH KERR
APPLICANT: KAPLAN, DONALD A
APPLICANT: SCHOLOM, JEFFREY
TITLE OF INVENTION: A NOVEL FAMILY OF HIGH AFFINITY,
TITLE OF INVENTION: MODIFIED ANTIBODIES FOR CANCER TREATMENT
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSER: DUANE C ULMER
STREET: P. O. BOX 1967
CITY: MIDLAND
STATE: MICHIGAN
COUNTRY: USA
ZIP: 48641-1967
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,285
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/040687
FILING DATE: 31-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: ULMER, DUANE C
REGISTRATION NUMBER: 34,941
REFERENCE/DOCKET NUMBER: C-37,075C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 636-8104
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 133 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-479-285-6

Query Match 76.4%; Score 68; DB 2; Length 133;
Best Local Similarity 75.0%; Pred. No. 0.0022;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IYFGNDISTYNQKFXG 17
| | | | | | | | | | | | | | | | | | | | | |
Db 70 ISFGNDIKYNEKFXG 85

RESULT 22
US-08-479-285-30
Sequence 30, Application US/08479285
Patent No. 6207815

GENERAL INFORMATION:
APPLICANT: MEZES, PETER S
APPLICANT: GOURLIE, BRIAN B
APPLICANT: RIXON, MARK W
APPLICANT: ANDERSON, WM KERR
APPLICANT: KAPLAN, DONALD A
APPLICANT: SCHOLOM, JEFFREY
TITLE OF INVENTION: A NOVEL FAMILY OF HIGH AFFINITY,
MODIFIED ANTIBODIES FOR CANCER TREATMENT
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: DUANE C ULMER
STREET: P.O. BOX 1967
CITY: MIDLAND
STATE: MICHIGAN
COUNTRY: USA
ZIP: 48641-1967
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,285
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/040687
FILING DATE: 31-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: ULMER, DUANE C
REGISTRATION NUMBER: 34,941
REFERENCE/DOCKET NUMBER: C-37,075C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 636-8104
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 133 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-479-285-30

Query Match 76.4%; Score 68; DB 2; Length 133;
Best Local Similarity 75.0%; Pred. No. 0.0022;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 IYPGNDISYNQKFXG 17
| | | | | | | | | | | | | | | | | | | | | |
DB 70 ISPQNDIKYNEKFXG 85

RESULT 23
US-08-961-309-48
Sequence 48, Application US/08961309
Patent No. 6495137
GENERAL INFORMATION:
APPLICANT: Mezes, Peter S.
APPLICANT: Richard, Ruth A.
APPLICANT: Johnson, Kimberly S.
APPLICANT: Schlom, Jeffrey
APPLICANT: Kashmiri, Syed V.S.
APPLICANT: Shu, Liming
APPLICANT: Padlan, Eduard A.
TITLE OF INVENTION: Composite Antibodies of Humanized Human Subgroup IV Light Chain
FILE REFERENCE: 37777E
CURRENT APPLICATION NUMBER: US/08/961,309
CURRENT FILING DATE: 1997-10-30
EARLIER APPLICATION NUMBER: US 60/030,173
EARLIER FILING DATE: 1996-10-31
EARLIER APPLICATION NUMBER: US 08/261,354

EARLIER FILING DATE: 1994-06-16
EARLIER APPLICATION NUMBER: US 07/964,536
EARLIER FILING DATE: 1992-10-20
EARLIER APPLICATION NUMBER: US 07/510,697
EARLIER FILING DATE: 1990-07-17
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Microsoft Word 97 SR-2
SEQ ID NO 48
LENGTH: 133
TYPE: PRT
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: CC83 VH
LOCATION: 1..133
US-08-961-309-48

Query Match 76.4%; Score 68; DB 2; Length 133;
Best Local Similarity 75.0%; Pred. No. 0.0022;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 IYPGNDISYNQKFXG 17
| | | | | | | | | | | | | | | | | | | | | |
DB 70 ISPQNDIKYNEKFXG 85

RESULT 24
US-09-503-653A-6
Sequence 6, Application US/09503653A
Patent No. 664199
GENERAL INFORMATION:
APPLICANT: Mezes, Peter S
APPLICANT: Gourlie, Brian B
APPLICANT: Rixon, Mark W
APPLICANT: Anderson, WM Kerr
APPLICANT: Kaplan, Donald A
APPLICANT: Schlom, Jeffrey
TITLE OF INVENTION: Probing Method for Identifying Antibodies
FILE REFERENCE: 37075H-CIP1
CURRENT APPLICATION NUMBER: US/09/503,653A
CURRENT FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: US 08/040,687
PRIOR FILING DATE: 1993-03-31
PRIOR APPLICATION NUMBER: US 07/424,362
PRIOR FILING DATE: 1989-10-19
PRIOR APPLICATION NUMBER: US 07/261,942
PRIOR FILING DATE: 1988-10-24
PRIOR APPLICATION NUMBER: US 07/259,943
NUMBER OF SEQ ID NOS: 74
SOFTWARE: MICROSOFT Word 97 SR-2
SEQ ID NO 6
LENGTH: 133
TYPE: PRT
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: SIGNAL
LOCATION: -19...-1
NAME/KEY: CHAIN
LOCATION: 1..114
US-09-503-653A-6

Query Match 76.4%; Score 68; DB 2; Length 133;
Best Local Similarity 75.0%; Pred. No. 0.0022;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 IYPGNDISYNQKFXG 17
| | | | | | | | | | | | | | | | | | | | | |
DB 70 ISPQNDIKYNEKFXG 85

RESULT 25
US-09-503-653A-30

```

Sequence 0, Application US/09503653A
Patent No. 6641999
GENERAL INFORMATION:
APPLICANT: Mezes, Peter S
APPLICANT: Gourlie, Brian B
APPLICANT: Rixon, Mark W
APPLICANT: Anderson, WH Kerr
APPLICANT: Kaplan, Donald A
APPLICANT: Schiom, Jeffrey
TITLE OF INVENTION: Profbing Method for Identifying Antibodies
TITLE OF INVENTION: Specific for Selected Antigens
FILE REFERENCE: 37075H-C1P1
CURRENT APPLICATION NUMBER: US/09/503,653A
CURRENT FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: US 08/040,687
PRIOR FILING DATE: 1993-03-31
PRIOR APPLICATION NUMBER: US 07/424,362
PRIOR FILING DATE: 1989-10-19
PRIOR APPLICATION NUMBER: US 07/261,942
PRIOR FILING DATE: 1988-10-24
PRIOR APPLICATION NUMBER: US 07/259,943
PRIOR FILING DATE: 1988-10-19
NUMBER OF SEQ ID NOS: 74
SOFTWARE: MICROSOFT Word 97 SR-2
SEQ ID NO 30
LENGTH: 133
TYPE: PRT
ORGANISM: Mus musculus
US-09-503-653A-30

```

Query Match	76.4%	Score 68	DB 2	Length 133
Best Local Similarity	75.0%	Pred. No. 0.0022		
Matches	12	Conservative	1	Mismatches 3
				Indels 0
				Gaps 0
QY	2	TYPGNDISYNOKFXG	17	
Db	70	ISPGNDIDIKYNEKFKG	85	

```

RESULT 26
5219996-17
; Patent No. 5219996
; APPLICANT: BOMMER, MARK W.; ADAIR, JOHN R.; WHITTLE, NIGEL R
; LYONS, ALAN H.; OWENS, RAYMOND J.
; TITLE OF INVENTION: RECOMBINANT ANTIBODIES AND METHODS FOR
; THEIR PRODUCTION IN WHICH SURFACE RESIDUES ARE ALTERED TO
; CYSTEINE RESIDUES FOR ATTACHMENT OF EFFECTOR OR RECEPTOR
; MOLECULES
; NUMBER OF SEQUENCES: 19
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/353,634
; FILING DATE: 05-SEP-1988
; SEQ ID NO.:17:
; LENGTH: 133
5219996-17

```

Query Match	76.4%	Score 68;	DB 6;	Length 133;
Best Local Similarity	75.0%	Pred. No. 0.0022;		
Matches	12;	conservative	1;	Mismatches 3; Indels 0;
Qy	2	TYPGNDISTNQKFXG	17	
Db	70	ISPGNDIDIKYNEKFKG	85	

RESULT 27
US-08-822-028-10
; Sequence 10, Application US/08822028
; Patent No. 5993813
; GENERAL INFORMATION:
; APPLICANT: MEZES, PETER S
; APPLICANT: GOURLIE, BRIAN B
; APPLICANT: RIXON, MARK W

```

1  APPLICANT:  ANDERSON, WM KEER
2  APPLICANT:  KAPLAN, DONALD A
3  APPLICANT:  SCHOLOM, JEFFREY
4  TITLE OF INVENTION:  A NOVEL FAMILY OF HIGH AFFINITY,
5  TITLE OF INVENTION:  MODIFIED ANTIBODIES FOR CANCER TREATMENT
6  NUMBER OF SEQUENCES:  74
7  CORRESPONDENCE ADDRESS:
8  ADDRESSEE:  DUANE C ULMER
9  STREET:  P.O. BOX 1967
10 CITY:  MIDLAND
11 STATE:  MICHIGAN
12 COUNTRY:  USA
13 ZIP:  48641-1967
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE:  floppy disk
16 COMPUTER:  IBM PC compatible
17 OPERATING SYSTEM:  PC-DOS/MS-DOS
18 SOFTWARE:  PatentIn Release #1.0, Version #1.25
19 CURRENT APPLICATION DATA:
20 APPLICATION NUMBER:  US/08/822,028
21 FILING DATE:
22 CLASSIFICATION:
23 PRIOR APPLICATION DATA:
24 APPLICATION NUMBER:  US 08/040,687
25 FILING DATE:
26 ATTORNEY/AGENT INFORMATION:
27 NAME:  ULMER, DUANE C
28 REGISTRATION NUMBER:  34,941
29 REFERENCE/DOCKET NUMBER:  C-37,075C
30 TELECOMMUNICATION INFORMATION:
31 TELEPHONE:  (517) 636-8104
32 INFORMATION FOR SEQ ID NO:  10:
33 SEQUENCE CHARACTERISTICS:
34     LENGTH:  134 amino acids
35     TYPE:  amino acid
36     TOPOLOGY:  linear
37 MOLECULE TYPE:  protein
38 US-08-822-028-10

```

		76.4%;	Score 68 ;	DB 1 ;	Length 134 ;
		Best Local Similarity	75.0% ;	Pred. No.	0.0022 ;
Matches	12 ;	Conservative	1 ;	Mismatches	3 ;
				Indels	0 ;
Gaps	0 ;				
OY	2	IYPGNDIDISYNOKFXG	17		
Db	70	ISP GNDIDIKYNEKEFG	85		

```

RESULT 28
US-08-479-285-10
; Sequence 10, Application US/08479285
; Patent No. 6207815
; GENERAL INFORMATION:
; APPLICANT: MEZES, PETER S
; APPLICANT: GOURLIE, BRIAN B
; APPLICANT: RIXON, MARK W
; APPLICANT: ANDERSON, WH KEER
; APPLICANT: KAPLAN, DONALD A
; APPLICANT: SCHOLOM, JEFFREY
; TITLE OF INVENTION: A NOVEL FAMILY OF HIGH AFFINITY,
; TITLE OF INVENTION: MODIFIED ANTIBODIES FOR CANCER TREATMENT
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: DUANE C ULMER
; STREET: P. O. BOX 1967
; CITY: MIDLAND
; STATE: MICHIGAN
; COUNTRY: USA
; ZIP: 48641-1967
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

```

```

1      SOFTWARE: Patent in Release #1.0, Version #1.25
2
3      CURRENT APPLICATION DATA:
4      APPLICATION NUMBER: US/08/479,265
5      FILING DATE: 07-JUN-1995
6
7      CLASSIFICATION: 536
8
9      PRIOR APPLICATION DATA:
10     APPLICATION NUMBER: US 08/040687
11     FILING DATE: 31-MAR-1993
12     ATTORNEY/AGENT INFORMATION:
13     NAME: UIMER, DUANE C
14     REGISTRATION NUMBER: 34,941
15     REFERENCE/DOCKET NUMBER: C-37, 075C
16
17     TELECOMMUNICATION INFORMATION:
18     TELEPHONE: (517) 636-8104
19
20     INFORMATION FOR SEQ ID NO: 10:
21
22     SEQUENCE CHARACTERISTICS:
23
24     LENGTH: 134 amino acids
25     TYPE: amino acid
26     TOPOLOGY: linear
27
28     MOLECULE TYPE: protein
29
30     US-08-479-285-10

```

Query Match	76.4%	Score 68	DB 2	Length 134
Best Local Similarity	75.0%	Pred. No. 0.0022		
Matches 12	Conservative 1	Mismatches 3	Indels 0	Gaps 0

```
QY      2 IYPGNDISYNQKFXG 17
          | ||||| | | : | | |
Db      70 ISPGNDDIKYNEKFKG 85
```

RESULT 29
US-08-961-309-49

Sequence 49 Application US/08961309
Patent No. 6495137
GENERAL INFORMATION:
APPLICANT: Mezes, Peter S.
APPLICANT: Richard, Ruth A.
APPLICANT: Johnson, Kimberly S.
APPLICANT: Schlom, Jeffrey
APPLICANT: Kashmiri, Syed V.S.
APPLICANT: Shu, Liming
APPLICANT: Padlan, Eduardo A.
TITLE OF INVENTION: Composite Antibodies of Humanized Human Subgroup IV Light Chain
TITLE OF INVENTION: Capable of Binding to TAg-72

Query Match	76.4%;	Score 68;	DB 2;	Length 134;
Best Local Similarity	75.0%;	Pred. No. 0.0022;		
Matches 12; Conservative	1;	Mismatches 3;	Indels 0;	Gaps 0;

QY 2 IYPGNDDISYNQKFXG 17
| | | | | | | : | | |

Db 70 ISPGND DIKYNEKFKG 85

```

RESULT 30
US-09-503-653A-10
: Sequence 10, Application US/09503653A
: Patent No. 6641999
: GENERAL INFORMATION:
: APPLICANT: Mezes, Peter S
: APPLICANT: Gourliat, Brian B
: APPLICANT: Rixon, Mark W
: APPLICANT: Anderson, WH Kerr
: APPLICANT: Kaplan, Donald A
: APPLICANT: Schiom, Jeffrey
: TITLE OF INVENTION: Probing Method for Identifying Antibodies
: TITLE OF INVENTION: Specific for Selected Antigens
: FILE REFERENCE: 37075H-CIP1
: CURRENT APPLICATION NUMBER: US/09/503,653A
: CURRENT FILING DATE: 2000-02-14
: PRIOR APPLICATION NUMBER: US 08/040,687
: PRIOR FILING DATE: 1993-03-31
: PRIOR APPLICATION NUMBER: US 07/424,362
: PRIOR FILING DATE: 1989-10-19
: PRIOR APPLICATION NUMBER: US 07/261,942
: PRIOR FILING DATE: 1988-10-24
: PRIOR APPLICATION NUMBER: US 07/259,943
: PRIOR FILING DATE: 1988-10-19
: NUMBER OF SEQ ID NOS: 74
: SOFTWARE: MICROSOFT word 97 SR-2
: SEQ ID NO 10
: LENGTH: 134
: TYPE: PRT
: ORGANISM: Mus musculus
: FEATURE:
: NAME/KEY: SIGNAL
: LOCATION: -19...-1
: NAME/KEY: CHAIN
: LOCATION: 1..115
: US-09-503-653A-10

```

Query Match 76.4%; Score 68; DB 2; Length 134;
Best Local Similarity 75.0%; Pred. No. 0.0022;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```
QY      2 IYPGNDDISYNQKFXG 17
          | ||||| |:|||
Db      70 ISPGNDIKYNEKFXG 85
```

```

1      RESULT 31
2      US-08-400-115-2
3      ; Sequence 2, Application US/08400115
4      ; Patent No. 5864019
5      ; GENERAL INFORMATION:
6      ; APPLICANT: KING, David John
7      ; APPLICANT: MOUNTAIN, Andrew
8      ; APPLICANT: OWENS, Raymond John
9      ; APPLICANT: YARANTON, Geoffrey Thomas
10     ; TITLE OF INVENTION: Multivalent Antigen-Binding Proteins
11     ; NUMBER OF SEQUENCES: 26
12     ; CORRESPONDENCE ADDRESSES:
13     ; ADDRESSEE: Foley & Lardner
14     ; STREET: 3000 K Street, N.W., Suite 500
15     ; CITY: Washington, D.C.
16     ; COUNTRY: USA
17     ; ZIP: 20007-5109
18     ; COMPUTER READABLE FORM:
19     ; MEDIUM TYPE: Floppy disk
20     ; COMPUTER: IBM PC compatible
21     ; OPERATING SYSTEM: PC-DOS/MS-DOS
22     ; SOFTWARE: PatentIn Release #1.0, Version #1.25
23     ; CURRENT APPLICATION DATA:
24     ; APPLICATION NUMBER: US/08/400.115

```



```

1      FLTING DATE: 06-MAR-1995
2      PRIOR APPLICATION DATE:
3      APPLICATION NUMBER: US 08/127,136
4      FLTING DATE: 27-SEP-1993
5      PRIOR APPLICATION DATA:
6      APPLICATION NUMBER: US 07/842,193
7      FLTING DATE: 17-MAR-1992
8      PRIOR APPLICATION DATA:
9      APPLICATION NUMBER: PCT/GB91/00935
10     FLTING DATE: 11-JUN-1991
11     PRIOR APPLICATION DATA:
12     APPLICATION NUMBER: GB 9012995.8
13     FLTING DATE: 11-JUN-1990
14     ATTORNEY/AGENT INFORMATION:
15     NAME: ISACSON, John P.
16     REGISTRATION NUMBER: 33,715
17     REFERENCE/DOCKET NUMBER: 040283/0106 CARA
18     TELECOMMUNICATION INFORMATION:
19     TELEPHONE: (202) 672-5300
20     TELEFAX: (202) 672-5399
21     TELEX: 904136
22     INFORMATION FOR SEQ ID NO: 2:
23     SEQUENCE CHARACTERISTICS:
24     LENGTH: 150 amino acids
25     TYPE: amino acid
26     TOPOLOGY: linear
27     MOLECULE TYPE: protein
28     US-08-400-115-2

```

```

; APPLICATION NUMBER: GB 9012995.8
; FILING DATE: 11-JUN-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: ISACSON, John P.
; REGISTRATION NUMBER: 33,715
; REFERENCE/DOCKET NUMBER: 040263/0106 CARA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 271 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-400-115-4

Query Match          76.4%; Score 68; DB 1; Length 271;
Best Local Similarity 75.0%; Pred. No. 0.0048,
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0.

QY      2 IYPGNDISYNOKFXG 17
| | | | | | | : | | |
Db      196 ISPGRDIDIKINKEFKG 211

```

RESULT 32
 US-08-400-115-4
 Sequence 4, Application US/08400115
 Patent No. 5864019
 GENERAL INFORMATION:
 APPLICANT: KING, David John
 APPLICANT: MOUNTAIN, Andrew
 APPLICANT: OWENS, Raymond John
 APPLICANT: VARANTON, Geoffrey Thomas
 TITLE OF INVENTION: Multivalent Antigen-Binding Proteins
 NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Foley & Lardner
 STREET: 3000 K Street, N.W., Suite 500
 CITY: Washington, D.C.
 COUNTRY: USA
 ZIP: 20007-5109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/400,115
 FILING DATE: 06-MAR-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/127,136
 FILING DATE: 27-SEP-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/842,193
 FILING DATE: 17-MAR-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/GB91/00935
 FILING DATE: 11-JUN-1991
 PRIOR APPLICATION DATA:

SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-403-853-18

Query Match 74.2%; Score 66; DB 1; Length 273;
Best Local Similarity 73.3%; Pred. No. 0.01;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VYFGNDISYNQKF 15
: ||||| :
Db 72 IFYFGNDISYNQKF 86

RESULT 34
US-09-419-788-113
Sequence 113, Application US/09419788
Patent No. 6825325
GENERAL INFORMATION:
APPLICANT: FISCHER, Rainer
APPLICANT: SCHILLBERG, Stefan
APPLICANT: NAHRING, Jorg
APPLICANT: SACK, Markus
APPLICANT: MONCKE, Michael
APPLICANT: LIAO, Yu-Cai
APPLICANT: SPIEGEL, Holger
APPLICANT: ZIMMERMAN, Sabine
APPLICANT: EMANS, Neil
TITLE OF INVENTION: Molecular Pathogenicity Mediated Plant Disease
TITLE OF INVENTION: Resistance
FILE REFERENCE: 0147-0189P
CURRENT APPLICATION NUMBER: US/09/419,788
CURRENT FILING DATE: 1999-10-18
EARLIER APPLICATION NUMBER: 98 11 9630.6 EP
EARLIER FILING DATE: 1998-10-16
EARLIER APPLICATION NUMBER: 66/BOM/1998 INDIA
EARLIER FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 163
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 113
LENGTH: 257
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic, no
OTHER INFORMATION: natural origin
US-09-419-788-113

Query Match 71.9%; Score 64; DB 2; Length 257;
Best Local Similarity 75.0%; Pred. No. 0.02;
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 IYFGNDISYNQKF 17
: ||||| :
Db 53 IYFGNDISYNQKF 68

RESULT 35
US-08-318-970B-4
Sequence 4, Application US/08318970B
Patent No. 5589573
GENERAL INFORMATION:
APPLICANT: HIDEAKI HAGIWARA, et al.
TITLE OF INVENTION: AMINO ACID SEQUENCES OF ANTI-IDIOTYPIC
TITLE OF INVENTION: ANTIBODIES AGAINST ANTI-CANCER HUMAN MONOCLONAL ANTIBODY
TITLE OF INVENTION: AND DNA BASE SEQUENCES ENCODING THOSE SEQUENCES
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Office of Sherman and Shalloway
STREET: 413 N. Washington Street
CITY: Alexandria

STATE: Virginia
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: Dell System 210; Intel 80 285 Microprocessor
OPERATING SYSTEM: MS DOS 3.3
SOFTWARE: Word Perfect, Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,970B
FILING DATE: October 6, 1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Richard A. Steinberg
REGISTRATION NUMBER: 26,588
REFERENCE/DOCKET NUMBER: S-2371
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 549-2282
TELEFAX: (703) 836-0106
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: H-CDR2-1
OTHER INFORMATION: hypervariable region
US-08-318-970B-4

Query Match 70.8%; Score 63; DB 1; Length 17;
Best Local Similarity 78.6%; Pred. No. 0.0014;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 IYFGNDISYNQKF 15
: ||||| :
Db 2 IYFGNDISYNQKF 15

RESULT 36
US-09-096-244-4
Sequence 4, Application US/09096244
Patent No. 6274143
GENERAL INFORMATION:
APPLICANT: Chatterjee, Malaya
APPLICANT: Boon, Kenneth A.
TITLE OF INVENTION: METHODS OF DELAYING DEVELOPMENT OF
TITLE OF INVENTION: HMF-G-ASSOCIATED TUMORS USING ANTI-IDIOTYPIC ANTIBODY 11D10
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/096,244
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Polizzi, Catherine M.
REGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 30414-20006.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
TELEX: 706141

```

; INFORMATION FOR SEQ ID NO: 4:
;
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 153 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;
US-09-036-244-4

```

Query Match	69.7%	Score 62	DB 2	Length 153
Best Local Similarity	68.8%	Pred. No. 0.023		
Matches 11; Conservative	1	Mismatches 4	Indels 0	Gaps 0

```
QY      2 IYPGNDISYNQKFXG 17
        | : ||| | ||||| |
Db      70 ITPGNGDTYNNQKFKG 85
```

RESULT 37
US-08-766-350B-4
; Sequence 4, Application US/08766350B
; Patent No. 6949244
; GENERAL INFORMATION:

Query Match	69.7%;	Score 62;	DB 2;	Length 153;
Best Local Similarity	68.8%;	Pred. No. 0.023;		
Matches 11; Conservative	1;	Mismatches 4;	Indels 0;	Gaps 0

```

QY      2 IYPGNDDISYNQKFXG 17
         |::||| | ||||| |
Db      70 IFPGNGDTYYNQKFKG 85

```

RESULT 38
US-08-822-028-2
; Sequence 2, Application US/08822028

```

1 Patent No. 5993813
2 GENERAL INFORMATION:
3 APPLICANT: MEZES, PETER S
4 APPLICANT: GOURLIE, BRIAN B
5 APPLICANT: RIXON, MARK W
6 APPLICANT: ANDERSON, WH KERR
7 APPLICANT: KAPLAN, DONALD A
8 APPLICANT: SCHOLOM, JEFFREY
9 TITLE OF INVENTION: A NOVEL FAMILY OF HIGH AFFINITY,
10 TITLE OF INVENTION: MODIFIED ANTIBODIES FOR CANCER TREATMENT
11 NUMBER OF SEQUENCES: 74
12 CORRESPONDENCE ADDRESS:
13 ADDRESSEE: DUANE C ULMER
14 STREET: P.O. BOX 1967
15 CITY: MIDLAND
16 STATE: MICHIGAN
17 COUNTRY: USA
18 ZIP: 48641-1967
19 COMPUTER READABLE FORM:
20 MEDIUM TYPE: Floppy disk
21 COMPUTER: IBM PC compatible
22 OPERATING SYSTEM: PC-DOS/MS-DOS
23 SOFTWARE: Patent in Release #1.0, Version #1.25
24 CURRENT APPLICATION DATA:
25 APPLICATION NUMBER: US/08/822,028
26 FILING DATE:
27 CLASSIFICATION:
28 PRIOR APPLICATION DATA:
29 APPLICATION NUMBER: US 08/040,687
30 FILING DATE:
31 ATTORNEY/AGENT INFORMATION:
32 NAME: ULMER, DUANE C
33 REGISTRATION NUMBER: 34,941
34 REFERENCE/DOCKET NUMBER: C-37,075C
35 TELECOMMUNICATION INFORMATION:
36 TELEPHONE: (517) 636-8104
37 INFORMATION FOR SEQ ID NO: 2:
38 SEQUENCE CHARACTERISTICS:
39 LENGTH: 117 amino acids
40 TYPE: amino acid
41 TOPOLOGY: linear
42 MOLECULE TYPE: protein
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Query Match	68.5%	Score 61;	DB 1;	Length 117;
Best Local Similarity	68.8%	Pred. No. 0.025;		
Matches 11; Conservative	1;	Mismatches 4;	Indels 0;	Gaps 0;

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QY      2 IYPGNDDISYNQKFXG 17
          ||||| | | | |
Db      70 ISPGNGDIKYNEKFKG 85
```

US-08-479-285-2
US-RESULT 39
Sequence 2, Application US/08479285
Patent No. 6207815
GENERAL INFORMATION:
APPLICANT: MEZES, PETER S
APPLICANT: GOURLIE, BRIAN B
APPLICANT: RIXON, MARK W
APPLICANT: ANDERSON, WH KERR
APPLICANT: KAPLAN, DONALD A
APPLICANT: SCHOLIM, JEFFREY
TITLE OF INVENTION: A NOVEL FAMILY OF HIGH AFFINITY,
MODIFIED ANTIBODIES FOR CANCER TREATMENT
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: DUANE C ULMER
STREET: P O BOX 1967
CITY: MIDLAND
STATE: MICHIGAN
COUNTRY: USA

ZIP: 48641-1967
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,285
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/040687
FILING DATE: 31-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: UMER, DUANE C
REGISTRATION NUMBER: 34,941
REFERENCE/DOCKET NUMBER: C-37,075C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 636-8104
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-479-285-2

Query Match 68.5%; Score 61; DB 2; Length 117;
Best Local Similarity 68.8%; Pred. No. 0.025;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 IYPGNDISYNOKFXG 17
| | | | | | | | | | | | | | | | | | | | | |
Db 70 ISPENGDIKYNKFXG 85

RESULT 40
US-08-961-309-45
Sequence 45, Application US/08961309
Patent No. 6493137
GENERAL INFORMATION:
APPLICANT: Mezes, Peter S.
APPLICANT: Richard, Ruth A.
APPLICANT: Johnson, Kimberly S.
APPLICANT: Schlom, Jeffrey
APPLICANT: Kashmitz, Syed V.S.
APPLICANT: Shu, Liming
TITLE OF INVENTION: Composite Antibodies of Humanized Human Subgroup IV Light Chain
FILE REFERENCE: 37777E
CURRENT APPLICATION NUMBER: US/08/961,309
CURRENT FILING DATE: 1997-10-30
EARLIER APPLICATION NUMBER: US 60/030,173
EARLIER FILING DATE: 1996-10-31
EARLIER APPLICATION NUMBER: US 08/261,354
EARLIER FILING DATE: 1994-06-16
EARLIER APPLICATION NUMBER: US 07/964,536
EARLIER FILING DATE: 1992-10-20
EARLIER APPLICATION NUMBER: US 07/510,697
EARLIER FILING DATE: 1990-07-17
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Microsoft Word 97 SR-2
SEQ ID NO 45
LENGTH: 117
TYPE: PRT
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: VHA TAG
LOCATION: 1..117
US-08-961-309-45

Query Match 68.5%; Score 61; DB 2; Length 117;

Best Local Similarity 68.8%; Pred. No. 0.025;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 IYPGNDISYNOKFXG 17
| | | | | | | | | | | | | | | | | | | | | |
Db 70 ISPENGDIKYNKFXG 85

RESULT 41
US-09-503-653A-2
Sequence 2, Application US/09503653A
Patent No. 6641999
GENERAL INFORMATION:
APPLICANT: Mezes, Peter S
APPLICANT: Gourlie, Brian B
APPLICANT: Rixon, Mark W
APPLICANT: Anderson, WH Kerr
APPLICANT: Kaplan, Donald A
APPLICANT: Schlom, Jeffrey
TITLE OF INVENTION: Probing Method for Identifying Antibodies
FILE REFERENCE: 37075H-CIP1
CURRENT APPLICATION NUMBER: US/09/503,653A
CURRENT FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: US 08/040,687
PRIOR FILING DATE: 1993-03-31
PRIOR APPLICATION NUMBER: US 07/424,362
PRIOR FILING DATE: 1989-10-19
PRIOR APPLICATION NUMBER: US 07/261,942
PRIOR FILING DATE: 1988-10-24
PRIOR APPLICATION NUMBER: US 07/259,943
PRIOR FILING DATE: 1988-10-19
NUMBER OF SEQ ID NOS: 74
SOFTWARE: MICROSOFT Word 97 SR-2
SEQ ID NO 2
LENGTH: 117
TYPE: PRT
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: SIGNAL
LOCATION: -19...-1
NAME/KEY: CHAIN
LOCATION: 1..98
US-09-503-653A-2

Query Match 68.5%; Score 61; DB 2; Length 117;
Best Local Similarity 68.8%; Pred. No. 0.025;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 IYPGNDISYNOKFXG 17
| | | | | | | | | | | | | | | | | | | | | |
Db 70 ISPENGDIKYNKFXG 85

RESULT 42
US-09-386-658A-2
Sequence 2, Application US/09386658A
Patent No. 6593137
GENERAL INFORMATION:
APPLICANT: Erlanger, Bernard F.
APPLICANT: Chen, Bi-Xing
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR FULLERENES
FILE REFERENCE: 0575/54182
CURRENT APPLICATION NUMBER: US/09/386,658A
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 132
TYPE: PRT
ORGANISM: Mouse
US-09-386-658A-2

Query Match 68.5%; Score 61; DB 2; Length 132;
Best Local Similarity 62.5%; Pred. No. 0.028;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Oy 2 IYPGNDISYNOKFXG 17
|||:|:|:|:|
Db 70 IYPGNDITYNKFKG 85

RESULT 43

US-08-875-811-57
Sequence 57, Application US/08875811
Patent No. 6045793

GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Luis
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998

CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996

ATTORNEY/AGENT INFORMATION:
NAME: Paris, Susan K.

REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:

LENGTH: 355 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-875-811-57

Query Match 67.4%; Score 60; DB 2; Length 355;
Best Local Similarity 62.5%; Pred. No. 0.12;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Oy 2 IYPGNDISYNOKFXG 17
|||:|:|:|:|
Db 169 IYPGNDITYNKFKG 184

RESULT 44

US-09-830-748B-5
Sequence 5, Application US/09830748B
Patent No. 6818749

GENERAL INFORMATION:

APPLICANT: The Government of the United States of America, as represented by The
APPLICANT: Secretary of the Department of Health and Human Services

APPLICANT: Kashmiri, Syed V.S.
APPLICANT: Padlan, Eduardo A.
APPLICANT: Jeffery, Schlom
TITLE OF INVENTION: VARIANTS OF HUMANIZED ANTI-CARCINOMA MONOCLONAL ANTIBODY CC49

FILE REFERENCE: 4239-61725
CURRENT APPLICATION NUMBER: US/09/830,748B

CURRENT FILING DATE: 2001-04-30
PRIOR APPLICATION NUMBER: PCT/US99/25552

PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: US 60/106,757

PRIOR FILING DATE: 1998-11-02
PRIOR APPLICATION NUMBER: US 60/106,534

PRIOR FILING DATE: 1998-10-31
NUMBER OF SEQ ID NOS: 44

SOFTWARE: Patent version 3.1
SEQ ID NO 5

LENGTH: 17
TYPE: PRT

ORGANISM: Mus musculus
US-09-830-748B-5

Query Match 66.3%; Score 59; DB 2; Length 17;
Best Local Similarity 64.3%; Pred. No. 0.0062;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Oy 4 PGNDISYNOKFXG 17
|||:|:|:|:|
Db 4 PGNDIFKINERFKG 17

RESULT 45

US-09-244-592-6
Sequence 6, Application US/09244592A
Patent No. 6365124

GENERAL INFORMATION:

APPLICANT: Babino, Alvaro
APPLICANT: Osinaga, Eduardo

APPLICANT: Barbera-Guillem, Emilio
TITLE OF INVENTION: Compositions for detecting and surgically removing lymphoid

TITLE OF INVENTION: tissue involved in tumor progression
FILE REFERENCE: B-18
CURRENT APPLICATION NUMBER: US/09/244,592A

CURRENT FILING DATE: 1999-02-04
EARLIER APPLICATION NUMBER: US 60/073882

EARLIER FILING DATE: 1998-02-06
EARLIER APPLICATION NUMBER: US 60/077970

EARLIER FILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 6

SEQ ID NO 6
LENGTH: 42

TYPE: PRT
ORGANISM: Artificial

FEATURE:
NAME/KEY:
LOCATION:
OTHER INFORMATION: synthesized

US-09-244-592-6

Query Match 66.3%; Score 59; DB 2; Length 42;
Best Local Similarity 71.4%; Pred. No. 0.017;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 4 PGNDISYNOKFXG 17
|||:|:|:|:|
Db 27 PGNDIKINERFKG 40

RESULT 46

US-09-244-592-3
Sequence 3, Application US/09244592A
Patent No. 6365124

GENERAL INFORMATION:

APPLICANT: Babino, Alvaro

```

; APPLICANT: Osinaga, Eduardo
; APPLICANT: Barbera-Guillem, Emilio
; TITLE OF INVENTION: Compositions for detecting and surgically removing lymphoid
; FILE REFERENCE: B-18
; CURRENT APPLICATION NUMBER: US/09/244,592A
; CURRENT FILING DATE: 1999-02-04
; EARLIER APPLICATION NUMBER: US 60/073882
; EARLIER FILING DATE: 1998-02-06
; EARLIER APPLICATION NUMBER: US 60/077970
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 3
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: synthesized
US-09-244-592-3

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Query Match      66.3%; Score 59; DB 2; Length 46;
Best Local Similarity 71.4%; Pred. No. 0.018;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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QY      4 PGNDISYNOKFXG 17
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Db      27 PGNGDIRYNEKFXG 40

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RESULT 47
US-09-244-592-4
; Sequence 4, Application US/09244592A
; Patent No. 6365124
; GENERAL INFORMATION:
; APPLICANT: Babino, Alvaro
; APPLICANT: Osinaga, Eduardo
; APPLICANT: Barbera-Guillem, Emilio
; TITLE OF INVENTION: Compositions for detecting and surgically removing lymphoid
; FILE REFERENCE: B-18
; CURRENT APPLICATION NUMBER: US/09/244,592A
; CURRENT FILING DATE: 1999-02-04
; EARLIER APPLICATION NUMBER: US 60/073882
; EARLIER FILING DATE: 1998-02-06
; EARLIER APPLICATION NUMBER: US 60/077970
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 4
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: synthesized
US-09-244-592-4

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Query Match      66.3%; Score 59; DB 2; Length 75;
Best Local Similarity 71.4%; Pred. No. 0.032;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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QY      4 PGNDISYNOKFXG 17
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Db      27 PGNGDIRYNEKFXG 40

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RESULT 48
US-09-244-592-5
; Sequence 5, Application US/09244592A
; Patent No. 6365124
; GENERAL INFORMATION:

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```

; APPLICANT: Babino, Alvaro
; APPLICANT: Osinaga, Eduardo
; APPLICANT: Barbera-Guillem, Emilio
; TITLE OF INVENTION: Compositions for detecting and surgically removing lymphoid
; FILE REFERENCE: B-18
; CURRENT APPLICATION NUMBER: US/09/244,592A
; CURRENT FILING DATE: 1999-02-04
; EARLIER APPLICATION NUMBER: US 60/073882
; EARLIER FILING DATE: 1998-02-06
; EARLIER APPLICATION NUMBER: US 60/077970
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 5
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: synthesized
US-09-244-592-5

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Query Match      66.3%; Score 59; DB 2; Length 75;
Best Local Similarity 71.4%; Pred. No. 0.032;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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QY      4 PGNDISYNOKFXG 17
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Db      53 PGNGDIRYNEKFXG 66

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RESULT 49
US-09-244-592-2
; Sequence 2, Application US/09244592A
; Patent No. 6365124
; GENERAL INFORMATION:
; APPLICANT: Babino, Alvaro
; APPLICANT: Osinaga, Eduardo
; APPLICANT: Barbera-Guillem, Emilio
; TITLE OF INVENTION: Compositions for detecting and surgically removing lymphoid
; FILE REFERENCE: B-18
; CURRENT APPLICATION NUMBER: US/09/244,592A
; CURRENT FILING DATE: 1999-02-04
; EARLIER APPLICATION NUMBER: US 60/073882
; EARLIER FILING DATE: 1998-02-06
; EARLIER APPLICATION NUMBER: US 60/077970
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 2
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: synthesized
US-09-244-592-2

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Query Match      66.3%; Score 59; DB 2; Length 90;
Best Local Similarity 71.4%; Pred. No. 0.039;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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Db      27 PGNGDIRYNEKFXG 40

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RESULT 50
US-08-263-911-4
; Sequence 4, Application US/08263911
; Patent No. 5877291

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GENERAL INFORMATION:
APPLICANT: Mezes, Peter S
APPLICANT: Goutlie, Brian B
TITLE OF INVENTION: MULTIVALENT SINGLE CHAIN ANTIBODIES
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Duane C. Ulmer
STREET: P.O. Box 1967
CITY: Midland
STATE: MI
COUNTRY: US
ZIP: 48641-1967
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/263,911
FILING DATE: 21-JUN-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,263
FILING DATE: 11-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Ulmer, Duane C
REGISTRATION NUMBER: 34,941
REFERENCE/DOCKET NUMBER: C-41,014
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 636-8104
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-263-911-4

Query Match 66.3%; Score 59; DB 1; Length 115;
Best Local Similarity 64.3%; Pred. No. 0.05;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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OM protein - protein search, using sw model

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Title: US-10-700-632-2

Perfect score: 89

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Searched: 1867569 seqs, 417829326 residues

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Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications_AA_Main:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

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7	73	82.0	17	US-10-240-353B-2	Sequence 2, Appl1
8	73	82.0	114	US-10-700-632-80	Sequence 80, Appl1
9	73	82.0	136	US-10-240-353B-8	Sequence 8, Appl1
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121	72	80.9	482	6	US-11-088-570-33	Sequence 33, App1	194	72	80.9	500	5	US-10-627-556-290	Sequence 290, App
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173	72	80.9	500	5	US-10-627-556-58	Sequence 58, App1	246	68	76.4	134	4	US-10-255-478-49	Sequence 49, App1

247	68	76.4	150	3	US-09-226-157-2	Sequence 2, Appl1	320	59	66.3	115	4	US-10-255-478-76	Sequence 76, Appl1
248	68	76.4	208	4	US-10-336-210-1	Sequence 1, Appl1	321	59	66.3	115	5	US-10-880-028-32	Sequence 32, Appl1
249	68	76.4	237	4	US-10-336-210-2	Sequence 2, Appl1	322	59	66.3	115	5	US-10-880-028-34	Sequence 34, Appl1
250	68	76.4	238	4	US-10-336-210-3	Sequence 3, Appl1	323	59	66.3	115	5	US-10-880-028-35	Sequence 35, Appl1
251	68	76.4	242	4	US-10-336-210-5	Sequence 5, Appl1	324	59	66.3	115	5	US-10-880-320-32	Sequence 32, Appl1
252	68	76.4	271	3	US-09-226-157-4	Sequence 4, Appl1	325	59	66.3	115	5	US-10-880-320-34	Sequence 34, Appl1
253	68	76.4	272	4	US-10-336-210-6	Sequence 6, Appl1	326	59	66.3	115	5	US-10-880-320-35	Sequence 35, Appl1
254	68	76.4	271	4	US-10-336-210-7	Sequence 7, Appl1	327	59	66.3	115	5	US-10-927-433-14	Sequence 14, Appl1
255	68	76.4	661	4	US-10-336-210-11	Sequence 11, Appl1	328	59	66.3	119	4	US-10-194-975-121	Sequence 12, App
256	67	75.3	17	5	US-10-849-615-31	Sequence 31, Appl1	329	59	66.3	134	4	US-10-255-478-46	Sequence 46, Appl1
257	67	75.3	120	4	US-10-010-729-19	Sequence 19, Appl1	330	59	66.3	134	4	US-10-255-478-47	Sequence 47, Appl1
258	67	75.3	121	5	US-10-849-615-55	Sequence 65, Appl1	331	59	66.3	136	4	US-10-160-232-88	Sequence 88, Appl1
259	66	74.2	122	5	US-10-895-135-55	Sequence 55, Appl1	332	59	66.3	136	4	US-10-160-232-91	Sequence 91, Appl1
260	64	71.9	216	5	US-10-488-074-85	Sequence 85, Appl1	333	59	66.3	136	4	US-10-160-232-95	Sequence 95, Appl1
261	64	71.9	452	5	US-10-861-049-46	Sequence 46, Appl1	334	59	66.3	241	3	US-09-791-578-62	Sequence 6, Appl1
262	64	71.9	452	6	US-11-021-874-46	Sequence 46, Appl1	335	59	66.3	241	3	US-09-791-540-6	Sequence 6, Appl1
263	63	70.8	113	4	US-10-468-496-1811	Sequence 1811, Ap	336	59	66.3	241	5	US-10-915-069-6	Sequence 6, Appl1
264	63	70.8	17	6	US-11-036-098-10	Sequence 10, Appl1	337	59	66.3	241	5	US-10-909-948-6	Sequence 6, Appl1
265	63	70.8	19	5	US-10-496-869-2	Sequence 2, Appl1	338	59	66.3	242	4	US-10-336-210-9	Sequence 9, Appl1
266	63	70.8	119	5	US-10-496-869-28	Sequence 28, Appl1	339	59	66.3	244	3	US-09-940-191-1	Sequence 1, Appl1
267	63	70.8	123	6	US-11-036-098-14	Sequence 14, Appl1	340	59	66.3	244	4	US-10-336-210-8	Sequence 8, Appl1
268	63	70.8	532	6	US-11-036-098-18	Sequence 18, Appl1	341	59	66.3	246	3	US-09-791-478-2	Sequence 2, Appl1
269	62	69.7	17	3	US-09-861-294-15	Sequence 15, Appl1	342	59	66.3	246	3	US-09-791-540-2	Sequence 2, Appl1
270	62	69.7	17	4	US-10-367-506-15	Sequence 15, Appl1	343	59	66.3	246	5	US-10-915-069-2	Sequence 2, Appl1
271	62	69.7	98	5	US-09-861-294-4	Sequence 24, Appl1	344	59	66.3	246	5	US-10-909-948-2	Sequence 2, Appl1
272	62	69.7	153	4	US-10-895-135-24	Sequence 4, Appl1	345	59	66.3	249	3	US-09-956-086-2	Sequence 2, Appl1
273	62	69.7	153	3	US-10-367-506-4	Sequence 4, Appl1	346	59	66.3	249	3	US-09-956-087-2	Sequence 2, Appl1
274	62	69.7	291	6	US-11-093-103-102	Sequence 102, App	347	59	66.3	257	3	US-09-791-478-4	Sequence 4, Appl1
275	62	69.7	322	6	US-11-093-103-96	Sequence 96, Appl1	348	59	66.3	257	3	US-09-791-540-4	Sequence 4, Appl1
276	62	69.7	729	6	US-11-093-103-94	Sequence 94, Appl1	349	59	66.3	257	3	US-09-983-980-2	Sequence 2, Appl1
277	61	68.5	17	5	US-10-895-135-2	Sequence 2, Appl1	350	59	66.3	257	3	US-09-985-442-2	Sequence 2, Appl1
278	61	68.5	117	4	US-10-255-478-45	Sequence 45, Appl1	351	59	66.3	257	5	US-10-915-069-4	Sequence 4, Appl1
279	61	68.5	132	4	US-10-197-080-2	Sequence 2, Appl1	352	59	66.3	257	5	US-10-909-948-4	Sequence 4, Appl1
280	61	68.5	132	4	US-10-484-031-2	Sequence 2, Appl1	353	59	66.3	260	4	US-10-255-478-6-4	Sequence 64, Appl1
281	60	67.4	17	5	US-10-849-615-29	Sequence 29, Appl1	354	59	66.3	262	4	US-10-336-210-4	Sequence 4, Appl1
282	59	66.3	17	4	US-10-160-232-16	Sequence 16, Appl1	355	59	66.3	269	3	US-09-983-980-4	Sequence 4, Appl1
283	59	66.3	17	5	US-10-927-433-5	Sequence 5, Appl1	356	59	66.3	269	3	US-09-985-442-4	Sequence 4, Appl1
284	59	66.3	115	3	US-09-999-025-1	Sequence 1, Appl1	357	59	66.3	274	4	US-10-255-478-6	Sequence 6, Appl1
285	59	66.3	115	3	US-09-999-025-3	Sequence 3, Appl1	358	59	66.3	284	4	US-10-255-478-70	Sequence 70, Appl1
286	59	66.3	115	3	US-09-999-025-4	Sequence 4, Appl1	359	59	66.3	347	5	US-10-880-028-18	Sequence 18, Appl1
287	59	66.3	115	3	US-09-999-025-5	Sequence 5, Appl1	360	59	66.3	347	5	US-10-880-320-18	Sequence 18, Appl1
288	59	66.3	115	3	US-09-999-025-6	Sequence 6, Appl1	361	59	66.3	360	5	US-10-880-028-22	Sequence 22, Appl1
289	59	66.3	115	3	US-09-999-025-10	Sequence 10, Appl1	362	59	66.3	360	5	US-10-880-320-22	Sequence 22, Appl1
290	59	66.3	115	3	US-09-999-025-11	Sequence 11, Appl1	363	59	66.3	362	5	US-10-880-028-23	Sequence 23, Appl1
291	59	66.3	115	3	US-09-999-040-1	Sequence 1, Appl1	364	59	66.3	362	5	US-10-880-028-26	Sequence 26, Appl1
292	59	66.3	115	3	US-09-999-040-3	Sequence 3, Appl1	365	59	66.3	362	5	US-10-880-320-23	Sequence 23, Appl1
293	59	66.3	115	3	US-09-999-040-4	Sequence 4, Appl1	366	59	66.3	362	5	US-10-880-320-26	Sequence 26, Appl1
294	59	66.3	115	3	US-09-999-040-5	Sequence 5, Appl1	367	59	66.3	444	4	US-10-013-173-49	Sequence 49, Appl1
295	59	66.3	115	3	US-09-999-040-6	Sequence 6, Appl1	368	59	66.3	444	4	US-10-150-762-49	Sequence 49, Appl1
296	59	66.3	115	3	US-09-999-040-10	Sequence 10, Appl1	369	59	66.3	444	4	US-10-244-821-49	Sequence 49, Appl1
297	59	66.3	115	3	US-09-999-040-11	Sequence 11, Appl1	370	58	65.2	17	5	US-10-484-480-9	Sequence 9, Appl1
298	59	66.3	115	3	US-09-998-817-1	Sequence 1, Appl1	371	58	65.2	111	6	US-11-070-697-30	Sequence 30, Appl1
299	59	66.3	115	3	US-09-998-817-3	Sequence 3, Appl1	372	58	65.2	112	6	US-11-070-697-34	Sequence 34, Appl1
300	59	66.3	115	3	US-09-998-817-4	Sequence 4, Appl1	373	58	65.2	112	6	US-11-070-697-38	Sequence 38, Appl1
301	59	66.3	115	3	US-09-998-817-5	Sequence 5, Appl1	374	58	65.2	119	4	US-10-411-037-53	Sequence 53, Appl1
302	59	66.3	115	3	US-09-998-817-6	Sequence 6, Appl1	375	58	65.2	119	4	US-10-411-037-54	Sequence 54, Appl1
303	59	66.3	115	3	US-09-998-817-10	Sequence 10, Appl1	376	58	65.2	119	4	US-10-411-037-55	Sequence 55, Appl1
304	59	66.3	115	3	US-09-998-817-11	Sequence 11, Appl1	377	58	65.2	119	4	US-10-411-026-54	Sequence 54, Appl1
305	59	66.3	115	3	US-09-999-021-1	Sequence 1, Appl1	378	58	65.2	119	4	US-10-410-862-53	Sequence 53, Appl1
306	59	66.3	115	3	US-09-999-021-3	Sequence 3, Appl1	379	58	65.2	119	4	US-10-410-962-54	Sequence 54, Appl1
307	59	66.3	115	3	US-09-999-021-4	Sequence 4, Appl1	380	58	65.2	119	4	US-10-411-049-53	Sequence 53, Appl1
308	59	66.3	115	3	US-09-999-021-5	Sequence 5, Appl1	381	58	65.2	119	4	US-10-411-049-54	Sequence 54, Appl1
309	59	66.3	115	3	US-09-999-021-6	Sequence 6, Appl1	382	58	65.2	119	4	US-10-410-930-53	Sequence 53, Appl1
310	59	66.3	115	3	US-09-999-021-10	Sequence 10, Appl1	383	58	65.2	119	4	US-10-410-930-54	Sequence 54, Appl1
311	59	66.3	115	3	US-09-999-021-11	Sequence 11, Appl1	384	58	65.2	119	4	US-10-410-937-53	Sequence 53, Appl1
312	59	66.3	115	4	US-10-040-997-1	Sequence 1, Appl1	385	58	65.2	119	4	US-10-410-997-54	Sequence 54, Appl1
313	59	66.3	115	4	US-10-040-997-3	Sequence 3, Appl1	386	58	65.2	119	4	US-10-411-012-53	Sequence 53, Appl1
314	59	66.3	115	4	US-10-040-997-4	Sequence 4, Appl1	387	58	65.2	119	4	US-10-411-012-54	Sequence 54, Appl1
315	59	66.3	115	4	US-10-040-997-5	Sequence 5, Appl1	388	58	65.2	119	4	US-10-287-994-53	Sequence 53, Appl1
316	59	66.3	115	4	US-10-040-997-6	Sequence 6, Appl1	389	58	65.2	119	4	US-10-287-994-54	Sequence 54, Appl1
317	59	66.3	115	4	US-10-040-997-10	Sequence 10, Appl1	390	58	65.2	119	4	US-10-410-913-53	Sequence 53, Appl1
318	59	66.3	115	4	US-10-040-997-11	Sequence 11, Appl1	391	58	65.2	119	4	US-10-410-913-54	Sequence 54, Appl1
319	59	66.3	115	4	US-10-255-478-74	Sequence 74, Appl1	392	58	65.2	119	5	US-10-410-980-53	Sequence 53, Appl1

393	58	65.2	119	5	US-10-410-980-54	Sequence 54, Appl	466	56	62.9	274	5	US-10-399-585-118	Sequence 118, App
394	58	65.2	119	5	US-10-410-897-53	Sequence 53, Appl	467	56	62.9	274	5	US-10-645-085A-90	Sequence 90, Appl
395	58	65.2	119	5	US-10-410-897-54	Sequence 54, Appl	468	56	62.9	274	3	US-10-917-410-6	Sequence 6, Appl
396	58	65.2	119	5	US-10-492-261-53	Sequence 53, Appl	469	55	61.8	17	4	US-10-447-257-6	Sequence 6, Appl
397	58	65.2	119	5	US-10-492-261-54	Sequence 54, Appl	470	55	61.8	17	4	US-10-312-316-6	Sequence 4, Appl
398	58	65.2	120	5	US-10-484-280-4	Sequence 4, Appl	471	55	61.8	17	4	US-10-745-102-4	Sequence 6, Appl
399	58	65.2	120	5	US-10-484-280-16	Sequence 16, Appl	472	55	61.8	17	5	US-10-496-628-6	Sequence 6, Appl
400	58	65.2	120	5	US-10-484-280-28	Sequence 28, Appl	473	55	61.8	103	5	US-10-683-547-15	Sequence 15, Appl
401	58	65.2	120	5	US-10-411-037-56	Sequence 56, Appl	474	55	61.8	112	4	US-10-251-085B-252	Sequence 252, App
402	58	65.2	448	4	US-10-411-026-56	Sequence 56, Appl	475	55	61.8	112	4	US-10-251-085B-253	Sequence 253, App
403	58	65.2	448	4	US-10-410-962-56	Sequence 56, Appl	476	55	61.8	112	4	US-10-251-085B-254	Sequence 254, App
404	58	65.2	448	4	US-10-411-049-56	Sequence 56, Appl	477	55	61.8	112	4	US-10-251-085B-255	Sequence 255, App
405	58	65.2	448	4	US-10-410-930-56	Sequence 56, Appl	478	55	61.8	112	4	US-10-737-252-752	Sequence 252, App
406	58	65.2	448	4	US-10-410-997-56	Sequence 56, Appl	479	55	61.8	112	4	US-10-737-252-253	Sequence 253, App
407	58	65.2	448	4	US-10-411-012-56	Sequence 56, Appl	480	55	61.8	112	4	US-10-737-252-254	Sequence 254, App
408	58	65.2	448	4	US-10-287-994-56	Sequence 56, Appl	481	55	61.8	112	4	US-10-737-252-255	Sequence 255, App
409	58	65.2	448	4	US-10-410-913-56	Sequence 56, Appl	482	55	61.8	113	4	US-10-745-102-14	Sequence 14, Appl
410	58	65.2	448	5	US-10-410-980-56	Sequence 56, Appl	483	55	61.8	116	5	US-10-700-532-74	Sequence 74, Appl
411	58	65.2	448	5	US-10-410-897-56	Sequence 56, Appl	484	55	61.8	117	5	US-10-447-257-2	Sequence 2, Appl
412	58	65.2	448	5	US-10-492-261-56	Sequence 56, Appl	485	55	61.8	117	5	US-10-729-441-76	Sequence 76, Appl
413	58	65.2	450	5	US-10-484-280-18	Sequence 18, Appl	486	55	61.8	117	5	US-10-683-547-14	Sequence 14, Appl
414	57	64.0	17	3	US-09-842-776A-29	Sequence 29, Appl	487	55	61.8	117	5	US-10-496-628-2	Sequence 2, Appl
415	57	64.0	17	5	US-10-297-371A-6	Sequence 6, Appl	488	55	61.8	117	5	US-10-895-135-54	Sequence 54, Appl
416	57	64.0	17	5	US-10-849-615-33	Sequence 33, Appl	489	55	61.8	117	5	US-10-897-406-76	Sequence 76, Appl
417	57	64.0	111	4	US-10-297-371A-2	Sequence 2, Appl	490	55	61.8	117	5	US-10-683-547-12	Sequence 12, Appl
418	57	64.0	119	4	US-10-412-703A-9	Sequence 9, Appl	491	55	61.8	122	4	US-10-312-316-43	Sequence 43, Appl
419	57	64.0	119	4	US-10-412-703A-10	Sequence 10, Appl	492	55	61.8	122	4	US-10-312-316-43	Sequence 43, Appl
420	57	64.0	119	4	US-10-412-703A-15	Sequence 15, Appl	493	55	61.8	139	4	US-10-207-655-262	Sequence 262, App
421	57	64.0	119	4	US-10-412-703A-16	Sequence 16, Appl	494	55	61.8	264	4	US-10-207-655-400	Sequence 400, App
422	57	64.0	121	5	US-10-938-992-42	Sequence 42, Appl	495	55	61.8	264	5	US-10-627-556-186	Sequence 186, App
423	57	64.0	123	3	US-09-842-776A-60	Sequence 60, Appl	496	55	61.8	378	5	US-10-743-697-1	Sequence 1, Appl
424	57	64.0	247	4	US-10-620-278-21	Sequence 21, Appl	497	55	61.8	451	4	US-10-679-620-118	Sequence 118, App
425	57	64.0	247	5	US-10-620-049-21	Sequence 21, Appl	498	55	61.8	451	6	US-11-132-143-118	Sequence 118, App
426	56	62.9	13	4	US-10-468-496-1810	Sequence 1810, Ap	499	55	61.8	483	4	US-10-679-620-112	Sequence 112, App
427	56	62.9	17	3	US-09-563-222-57	Sequence 57, Appl	500	55	61.8	483	6	US-11-132-143-122	Sequence 122, App
428	56	62.9	17	5	US-10-783-950-57	Sequence 57, Appl	501	55	61.8	548	4	US-10-207-655-572	Sequence 572, Appl
429	56	62.9	121	5	US-10-842-011-22	Sequence 22, Appl	502	55	61.8	548	5	US-10-627-556-56	Sequence 56, Appl
430	56	62.9	125	3	US-09-929-655-20	Sequence 20, Appl	503	54	60.7	10	5	US-10-700-632-59	Sequence 59, Appl
431	56	62.9	125	3	US-09-929-655-20	Sequence 20, Appl	504	54	60.7	17	4	US-10-032-482-15	Sequence 15, Appl
432	56	62.9	125	3	US-09-929-656-20	Sequence 20, Appl	505	54	60.7	17	4	US-10-307-276B-33	Sequence 33, Appl
433	56	62.9	125	4	US-10-160-506-79	Sequence 79, Appl	506	54	60.7	17	6	US-11-061-956-93	Sequence 93, Appl
434	56	62.9	125	4	US-10-449-379-79	Sequence 79, Appl	507	54	60.7	17	6	US-11-129-359-15	Sequence 15, Appl
435	56	62.9	125	4	US-10-688-015-79	Sequence 79, Appl	508	54	60.7	96	5	US-10-700-632-61	Sequence 61, Appl
436	56	62.9	125	4	US-10-160-505-79	Sequence 79, Appl	509	54	60.7	111	4	US-10-032-482-5	Sequence 5, Appl
437	56	62.9	136	4	US-10-138-505-8	Sequence 8, Appl	510	54	60.7	111	6	US-11-129-359-5	Sequence 5, Appl
438	56	62.9	136	4	US-10-237-864A-86	Sequence 86, Appl	511	54	60.7	112	4	US-10-251-085B-247	Sequence 247, App
439	56	62.9	136	4	US-10-221-131-91	Sequence 91, Appl	512	54	60.7	112	4	US-10-251-085B-248	Sequence 248, App
440	56	62.9	136	4	US-10-399-518-115	Sequence 115, App	513	54	60.7	112	4	US-10-251-085B-249	Sequence 249, App
441	56	62.9	136	5	US-10-399-585-115	Sequence 115, App	514	54	60.7	112	4	US-10-251-085B-250	Sequence 250, App
442	56	62.9	136	5	US-10-645-085A-86	Sequence 86, Appl	515	54	60.7	112	4	US-10-251-085B-251	Sequence 251, App
443	56	62.9	247	4	US-10-620-278-23	Sequence 23, Appl	516	54	60.7	112	4	US-10-737-252-147	Sequence 247, App
444	56	62.9	247	4	US-10-620-278-25	Sequence 25, Appl	517	54	60.7	112	4	US-10-737-252-248	Sequence 248, App
445	56	62.9	247	5	US-10-620-049-23	Sequence 23, Appl	518	54	60.7	112	4	US-10-737-252-249	Sequence 249, App
446	56	62.9	247	5	US-10-620-049-25	Sequence 25, Appl	519	54	60.7	112	4	US-10-737-252-250	Sequence 250, App
447	56	62.9	249	3	US-09-984-186-18	Sequence 18, Appl	520	54	60.7	112	4	US-10-737-252-251	Sequence 251, App
448	56	62.9	249	4	US-10-237-667-18	Sequence 18, Appl	521	54	60.7	113	4	US-10-307-276B-3	Sequence 3, Appl
449	56	62.9	249	4	US-10-237-708-18	Sequence 18, Appl	522	54	60.7	113	4	US-10-307-276B-5	Sequence 5, Appl
450	56	62.9	249	4	US-10-237-708-18	Sequence 18, Appl	523	54	60.7	113	4	US-10-307-276B-7	Sequence 7, Appl
451	56	62.9	249	4	US-10-237-866-18	Sequence 18, Appl	524	54	60.7	113	4	US-10-307-276B-8	Sequence 8, Appl
452	56	62.9	249	4	US-10-237-871-18	Sequence 18, Appl	525	54	60.7	113	4	US-10-307-276B-9	Sequence 9, Appl
453	56	62.9	249	4	US-10-702-624-18	Sequence 18, Appl	526	54	60.7	113	4	US-10-307-276B-10	Sequence 10, Appl
454	56	62.9	249	4	US-10-702-636-18	Sequence 18, Appl	527	54	60.7	113	4	US-10-307-276B-11	Sequence 11, Appl
455	56	62.9	249	6	US-11-146-077-18	Sequence 18, Appl	528	54	60.7	113	6	US-11-061-956-3	Sequence 3, Appl
456	56	62.9	271	4	US-10-138-505-30	Sequence 30, Appl	529	54	60.7	113	6	US-11-061-956-5	Sequence 5, Appl
457	56	62.9	271	4	US-10-257-864A-91	Sequence 91, Appl	530	54	60.7	113	6	US-11-061-956-7	Sequence 7, Appl
458	56	62.9	271	4	US-10-221-131-91	Sequence 91, Appl	531	54	60.7	113	6	US-11-061-956-8	Sequence 8, Appl
459	56	62.9	271	4	US-10-221-131-96	Sequence 96, Appl	532	54	60.7	113	6	US-11-061-956-9	Sequence 9, Appl
460	56	62.9	271	4	US-10-399-518-120	Sequence 120, App	533	54	60.7	113	6	US-11-061-956-10	Sequence 10, Appl
461	56	62.9	271	5	US-10-399-585-119	Sequence 119, App	534	54	60.7	113	6	US-11-061-956-11	Sequence 11, Appl
462	56	62.9	271	5	US-10-645-085A-91	Sequence 91, Appl	535	54	60.7	118	5	US-10-700-632-76	Sequence 76, Appl
463	56	62.9	274	4	US-10-138-505-26	Sequence 26, Appl	536	54	60.7	119	5	US-10-895-135-56	Sequence 56, Appl
464	56	62.9	274	4	US-10-257-864A-90	Sequence 90, Appl	537	54	60.7	120	4	US-10-310-674A-38	Sequence 38, Appl
465	56	62.9	274	4	US-10-399-518-119	Sequence 119, App	538	54	60.7	120	4	US-10-389-679-14	Sequence 14, Appl

539	54	60.7	120	4	US-10-389-679-19	Sequence 19, App1	612	53	59.6	139	3	US-09-509-098-4	Sequence 4, App11
540	54	60.7	138	2	US-08-779-784-31	Sequence 31, App1	613	53	59.6	139	3	US-09-509-098-16	Sequence 16, App1
541	54	60.7	138	4	US-10-010-729-67	Sequence 67, App1	614	53	59.6	139	3	US-09-509-098-18	Sequence 18, App1
542	54	60.7	139	4	US-10-006-773-13	Sequence 13, App1	615	53	59.6	139	3	US-09-509-098-20	Sequence 20, App1
543	53	59.6	15	6	US-11-070-697-5	Sequence 5, App11	616	53	59.6	139	3	US-09-509-098-22	Sequence 22, App1
544	53	59.6	17	3	US-09-269-921-7	Sequence 7, App11	617	53	59.6	139	3	US-09-509-098-24	Sequence 24, App1
545	53	59.6	17	4	US-10-160-232-10	Sequence 10, App11	618	53	59.6	139	3	US-09-509-098-26	Sequence 26, App1
546	53	59.6	17	4	US-10-218-253-7	Sequence 7, App11	619	53	59.6	139	3	US-09-509-098-28	Sequence 28, App1
547	53	59.6	17	5	US-10-812-366-6	Sequence 6, App11	620	53	59.6	139	3	US-09-509-098-30	Sequence 30, App1
548	53	59.6	17	5	US-10-813-977-19	Sequence 19, App11	621	53	59.6	139	3	US-09-509-098-32	Sequence 32, App1
549	53	59.6	49	3	US-09-509-098-156	Sequence 156, App	622	53	59.6	139	3	US-09-509-098-34	Sequence 34, App1
550	53	59.6	49	3	US-09-509-098-159	Sequence 159, App	623	53	59.6	139	3	US-09-509-098-36	Sequence 36, App1
551	53	59.6	49	3	US-09-509-098-160	Sequence 160, App	624	53	59.6	139	3	US-09-509-098-38	Sequence 38, App1
552	53	59.6	49	3	US-09-509-098-161	Sequence 161, App	625	53	59.6	139	3	US-09-509-098-40	Sequence 40, App1
553	53	59.6	49	3	US-09-509-098-162	Sequence 162, App	626	53	59.6	139	3	US-09-509-098-42	Sequence 42, App1
554	53	59.6	49	3	US-09-509-098-163	Sequence 163, App	627	53	59.6	139	3	US-09-509-098-44	Sequence 44, App1
555	53	59.6	49	3	US-09-509-098-164	Sequence 164, App	628	53	59.6	139	3	US-09-509-098-46	Sequence 46, App1
556	53	59.6	49	3	US-09-509-098-165	Sequence 165, App	629	53	59.6	139	3	US-09-509-098-48	Sequence 48, App1
557	53	59.6	49	3	US-09-509-098-166	Sequence 166, App	630	53	59.6	139	3	US-09-509-098-50	Sequence 50, App1
558	53	59.6	49	3	US-09-509-098-167	Sequence 167, App	631	53	59.6	139	3	US-09-509-098-98	Sequence 98, App1
559	53	59.6	49	3	US-09-509-098-168	Sequence 168, App	632	53	59.6	139	3	US-09-509-098-100	Sequence 100, App
560	53	59.6	49	3	US-09-509-098-169	Sequence 169, App	633	53	59.6	139	3	US-09-509-098-127	Sequence 127, App
561	53	59.6	49	3	US-09-509-098-170	Sequence 170, App	634	53	59.6	139	4	US-10-315-123-7	Sequence 7, App11
562	53	59.6	49	3	US-09-509-098-171	Sequence 171, App	635	53	59.6	139	4	US-10-315-125-8	Sequence 8, App11
563	53	59.6	49	3	US-09-509-098-172	Sequence 172, App	636	53	59.6	139	4	US-10-218-253-105	Sequence 105, App
564	53	59.6	49	3	US-09-509-098-173	Sequence 173, App	637	53	59.6	139	4	US-10-218-253-108	Sequence 108, App
565	53	59.6	49	3	US-09-509-098-174	Sequence 174, App	638	53	59.6	139	4	US-10-218-253-109	Sequence 109, App
566	53	59.6	49	3	US-09-509-098-175	Sequence 175, App	639	53	59.6	139	4	US-10-218-253-110	Sequence 110, App
567	53	59.6	49	3	US-09-509-098-176	Sequence 176, App	640	53	59.6	139	4	US-10-218-253-111	Sequence 111, App
568	53	59.6	96	5	US-10-764-730-2	Sequence 2, App11	641	53	59.6	139	4	US-10-218-253-112	Sequence 112, App
569	53	59.6	113	4	US-10-251-085B-260	Sequence 260, App	642	53	59.6	139	4	US-10-218-253-113	Sequence 113, App
570	53	59.6	113	4	US-10-251-085B-261	Sequence 261, App	643	53	59.6	139	4	US-10-218-253-114	Sequence 114, App
571	53	59.6	113	4	US-10-251-085B-262	Sequence 262, App	644	53	59.6	139	4	US-10-218-253-115	Sequence 115, App
572	53	59.6	113	4	US-10-251-085B-264	Sequence 264, App	645	53	59.6	139	4	US-10-218-253-116	Sequence 116, App
573	53	59.6	113	4	US-10-737-252-260	Sequence 260, App	646	53	59.6	139	4	US-10-218-253-117	Sequence 117, App
574	53	59.6	113	4	US-10-737-252-261	Sequence 261, App	647	53	59.6	139	4	US-10-218-253-118	Sequence 118, App
575	53	59.6	113	4	US-10-737-252-262	Sequence 262, App	648	53	59.6	139	4	US-10-218-253-119	Sequence 119, App
576	53	59.6	113	4	US-10-737-252-264	Sequence 264, App	649	53	59.6	139	4	US-10-218-253-120	Sequence 120, App
577	53	59.6	118	4	US-10-251-085B-263	Sequence 263, App	650	53	59.6	139	4	US-10-218-253-121	Sequence 121, App
578	53	59.6	118	4	US-10-737-252-263	Sequence 263, App	651	53	59.6	139	4	US-10-218-253-122	Sequence 122, App
579	53	59.6	120	3	US-09-509-098-198	Sequence 198, App	652	53	59.6	139	4	US-10-218-253-123	Sequence 123, App
580	53	59.6	120	3	US-09-509-098-201	Sequence 201, App	653	53	59.6	139	4	US-10-218-253-124	Sequence 124, App
581	53	59.6	120	3	US-09-509-098-202	Sequence 202, App	654	53	59.6	139	4	US-10-218-253-125	Sequence 125, App
582	53	59.6	120	5	US-10-812-366-3	Sequence 3, App11	655	53	59.6	139	4	US-10-218-253-126	Sequence 126, App
583	53	59.6	122	3	US-09-215-163-19	Sequence 19, App1	656	53	59.6	139	4	US-10-218-253-127	Sequence 127, App
584	53	59.6	138	4	US-10-160-232-86	Sequence 86, App1	657	53	59.6	139	4	US-10-218-253-128	Sequence 128, App
585	53	59.6	138	4	US-10-160-232-90	Sequence 90, App1	658	53	59.6	139	4	US-10-428-085-7	Sequence 7, App11
586	53	59.6	139	3	US-09-760-723-7	Sequence 7, App11	659	53	59.6	139	4	US-10-428-085-8	Sequence 8, App11
587	53	59.6	139	3	US-09-760-723-8	Sequence 8, App11	660	53	59.6	139	4	US-10-474-714-6	Sequence 6, App11
588	53	59.6	139	3	US-09-355-925-7	Sequence 7, App11	661	53	59.6	139	4	US-10-360-053-6	Sequence 6, App11
589	53	59.6	139	3	US-09-355-925-8	Sequence 8, App11	662	53	59.6	139	4	US-10-360-053-8	Sequence 8, App11
590	53	59.6	139	3	US-09-269-921-110	Sequence 110, App	663	53	59.6	139	4	US-10-360-053-10	Sequence 10, App1
591	53	59.6	139	3	US-09-269-921-105	Sequence 105, App	664	53	59.6	139	4	US-10-813-977-17	Sequence 17, App1
592	53	59.6	139	3	US-09-269-921-108	Sequence 108, App	665	53	59.6	139	4	US-10-813-977-17	Sequence 17, App1
593	53	59.6	139	3	US-09-269-921-109	Sequence 109, App	666	53	59.6	139	4	US-10-813-977-17	Sequence 17, App1
594	53	59.6	139	3	US-09-269-921-111	Sequence 111, App	667	53	59.6	139	4	US-10-813-977-17	Sequence 17, App1
595	53	59.6	139	3	US-09-269-921-112	Sequence 112, App	668	53	59.6	139	4	US-10-813-977-17	Sequence 17, App1
596	53	59.6	139	3	US-09-269-921-113	Sequence 113, App	669	53	59.6	139	4	US-10-813-977-17	Sequence 17, App1
597	53	59.6	139	3	US-09-269-921-114	Sequence 114, App	670	53	59.6	139	4	US-10-813-977-17	Sequence 17, App1
598	53	59.6	139	3	US-09-269-921-115	Sequence 115, App	671	53	59.6	139	4	US-10-813-977-17	Sequence 17, App1
599	53	59.6	139	3	US-09-269-921-116	Sequence 116, App	672	53	59.6	139	4	US-10-813-977-17	Sequence 17, App1
600	53	59.6	139	3	US-09-269-921-117	Sequence 117, App	673	53	59.6	139	4	US-10-813-977-17	Sequence 17, App1
601	53	59.6	139	3	US-09-269-921-118	Sequence 118, App	674	53	59.6	139	4	US-10-813-977-17	Sequence 17, App1
602	53	59.6	139	3	US-09-269-921-119	Sequence 119, App	675	53	59.6	139	4	US-10-813-977-17	Sequence 17, App1
603	53	59.6	139	3	US-09-269-921-120	Sequence 120, App	676	53	59.6	139	4	US-10-813-977-17	Sequence 17, App1
604	53	59.6	139	3	US-09-269-921-121	Sequence 121, App	677	53	59.6	139	4	US-10-813-977-17	Sequence 17, App1
605	53	59.6	139	3	US-09-269-921-122	Sequence 122, App	678	53	59.6	139	4	US-10-813-977-17	Sequence 17, App1
606	53	59.6	139	3	US-09-269-921-123	Sequence 123, App	679	53	59.6	139	4	US-10-813-977-17	Sequence 17, App1
607	53	59.6	139	3	US-09-269-921-124	Sequence 124, App	680	53	59.6	139	4	US-10-813-977-17	Sequence 17, App1
608	53	59.6	139	3	US-09-269-921-125	Sequence 125, App	681	53	59.6	139	4	US-10-813-977-17	Sequence 17, App1
609	53	59.6	139	3	US-09-269-921-126	Sequence 126, App	682	53	59.6	139	4	US-10-813-977-17	Sequence 17, App1
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611	53	59.6	139	3	US-09-269-921-128	Sequence 128, App	684	53	59.6	139	5	US-10-813-977-17	Sequence 17, App1

685	52	58.4	119	5	US-10-981-738-42	Sequence 42, Appl	758	51	57.3	245	4	US-10-221-131-100	Sequence 100, App
686	52	58.4	119	5	US-10-981-738-44	Sequence 44, Appl	759	51	57.3	245	4	US-10-399-518-124	Sequence 124, App
687	52	58.4	119	5	US-10-981-738-46	Sequence 46, Appl	760	51	57.3	245	5	US-10-399-585-123	Sequence 123, App
688	52	58.4	119	5	US-10-981-738-52	Sequence 52, Appl	761	51	57.3	245	5	US-10-645-085A-95	Sequence 95, Appl
689	52	58.4	119	5	US-10-981-738-56	Sequence 56, Appl	762	51	57.3	246	4	US-10-257-864A-97	Sequence 97, Appl
690	52	58.4	119	5	US-10-981-738-58	Sequence 58, Appl	763	51	57.3	246	4	US-10-353-708-41	Sequence 41, Appl
691	52	58.4	119	5	US-10-981-738-60	Sequence 60, Appl	764	51	57.3	246	4	US-10-221-131-102	Sequence 102, App
692	52	58.4	119	5	US-10-981-738-62	Sequence 62, Appl	765	51	57.3	246	4	US-10-221-131-103	Sequence 103, App
693	52	58.4	119	5	US-10-981-738-64	Sequence 64, Appl	766	51	57.3	246	4	US-10-399-518-126	Sequence 126, App
694	52	58.4	119	5	US-10-981-738-66	Sequence 66, Appl	767	51	57.3	246	4	US-10-399-518-127	Sequence 125, App
695	52	58.4	119	5	US-10-981-738-68	Sequence 68, Appl	768	51	57.3	246	5	US-10-399-585-125	Sequence 126, App
696	52	58.4	119	5	US-10-981-738-70	Sequence 70, Appl	769	51	57.3	246	5	US-10-645-085A-96	Sequence 96, Appl
697	52	58.4	119	5	US-10-981-738-72	Sequence 72, Appl	770	51	57.3	246	5	US-10-645-085A-98	Sequence 98, Appl
698	52	58.4	121	4	US-10-308-817-187	Sequence 187, App	771	51	57.3	246	5	US-10-353-708-54	Sequence 54, Appl
699	52	58.4	121	4	US-10-453-698-10	Sequence 187, App	772	51	57.3	246	5	US-10-353-708-55	Sequence 55, Appl
700	52	58.4	121	4	US-10-307-276B-12	Sequence 12, Appl	773	51	57.3	246	5	US-10-399-585-126	Sequence 125, App
701	52	58.4	121	6	US-11-061-956-12	Sequence 12, Appl	774	51	57.3	246	5	US-10-399-585-127	Sequence 126, App
702	52	58.4	123	4	US-10-466-242-49	Sequence 49, Appl	775	51	57.3	246	5	US-10-645-085A-97	Sequence 97, Appl
703	52	58.4	124	5	US-10-903-858-4	Sequence 4, Appli	776	51	57.3	246	5	US-10-353-708-56	Sequence 56, Appl
704	52	58.4	124	5	US-10-903-858-9	Sequence 9, Appli	777	51	57.3	246	5	US-10-353-708-57	Sequence 57, Appl
705	52	58.4	124	5	US-10-903-858-10	Sequence 10, Appl	778	51	57.3	246	5	US-10-353-708-58	Sequence 58, Appl
706	52	58.4	124	5	US-10-903-858-15	Sequence 15, Appl	779	51	57.3	246	5	US-10-353-708-59	Sequence 59, Appl
707	52	58.4	129	5	US-10-627-556-390	Sequence 390, App	780	51	57.3	246	4	US-10-257-864A-92	Sequence 92, Appl
708	52	58.4	129	5	US-10-627-556-394	Sequence 394, App	781	51	57.3	244	5	US-10-399-518-121	Sequence 121, App
709	52	58.4	164	4	US-10-471-475A-23	Sequence 23, Appl	782	51	57.3	244	5	US-10-399-585-120	Sequence 120, App
710	52	58.4	164	4	US-10-471-475A-24	Sequence 24, Appl	783	51	57.3	244	5	US-10-645-085A-92	Sequence 92, Appl
711	52	58.4	271	4	US-10-207-635-12	Sequence 12, Appl	784	51	57.3	244	4	US-10-171-452A-42	Sequence 42, Appl
712	52	58.4	271	4	US-10-053-530-12	Sequence 12, Appl	785	51	57.3	448	4	US-10-171-452A-48	Sequence 48, Appl
713	52	58.4	271	6	US-11-089-511-12	Sequence 12, Appl	786	51	57.3	448	4	US-10-171-452A-54	Sequence 54, Appl
714	52	58.4	271	6	US-11-089-190-12	Sequence 12, Appl	787	51	57.3	448	4	US-10-171-452A-60	Sequence 60, Appl
715	52	58.4	271	6	US-11-088-570-12	Sequence 12, Appl	788	51	57.3	448	4	US-10-353-708-48	Sequence 48, Appl
716	52	58.4	271	6	US-11-088-737-12	Sequence 12, Appl	789	51	57.3	448	4	US-10-353-708-48	Sequence 48, Appl
717	52	58.4	271	6	US-11-088-569-12	Sequence 12, Appl	790	51	57.3	448	4	US-10-353-708-54	Sequence 54, Appl
718	52	58.4	271	6	US-11-088-693-12	Sequence 12, Appl	791	51	57.3	448	4	US-10-353-708-60	Sequence 60, Appl
719	52	58.4	271	6	US-11-089-367-12	Sequence 12, Appl	792	51	57.3	448	4	US-10-731-984-8	Sequence 8, Appli
720	52	58.4	271	6	US-11-089-368-12	Sequence 12, Appl	793	51	57.3	448	4	US-10-731-984-16	Sequence 16, Appl
721	52	58.4	273	5	US-10-627-556-392	Sequence 392, App	794	51	57.3	448	4	US-10-731-984-24	Sequence 24, Appl
722	52	58.4	273	5	US-10-627-556-396	Sequence 396, App	795	51	57.3	448	4	US-10-731-984-32	Sequence 32, Appl
723	52	58.4	401	4	US-10-002-631C-114	Sequence 114, App	796	51	57.3	467	4	US-10-171-452A-41	Sequence 41, Appl
724	52	58.4	468	5	US-10-964-195-13	Sequence 13, Appl	797	51	57.3	467	4	US-10-171-452A-47	Sequence 47, Appl
725	52	58.4	498	5	US-10-964-195-13	Sequence 13, Appl	798	51	57.3	467	4	US-10-171-452A-53	Sequence 53, Appl
726	52	58.4	505	5	US-10-627-556-400	Sequence 400, App	799	51	57.3	467	4	US-10-171-452A-59	Sequence 59, Appl
727	52	58.4	505	5	US-10-627-556-402	Sequence 402, App	800	51	57.3	467	4	US-10-353-708-41	Sequence 41, Appl
728	52	58.4	506	5	US-10-627-556-402	Sequence 402, App	801	51	57.3	467	4	US-10-353-708-47	Sequence 47, Appl
729	52	58.4	521	5	US-10-964-195-11	Sequence 11, Appl	802	51	57.3	467	4	US-10-353-708-53	Sequence 53, Appl
730	51	57.3	13	4	US-10-468-496-1809	Sequence 1809, Ap	803	51	57.3	467	4	US-10-353-708-59	Sequence 59, Appl
731	51	57.3	17	5	US-10-849-615-37	Sequence 37, Appl	804	51	57.3	467	4	US-10-731-984-7	Sequence 7, Appli
732	51	57.3	17	5	US-10-891-658-93	Sequence 93, Appl	805	51	57.3	467	4	US-10-731-984-15	Sequence 15, Appl
733	51	57.3	31	3	US-09-956-206A-34	Sequence 34, Appl	806	51	57.3	467	4	US-10-731-984-23	Sequence 23, Appl
734	51	57.3	31	5	US-10-965-616-34	Sequence 34, Appl	807	51	57.3	467	4	US-10-731-984-31	Sequence 31, Appl
735	51	57.3	98	3	US-09-905-243-36	Sequence 47, Appl	808	51	57.3	533	4	US-10-257-864A-96	Sequence 96, Appl
736	51	57.3	98	3	US-10-041-860-368	Sequence 368, App	809	51	57.3	533	4	US-10-399-518-125	Sequence 125, App
737	51	57.3	98	6	US-11-099-331-47	Sequence 47, Appl	810	51	57.3	533	4	US-10-399-585-124	Sequence 124, App
738	51	57.3	115	5	US-09-940-727B-16	Sequence 16, Appl	811	51	57.3	533	5	US-10-645-085A-95	Sequence 95, Appl
739	51	57.3	119	5	US-10-981-738-30	Sequence 30, Appl	812	51	57.3	533	5	US-10-645-085A-96	Sequence 96, Appl
740	51	57.3	119	5	US-10-981-738-48	Sequence 48, Appl	813	51	57.3	533	5	US-09-940-727B-65	Sequence 106, App
741	51	57.3	119	5	US-10-981-738-54	Sequence 54, Appl	814	51	57.3	533	5	US-10-195-782-106	Sequence 106, App
742	51	57.3	125	5	US-10-895-135-58	Sequence 58, Appl	815	51	57.3	533	5	US-10-384-060-40	Sequence 40, Appl
743	51	57.3	125	5	US-10-891-658-79	Sequence 79, Appl	816	51	57.3	533	5	US-10-374-992-6	Sequence 6, Appli
744	51	57.3	126	4	US-10-041-860-46	Sequence 46, Appl	817	51	57.3	533	5	US-10-374-992-6	Sequence 6, Appli
745	51	57.3	126	4	US-10-041-860-217	Sequence 217, App	818	51	57.3	533	5	US-10-128-500-169	Sequence 9, Appli
746	51	57.3	126	4	US-10-041-860-366	Sequence 366, App	819	51	57.3	533	5	US-10-846-981-9	Sequence 16, Appl
747	51	57.3	126	4	US-10-665-383-70	Sequence 70, Appl	820	51	57.3	533	5	US-10-473-977-16	Sequence 16, Appl
748	51	57.3	127	4	US-10-041-860-252	Sequence 252, App	821	51	57.3	533	5	US-10-644-987-35	Sequence 35, Appl
749	51	57.3	136	4	US-10-138-505-12	Sequence 12, Appl	822	51	57.3	533	5	US-10-919-993-9	Sequence 9, Appli
750	51	57.3	136	4	US-10-257-864A-88	Sequence 88, Appl	823	51	57.3	533	5	US-10-638-285-95	Sequence 95, Appl
751	51	57.3	136	4	US-10-221-131-93	Sequence 93, Appl	824	51	57.3	533	5	US-10-726-332-55	Sequence 55, Appl
752	51	57.3	136	4	US-10-399-518-117	Sequence 117, App	825	51	57.3	533	5	US-10-726-332-73	Sequence 73, Appl
753	51	57.3	136	4	US-10-399-585-117	Sequence 117, App	826	51	57.3	533	5	US-10-726-332-88	Sequence 88, Appl
754	51	57.3	136	4	US-10-645-085A-88	Sequence 88, Appl	827	51	57.3	533	5	US-10-726-332-91	Sequence 91, Appl
755	51	57.3	144	5	US-10-516-429-10	Sequence 10, Appl	828	51	57.3	533	5	US-10-982-725-6	Sequence 6, Appli
756	51	57.3	245	4	US-10-138-505-40	Sequence 40, Appl	829	51	57.3	533	5	US-10-982-725-6	Sequence 6, Appli
757	51	57.3	245	4	US-10-257-864A-95	Sequence 95, Appl	830	51	57.3	533	5	US-10-982-725-6	Sequence 6, Appli

831	50	56.2	98	4	US-10-194-975-45	Sequence 45, Appl	904	50	56.2	118	5	US-10-726-322-145	Sequence 145, App
832	50	56.2	98	4	US-10-125-687-16	Sequence 16, Appl	905	50	56.2	119	4	US-10-372-441-9	Sequence 9, Appl
833	50	56.2	98	4	US-10-041-860-6	Sequence 6, Appl	906	50	56.2	119	4	US-10-371-797-9	Sequence 9, Appl
834	50	56.2	98	4	US-10-041-860-301	Sequence 301, App	907	50	56.2	119	5	US-10-473-677-6	Sequence 67, Appl
835	50	56.2	98	4	US-10-041-860-302	Sequence 302, App	908	50	56.2	120	4	US-10-125-607-6	Sequence 6, Appl
836	50	56.2	98	4	US-10-041-860-312	Sequence 312, App	909	50	56.2	120	5	US-10-638-245-52	Sequence 62, Appl
837	50	56.2	98	4	US-10-041-860-314	Sequence 314, App	910	50	56.2	120	5	US-10-638-245-78	Sequence 78, Appl
838	50	56.2	98	4	US-10-041-860-318	Sequence 318, App	911	50	56.2	120	5	US-10-996-191-6	Sequence 6, Appl
839	50	56.2	98	4	US-10-041-860-330	Sequence 320, App	912	50	56.2	121	4	US-10-078-958-6	Sequence 6, Appl
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842	50	56.2	98	4	US-10-041-860-367	Sequence 367, App	915	50	56.2	125	3	US-09-144-886-51	Sequence 51, Appl
843	50	56.2	98	4	US-10-308-817-88	Sequence 88, Appl	916	50	56.2	125	3	US-09-144-886-52	Sequence 52, Appl
844	50	56.2	98	4	US-10-033-037B-106	Sequence 106, App	917	50	56.2	125	4	US-10-632-706-48	Sequence 48, Appl
845	50	56.2	98	4	US-10-033-037B-107	Sequence 107, App	918	50	56.2	125	4	US-10-632-706-49	Sequence 49, Appl
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847	50	56.2	98	4	US-10-029-988B-106	Sequence 106, App	920	50	56.2	126	4	US-10-041-860-27	Sequence 27, Appl
848	50	56.2	98	4	US-10-029-988B-107	Sequence 106, App	921	50	56.2	126	4	US-10-041-860-35	Sequence 35, Appl
849	50	56.2	98	4	US-10-029-988B-108	Sequence 108, App	922	50	56.2	126	4	US-10-041-860-214	Sequence 214, App
850	50	56.2	98	4	US-10-033-423A-106	Sequence 106, App	923	50	56.2	126	4	US-10-041-860-216	Sequence 216, App
851	50	56.2	98	4	US-10-033-423A-107	Sequence 107, App	924	50	56.2	126	4	US-10-041-860-248	Sequence 248, App
852	50	56.2	98	4	US-10-033-423A-108	Sequence 108, App	925	50	56.2	126	4	US-10-041-860-249	Sequence 249, App
853	50	56.2	98	4	US-10-453-658-88	Sequence 88, Appl	926	50	56.2	126	4	US-10-041-860-251	Sequence 251, App
854	50	56.2	98	4	US-10-029-926B-106	Sequence 106, App	927	50	56.2	126	4	US-10-041-860-300	Sequence 300, App
855	50	56.2	98	4	US-10-029-926B-107	Sequence 107, App	928	50	56.2	126	4	US-10-041-860-313	Sequence 313, App
856	50	56.2	98	4	US-10-029-926B-108	Sequence 108, App	929	50	56.2	126	4	US-10-041-860-337	Sequence 337, App
857	50	56.2	98	4	US-10-379-392-53	Sequence 53, Appl	930	50	56.2	126	4	US-10-665-383-26	Sequence 26, Appl
858	50	56.2	98	5	US-10-769-144-30	Sequence 30, Appl	931	50	56.2	126	4	US-10-665-383-34	Sequence 34, Appl
859	50	56.2	98	5	US-10-996-191-16	Sequence 16, Appl	932	50	56.2	126	4	US-10-665-383-50	Sequence 50, Appl
860	50	56.2	98	5	US-10-903-191-30	Sequence 30, Appl	933	50	56.2	127	4	US-10-320-231A-38	Sequence 38, Appl
861	50	56.2	98	6	US-11-009-721-49	Sequence 49, Appl	934	50	56.2	127	5	US-10-867-506-38	Sequence 38, Appl
862	50	56.2	109	4	US-10-800-197-144	Sequence 144, App	935	50	56.2	127	5	US-10-505-313-337	Sequence 337, App
863	50	56.2	109	4	US-10-800-197-145	Sequence 145, App	936	50	56.2	129	4	US-10-041-860-29	Sequence 29, Appl
864	50	56.2	109	4	US-10-800-197-146	Sequence 146, App	937	50	56.2	129	4	US-10-041-860-315	Sequence 315, App
865	50	56.2	109	5	US-10-727-155-283	Sequence 283, App	938	50	56.2	129	4	US-10-041-860-250	Sequence 250, App
866	50	56.2	109	5	US-10-727-155-291	Sequence 291, App	939	50	56.2	129	4	US-10-041-860-319	Sequence 319, App
867	50	56.2	110	3	US-09-940-727B-86	Sequence 86, Appl	940	50	56.2	129	4	US-10-665-383-88	Sequence 88, Appl
868	50	56.2	110	5	US-10-726-332-217	Sequence 217, App	941	50	56.2	130	4	US-10-226-615-2	Sequence 2, Appl
869	50	56.2	110	5	US-10-726-332-218	Sequence 218, App	942	50	56.2	130	4	US-10-374-932-2	Sequence 2, Appl
870	50	56.2	110	5	US-10-726-332-219	Sequence 219, App	943	50	56.2	130	4	US-10-379-741-2	Sequence 2, Appl
871	50	56.2	111	4	US-10-803-622-171	Sequence 171, App	944	50	56.2	130	5	US-10-982-725-2	Sequence 2, Appl
872	50	56.2	111	4	US-10-803-653-171	Sequence 171, App	945	50	56.2	138	4	US-10-395-994-27	Sequence 27, Appl
873	50	56.2	114	5	US-10-846-981-7	Sequence 7, Appl	946	50	56.2	138	4	US-10-695-667-27	Sequence 27, Appl
874	50	56.2	114	5	US-10-919-923-7	Sequence 7, Appl	947	50	56.2	138	5	US-10-976-352-27	Sequence 27, Appl
875	50	56.2	114	5	US-10-787-219A-47	Sequence 47, Appl	948	50	56.2	144	4	US-10-195-752-112	Sequence 112, App
876	50	56.2	115	5	US-10-727-155-100	Sequence 100, App	949	50	56.2	222	4	US-10-128-520-169	Sequence 169, App
877	50	56.2	117	3	US-09-144-886-71	Sequence 71, Appl	950	50	56.2	224	4	US-10-128-520-164	Sequence 164, App
878	50	56.2	117	4	US-10-633-706-68	Sequence 68, Appl	951	50	56.2	224	4	US-10-128-520-165	Sequence 165, App
879	50	56.2	117	5	US-10-684-957-6	Sequence 6, Appl	952	50	56.2	224	4	US-10-128-520-167	Sequence 167, App
880	50	56.2	117	5	US-10-684-957-10	Sequence 10, Appl	953	50	56.2	224	4	US-10-128-520-170	Sequence 170, App
881	50	56.2	117	5	US-10-684-957-14	Sequence 14, Appl	954	50	56.2	224	4	US-10-128-520-176	Sequence 176, App
882	50	56.2	117	5	US-10-684-957-30	Sequence 30, Appl	955	50	56.2	224	4	US-10-128-520-180	Sequence 180, App
883	50	56.2	117	5	US-10-726-332-9	Sequence 9, Appl	956	50	56.2	224	4	US-10-128-520-181	Sequence 181, App
884	50	56.2	117	5	US-10-726-332-11	Sequence 11, Appl	957	50	56.2	224	4	US-10-128-520-182	Sequence 182, App
885	50	56.2	117	5	US-10-726-332-138	Sequence 138, App	958	50	56.2	225	4	US-10-128-520-157	Sequence 157, App
886	50	56.2	117	5	US-10-726-332-144	Sequence 144, App	959	50	56.2	225	4	US-10-128-520-158	Sequence 158, App
887	50	56.2	118	5	US-10-726-332-3	Sequence 3, Appl	960	50	56.2	225	4	US-10-128-520-162	Sequence 162, App
888	50	56.2	118	5	US-10-726-332-5	Sequence 5, Appl	961	50	56.2	225	4	US-10-128-520-166	Sequence 166, App
889	50	56.2	118	5	US-10-726-332-7	Sequence 7, Appl	962	50	56.2	225	4	US-10-128-520-173	Sequence 173, App
890	50	56.2	118	5	US-10-726-332-13	Sequence 13, Appl	963	50	56.2	226	4	US-10-128-520-178	Sequence 178, App
891	50	56.2	118	5	US-10-726-332-15	Sequence 15, Appl	964	50	56.2	226	4	US-10-128-520-159	Sequence 159, App
892	50	56.2	118	5	US-10-726-332-17	Sequence 17, Appl	965	50	56.2	226	4	US-10-128-520-179	Sequence 179, App
893	50	56.2	118	5	US-10-726-332-19	Sequence 19, Appl	966	50	56.2	243	4	US-10-097-958-2	Sequence 2, Appl
894	50	56.2	118	5	US-10-726-332-27	Sequence 27, Appl	967	50	56.2	243	4	US-10-097-958-3	Sequence 3, Appl
895	50	56.2	118	5	US-10-726-332-29	Sequence 29, Appl	968	50	56.2	243	5	US-10-505-658-2	Sequence 2, Appl
896	50	56.2	118	5	US-10-726-332-30	Sequence 30, Appl	969	50	56.2	243	5	US-10-505-658-3	Sequence 3, Appl
897	50	56.2	118	5	US-10-726-332-31	Sequence 31, Appl	970	50	56.2	252	3	US-09-880-748-1537	Sequence 1537, App
898	50	56.2	118	5	US-10-726-332-134	Sequence 134, App	971	50	56.2	252	4	US-10-293-418-1537	Sequence 1537, App
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900	50	56.2	118	5	US-10-726-332-139	Sequence 139, App	973	50	56.2	264	5	US-10-930-548-46	Sequence 46, Appl
901	50	56.2	118	5	US-10-726-332-140	Sequence 140, App	974	50	56.2	447	5	US-10-684-957-17	Sequence 17, Appl
902	50	56.2	118	5	US-10-726-332-141	Sequence 141, App	975	50	56.2	447	5	US-10-684-957-19	Sequence 19, Appl
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577 50 56.2 447 5 US-10-684-957-32 Sequence 32, Appl
578 50 56.2 474 4 US-10-291-265-284 Sequence 284, App
579 49 55.1 17 4 US-10-146-305-13 Sequence 13, Appl
580 49 55.1 17 5 US-10-769-144-14 Sequence 14, Appl
581 49 55.1 17 5 US-10-903-191-14 Sequence 14, Appl
582 49 55.1 110 4 US-10-251-085B-242 Sequence 242, App
583 49 55.1 110 4 US-10-251-085B-243 Sequence 243, App
584 49 55.1 110 4 US-10-251-085B-244 Sequence 244, App
585 49 55.1 110 4 US-10-251-085B-246 Sequence 246, App
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588 49 55.1 110 4 US-10-737-252-244 Sequence 246, App
589 49 55.1 110 4 US-10-737-252-246 Sequence 246, App
590 49 55.1 112 4 US-10-471-475A-10 Sequence 10, Appl
591 49 55.1 113 4 US-10-251-085B-238 Sequence 238, App
592 49 55.1 113 4 US-10-737-252-238 Sequence 238, App
593 49 55.1 116 3 US-09-851-614-4 Sequence 4, Appl1
594 49 55.1 116 4 US-10-035-637-4 Sequence 4, Appl1
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596 49 55.1 116 5 US-10-901-842-1 Sequence 1, Appl1
597 49 55.1 116 5 US-10-903-191-4 Sequence 4, Appl1
598 49 55.1 117 3 US-09-726-258-48 Sequence 48, Appl
599 49 55.1 117 3 US-09-726-258-49 Sequence 49, Appl
1000 49 55.1 117 6 US-11-009-443-84 Sequence 84, Appl
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ALIGNMENTS

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RESULT 1
US-10-700-632-2
; Sequence 2, Application US/10700632
; Publication No. US20050118183A1
; GENERAL INFORMATION:
; APPLICANT: Immunogen, Inc.
; TITLE OF INVENTION: ANTI-CD3 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID
; TITLE OF INVENTION: LEUKEMIA USING THE SAME
; FILE REFERENCE: A8427
; CURRENT APPLICATION NUMBER: US/10/700,632
; CURRENT FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: US 60/424,332
; PRIOR FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (16)..(16)
; OTHER INFORMATION: "X" may be K or Q
US-10-700-632-2

Query Match          98.9%; Score 88; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 VIYPGNDDISYNQKFXG 17
Db      1 VIYPGNDDISYNQKFXG 17

RESULT 2
US-10-700-632-57
; Sequence 57, Application US/10700632
; Publication No. US20050118183A1
; GENERAL INFORMATION:
; APPLICANT: Immunogen, Inc.
; TITLE OF INVENTION: ANTI-CD3 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID
; TITLE OF INVENTION: LEUKEMIA USING THE SAME
; FILE REFERENCE: A8427
; CURRENT APPLICATION NUMBER: US/10/700,632
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; CURRENT FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: US 60/424,332
; PRIOR FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-700-632-57

Query Match          98.9%; Score 88; DB 5; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.7e-07;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db      1 VIYPGNDDISYNQKFXG 17
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RESULT 3
US-10-700-632-73
; Sequence 73, Application US/10700632
; Publication No. US20050118183A1
; GENERAL INFORMATION:
; APPLICANT: Immunogen, Inc.
; TITLE OF INVENTION: ANTI-CD3 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID
; TITLE OF INVENTION: LEUKEMIA USING THE SAME
; FILE REFERENCE: A8427
; CURRENT APPLICATION NUMBER: US/10/700,632
; CURRENT FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: US 60/424,332
; PRIOR FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 73
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-700-632-73

Query Match          98.9%; Score 88; DB 5; Length 117;
Best Local Similarity 94.1%; Pred. No. 1.4e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy      1 VIYPGNDDISYNQKFXG 17
Db      50 VIYPGNDDISYNQKFXG 66

RESULT 4
US-10-700-632-7
; Sequence 7, Application US/10700632
; Publication No. US20050118183A1
; GENERAL INFORMATION:
; APPLICANT: Immunogen, Inc.
; TITLE OF INVENTION: ANTI-CD3 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID
; TITLE OF INVENTION: LEUKEMIA USING THE SAME
; FILE REFERENCE: A8427
; CURRENT APPLICATION NUMBER: US/10/700,632
; CURRENT FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: US 60/424,332
; PRIOR FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-700-632-7

Query Match          98.9%; Score 88; DB 5; Length 118;
Best Local Similarity 94.1%; Pred. No. 1.5e-06;
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Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VYPGNDISYNQKFXG 17
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Db 50 VYPGNDISYNQKFXG 66

RESULT 5
US-10-700-632-9
; Sequence 9, Application US/10700632
; Publication No. US20050118183A1
; GENERAL INFORMATION:
; APPLICANT: Immunogen, Inc.
; TITLE OF INVENTION: ANTI-CD33 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID
; TITLE OF INVENTION: LEUKEMIA USING THE SAME
; FILE REFERENCE: A8427
; CURRENT APPLICATION NUMBER: US/10/700,632
; PRIOR FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: US 60/424,332
; PRIOR FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized My9-6 antibody heavy chain variable region
US-10-700-632-9

Query Match 98.9%; Score 88; DB 5; Length 118;
Best Local Similarity 94.1%; Pred. No. 1.5e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VYPGNDISYNQKFXG 17
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Db 50 VYPGNDISYNQKFXG 66

RESULT 6
US-09-770-002-2
; Sequence 2, Application US/09770002
; Patent No. US20020110558A1
; GENERAL INFORMATION:
; APPLICANT: Peter Lloyd Amiot
; APPLICANT: Max H. Schreier
; APPLICANT: Karin Schreier
; TITLE OF INVENTION: Use of CD25 binding molecules in the
; TITLE OF INVENTION: treatment of rheumatoid arthritis or skin diseases.
; FILE REFERENCE: 4-30583A/30967C1
; CURRENT APPLICATION NUMBER: US/09/770,002
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: PCT/EP99/05316
; PRIOR FILING DATE: 1999-07-26
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-770-002-2

Query Match 82.0%; Score 73; DB 3; Length 17;
Best Local Similarity 81.2%; Pred. No. 5e-05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IYPGNDISYNQKFXG 17
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Db 2 IYPGNDISYNQKFXG 17

RESULT 7
US-10-240-353B-2

; Sequence 2, Application US/10240353B
; Publication No. US20050226872A1
; GENERAL INFORMATION:
; APPLICANT: Hansjorg Adam
; APPLICANT: Lothar Farber
; TITLE OF INVENTION: Use of CD25 binding molecules in the
; TITLE OF INVENTION: treatment of inflammatory diseases of the gastrointestinal
; FILE REFERENCE: 4-31368A
; CURRENT APPLICATION NUMBER: US/10/240,353B
; PRIOR FILING DATE: 2002-09-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-240-353B-2

Query Match 82.0%; Score 73; DB 5; Length 17;
Best Local Similarity 81.2%; Pred. No. 5e-05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IYPGNDISYNQKFXG 17
|||||

Db 2 IYPGNDISYNQKFXG 17

RESULT 8
US-10-700-632-80
; Sequence 80, Application US/10700632
; Publication No. US20050118183A1
; GENERAL INFORMATION:
; APPLICANT: Immunogen, Inc.
; TITLE OF INVENTION: ANTI-CD33 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID
; TITLE OF INVENTION: LEUKEMIA USING THE SAME
; FILE REFERENCE: A8427
; CURRENT APPLICATION NUMBER: US/10/700,632
; PRIOR FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: US 60/424,332
; PRIOR FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 80
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-700-632-80

Query Match 82.0%; Score 73; DB 5; Length 114;
Best Local Similarity 81.2%; Pred. No. 0.00042;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IYPGNDISYNQKFXG 17
|||||

Db 49 IYPGNDISYNQKFXG 64

RESULT 9
US-10-240-353B-8
; Sequence 8, Application US/10240353B
; Publication No. US20050226872A1
; GENERAL INFORMATION:
; APPLICANT: Hansjorg Adam
; APPLICANT: Lothar Farber
; TITLE OF INVENTION: Use of CD25 binding molecules in the
; TITLE OF INVENTION: treatment of inflammatory diseases of the gastrointestinal
; FILE REFERENCE: 4-31368A
; CURRENT APPLICATION NUMBER: US/10/240,353B
; PRIOR FILING DATE: 2002-09-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0

```

; SEQ ID NO 8
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-240-353B-8

```

```

Query Match      82.0%; Score 73; DB 5; Length 136,
Best Local Similarity 81.2%; Pred. No. 0.00051;
Matches 13; Conservative 0; Mismatches 3; Indels

```

QY	2	IYPGNDISYNQKFXG	17
Db	70	IYPGNSDTSYNQKFEQ	85

RESULT 10
US-10-366-709-9
; Sequence 9, Application US/10366709
; Publication No. US20030219433A1

```

1  APPLICANT: OU, ZHENGXING
2  APPLICANT: GOLDENBERG, DAVID M.
3  TITLE OF INVENTION: ANTI-CR20 ANTIBODIES AND FUSION PROTEINS THEREOF AND
4  TITLE OF INVENTION: METHODS OF USE
5  FILE REFERENCE: 18733/115
6  CURRENT APPLICATION NUMBER: US/10/366,709
7  CURRENT FILING DATE: 2003-02-14
8  PRIOR APPLICATION NUMBER: 60/356,132
9  PRIOR FILING DATE: 2002-02-14
10 PRIOR APPLICATION NUMBER: 60/116,232
11 PRIOR FILING DATE: 2002-10-07
12 NUMBER OF SEQ ID NOS: 55
13 SOFTWARE: PatentIn Ver. 2.1
14 SEQ ID NO 9
15 LENGTH: 17
16 TYPE: PRT
17 ORGANISM: Artificial Sequence
18 FEATURE:
19 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
20 OTHER INFORMATION: peptide
21 US-10-366-709-9

```

Query Match	80.9%	Score 72;	DB 4;	Length 17;
Best Local Similarity	81.2%;	Pred. No. 7.3e-05;		
Matches 13;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;

QY 2 IYPGNDDISYNQKFXG 17
||| | | | | |
Db 2 IYPGNGDTSYNQKFXG 17

RESULT 11
 US-10-337-663-9
 ; Sequence 9, Application US/10327663
 ; Publication No. US20040093621A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kenya SHITARA
 ; APPLICANT: Mikiko SAKURADA
 ; APPLICANT: Kazuhisa UCHIDA
 ; APPLICANT: Toyohide SHINKAWA
 ; APPLICANT: Mitsuo SATOH
 ; APPLICANT: Ryoosuke NAKANO
 ; TITLE OF INVENTION: ANTIBODY COMPOSITION WHICH SPECIFICALLY BINDS TO CD20
 ; FILE REFERENCE: 249-289
 ; CURRENT APPLICATION NUMBER: US/10/327,663
 ; CURRENT FILING DATE: 2002-12-24
 ; PRIOR APPLICATION NUMBER: JP 2001-392753
 ; PRIOR FILING DATE: 2001-12-25
 ; PRIOR APPLICATION NUMBER: JP 2002-106948
 ; PRIOR FILING DATE: 2002-04-09
 ; PRIOR APPLICATION NUMBER: JP 2002-319975
 ; PRIOR FILING DATE: 2001-11-01

```

; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patentin Ver. 2.11
; SEQ ID NO 9
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-327-663-9

```

Query Match	80.9%	Score 72;	DB 4;	Length 17;
Best Local Similarity	81.2%	Pred. No. 7.3e-05;		
Matches 13; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

Qy	2	IYPGNDISYNQKFXG	17
Db	2	IYPGNGDTSYNQKFKG	17

```

RESULTS 2
US-10-849-615-27
; Sequence 27, Application US/10849615
; Publication No. US20050025764A1
; GENERAL INFORMATION:
; APPLICANT: Allan, Barrett W.
; APPLICANT: Davies, Julian
; APPLICANT: Margulis, David M.
; APPLICANT: Oudek, Brian
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: CD20 BINDING MOLECULES
; FILE REFERENCE: AHE-09016
; CURRENT APPLICATION NUMBER: US/10/849,615
; CURRENT FILING DATE: 2004-05-20
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27
; LENGTH: 17
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(17)
; OTHER INFORMATION: CDRH2
US-10-849-615-27

```

Query Match	80.9%	Score 72;	DB 5;	Length 17;
Best Local Similarity	81.2%	Pred. No. 7.3e-05;		
Matches 13;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;

QY	2	IYPGNDISYNQKFXG	17
Db	2	IYPGNGDTSYNQKFXG	17

RESULT 13
US-10-661-049-44
Sequence 44, Application US/10861049
Publication No US20050095243A1
GENERAL INFORMATION:
APPLICANT: Andrew Chan
APPLICANT: Qian Gong
APPLICANT: Flavius Martin
TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDER
FILE REFERENCE: P2040RUS
CURRENT APPLICATION NUMBER: US/10/861,049.
CURRENT FILING DATE: 2004-06-04
PRIOR APPLICATION NUMBER: US 60/476,531
PRIOR FILING DATE: 2003-06-06
PRIOR APPLICATION NUMBER: US 60/476,481
PRIOR FILING DATE: 2003-06-05
PRIOR APPLICATION NUMBER: US 60/476,414
PRIOR FILING DATE: 2003-06-05
NUMBER OF SEQ ID NOS: 145

SEQ ID NO 44
LENGTH: 17
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: sequence is synthesized
US-10-861-049-44

Query Match 80.9%; Score 72; DB 5; Length 17;
Best Local Similarity 81.2%; Pred. No. 7.3e-05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGNDISYNOKFXG 17
Db 2 IYPGNGDTSYNOKFXG 17

RESULT 14
US-11-021-874-44
Sequence 44, Application US/11021874
Publication No. US20050163775A1
GENERAL INFORMATION:
APPLICANT: Andrew Chan
APPLICANT: Qian Gong
APPLICANT: Flavius Martin
TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS
FILE REFERENCE: P2040R1P1
CURRENT APPLICATION NUMBER: US/11/021,874
CURRENT FILING DATE: 2004-12-22
PRIOR APPLICATION NUMBER: US 10/861,049
PRIOR FILING DATE: 2004-06-04
PRIOR APPLICATION NUMBER: US 60/476,531
PRIOR FILING DATE: 2003-06-06
PRIOR APPLICATION NUMBER: US 60/476,481
PRIOR FILING DATE: 2003-06-05
PRIOR APPLICATION NUMBER: US 60/476,414
PRIOR FILING DATE: 2003-06-05
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 44
LENGTH: 17
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: sequence is synthesized
US-11-021-874-44

Query Match 80.9%; Score 72; DB 6; Length 17;
Best Local Similarity 81.2%; Pred. No. 7.3e-05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGNDISYNOKFXG 17
Db 2 IYPGNGDTSYNOKFXG 17

RESULT 15
US-10-366-709-35
Sequence 35, Application US/10366709
Publication No. US20030219433A1
GENERAL INFORMATION:
APPLICANT: HANSEN, HANS
APPLICANT: OU, ZHENGXING
APPLICANT: GOLDENBERG, DAVID M.
TITLE OF INVENTION: ANTI-CD20 ANTIBODIES AND FUSION PROTEINS THEREOF AND
FILE REFERENCE: 18733/115
CURRENT APPLICATION NUMBER: US/10/366,709
CURRENT FILING DATE: 2003-02-14
PRIOR APPLICATION NUMBER: 60/356,132
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: 60/416,232
PRIOR FILING DATE: 2002-10-07
NUMBER OF SEQ ID NOS: 55

SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 35
LENGTH: 120
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic heavy
US-10-366-709-35

Query Match 80.9%; Score 72; DB 4; Length 120;
Best Local Similarity 81.2%; Pred. No. 0.00064;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGNDISYNOKFXG 17
Db 50 IYPGNGDTSYNOKFXG 65

RESULT 16
US-10-366-709-39
Sequence 39, Application US/10366709
Publication No. US20030219433A1
GENERAL INFORMATION:
APPLICANT: HANSEN, HANS
APPLICANT: OU, ZHENGXING
APPLICANT: GOLDENBERG, DAVID M.
TITLE OF INVENTION: ANTI-CD20 ANTIBODIES AND FUSION PROTEINS THEREOF AND
FILE REFERENCE: 18733/115
CURRENT APPLICATION NUMBER: US/10/366,709
CURRENT FILING DATE: 2003-02-14
PRIOR APPLICATION NUMBER: 60/356,132
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: 60/416,232
PRIOR FILING DATE: 2002-10-07
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 39
LENGTH: 121
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic heavy
US-10-366-709-39

Query Match 80.9%; Score 72; DB 4; Length 121;
Best Local Similarity 81.2%; Pred. No. 0.00065;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGNDISYNOKFXG 17
Db 51 IYPGNGDTSYNOKFXG 66

RESULT 17
US-10-366-709-41
Sequence 41, Application US/10366709
Publication No. US20030219433A1
GENERAL INFORMATION:
APPLICANT: HANSEN, HANS
APPLICANT: OU, ZHENGXING
APPLICANT: GOLDENBERG, DAVID M.
TITLE OF INVENTION: ANTI-CD20 ANTIBODIES AND FUSION PROTEINS THEREOF AND
FILE REFERENCE: 18733/115
CURRENT APPLICATION NUMBER: US/10/366,709
CURRENT FILING DATE: 2003-02-14
PRIOR APPLICATION NUMBER: 60/356,132
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: 60/416,232
PRIOR FILING DATE: 2002-10-07

RESULT 21
US-10-917-599-3
Sequence 3, Application US/10917599
Publication No. US20050069545A1
GENERAL INFORMATION:
APPLICANT: CARB, Francis Joseph
APPLICANT: WILLIAMS, Stephen
APPLICANT: GILLIES, Stephen D.
TITLE OF INVENTION: CD20-BINDING POLYPEPTIDE COMPOSITIONS
TITLE OF INVENTION: AND METHODS
FILE REFERENCE: MER-125
CURRENT APPLICATION NUMBER: US/10/917,599
CURRENT FILING DATE: 2004-08-13
PRIOR APPLICATION NUMBER: 60/520,171
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: EP03018480.8
PRIOR FILING DATE: 2003-08-14

; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: ANTIBODY VARIABLE REGION FRAGMENT
US-10-917-599-3

Query Match 80.9%; Score 72; DB 5; Length 121;
Best Local Similarity 81.2%; Pred. No. 0.00065;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IYPGNDISYNQKFXG 17
|||||
Db 51 IYPGNGDTSYNQKFXG 66

RESULT 22
US-10-861-049-23
; Sequence 23, Application US/10861049
; Publication No. US20050095243A1
; GENERAL INFORMATION:
; APPLICANT: Andrew Chan
; APPLICANT: Qian Gong
; APPLICANT: Flavius Martin
; TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS
; FILE REFERENCE: P2040R1US
; CURRENT APPLICATION NUMBER: US/10/861,049
; CURRENT FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 60/476,531
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/476,481
; PRIOR FILING DATE: 2003-06-05
; PRIOR APPLICATION NUMBER: US 60/476,414
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 23
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-861-049-23

Query Match 80.9%; Score 72; DB 5; Length 121;
Best Local Similarity 81.2%; Pred. No. 0.00065;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IYPGNDISYNQKFXG 17
|||||
Db 51 IYPGNGDTSYNQKFXG 66

RESULT 23
US-11-021-874-23
; Sequence 23, Application US/11021874
; Publication No. US20050163775A1
; GENERAL INFORMATION:
; APPLICANT: Andrew Chan
; APPLICANT: Qian Gong
; APPLICANT: Flavius Martin
; TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS
; FILE REFERENCE: P2040R1P1
; CURRENT APPLICATION NUMBER: US/11/021,874
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: US 10/861,049
; PRIOR FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 60/476,531
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/476,481
; PRIOR FILING DATE: 2003-06-05
; PRIOR APPLICATION NUMBER: US 60/476,414
; PRIOR FILING DATE: 2003-06-05

; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 23
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-021-874-23

Query Match 80.9%; Score 72; DB 6; Length 121;
Best Local Similarity 81.2%; Pred. No. 0.00065;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IYPGNDISYNQKFXG 17
|||||
Db 51 IYPGNGDTSYNQKFXG 66

RESULT 24
US-10-818-765-2
; Sequence 2, Application US/10818765
; Publication No. US20040202658A1
; GENERAL INFORMATION:
; APPLICANT: Benyunes, Mark C.
; TITLE OF INVENTION: THERAPY OF AUTOIMMUNE DISEASE IN A PATIENT WITH AN
; FILE REFERENCE: P2027R1-US
; CURRENT APPLICATION NUMBER: US/10/818,765
; CURRENT FILING DATE: 2004-04-06
; PRIOR APPLICATION NUMBER: US 60/461,4819
; PRIOR FILING DATE: 2003-04-09
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 2
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: humanized sequence
US-10-818-765-2

Query Match 80.9%; Score 72; DB 4; Length 122;
Best Local Similarity 81.2%; Pred. No. 0.00066;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IYPGNDISYNQKFXG 17
|||||
Db 51 IYPGNGDTSYNQKFXG 66

RESULT 25
US-10-877-363-2
; Sequence 2, Application US/10877363
; Publication No. US20050032130A1
; GENERAL INFORMATION:
; APPLICANT: BERESINI, MAUREEN
; APPLICANT: SONG, AN
; TITLE OF INVENTION: NEUTRALIZING ANTIBODY ASSAY AND USES THEREFOR
; FILE REFERENCE: P2032R1
; CURRENT APPLICATION NUMBER: US/10/877,363
; CURRENT FILING DATE: 2004-06-24
; PRIOR APPLICATION NUMBER: US 60/490,678
; PRIOR FILING DATE: 2003-07-29
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 2
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized.
US-10-877-363-2

Query Match 80.9%; Score 72; DB 5; Length 122;
Best Local Similarity 81.2%; Pred. No. 0.00066;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGNDISYNOKFXG 17
| | | | | | | | | |
DB 51 IYPGNGDTSYNOKFXG 66

RESULT 26

US-10-922-651-2
; Sequence 2, Application US/10922651
; Publication No. US20050053602A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G.
; TITLE OF INVENTION: Therapy of Ocular Disorders
; FILE REFERENCE: P2029R1
; CURRENT APPLICATION NUMBER: US/10/922,651
; PRIOR FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: US 60/498,791
; PRIOR FILING DATE: 2003-08-29
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 2
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized.
US-10-922-651-2

Query Match 80.9%; Score 72; DB 5; Length 122;
Best Local Similarity 81.2%; Pred. No. 0.00066;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGNDISYNOKFXG 17
| | | | | | | | | |
DB 51 IYPGNGDTSYNOKFXG 66

RESULT 27

US-10-917-599-9
; Sequence 9, Application US/10917599
; Publication No. US20050069545A1
; GENERAL INFORMATION:
; APPLICANT: CARR, Francis Joseph
; APPLICANT: WILLIAMS, Stephen D.
; TITLE OF INVENTION: CD20-BINDING POLYPEPTIDE COMPOSITIONS
; TITLE OF INVENTION: AND METHODS
; FILE REFERENCE: MER-125
; CURRENT APPLICATION NUMBER: US/10/917,599
; CURRENT FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: 60/520,171
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: EP03018480.8
; PRIOR FILING DATE: 2003-08-14
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: ANTIBODY VARIABLE REGION FRAGMENT
US-10-917-599-9

Query Match 80.9%; Score 72; DB 5; Length 122;
Best Local Similarity 81.2%; Pred. No. 0.00066;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGNDISYNOKFXG 17
| | | | | | | | | |
DB 51 IYPGNGDTSYNOKFXG 66

RESULT 28

US-10-917-599-10

; Sequence 10, Application US/10917599
; Publication No. US20050069545A1
; GENERAL INFORMATION:
; APPLICANT: CARR, Francis Joseph
; APPLICANT: WILLIAMS, Stephen D.
; TITLE OF INVENTION: CD20-BINDING POLYPEPTIDE COMPOSITIONS
; TITLE OF INVENTION: AND METHODS
; FILE REFERENCE: MER-125
; CURRENT APPLICATION NUMBER: US/10/917,599
; CURRENT FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: 60/520,171
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: EP03018480.8
; PRIOR FILING DATE: 2003-08-14
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: ANTIBODY VARIABLE REGION FRAGMENT
US-10-917-599-10

Query Match 80.9%; Score 72; DB 5; Length 122;
Best Local Similarity 81.2%; Pred. No. 0.00066;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGNDISYNOKFXG 17
| | | | | | | | | |
DB 51 IYPGNGDTSYNOKFXG 66

RESULT 29

US-10-861-049-14
; Sequence 14, Application US/10861049
; Publication No. US20050095243A1
; GENERAL INFORMATION:
; APPLICANT: Andrew Chan
; APPLICANT: Qian Gong
; APPLICANT: Flavius Martin
; TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS
; FILE REFERENCE: P2040R1US
; CURRENT APPLICATION NUMBER: US/10/861,049
; CURRENT FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 60/476,531
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/476,481
; PRIOR FILING DATE: 2003-06-05
; PRIOR APPLICATION NUMBER: US 60/476,414
; PRIOR FILING DATE: 2003-06-05
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 14
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-10-861-049-14

Query Match 80.9%; Score 72; DB 5; Length 122;
Best Local Similarity 81.2%; Pred. No. 0.00066;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGNDISYNOKFXG 17
| | | | | | | | | |
DB 51 IYPGNGDTSYNOKFXG 66

RESULT 30

US-10-627-556-242
; Sequence 242, Application US/10627556

```
/ Publication No. US20050136049A1
/ GENERAL INFORMATION:
/ APPLICANT: LEDBETTER, JEFFREY A.
/ APPLICANT: HAYDEN-LEDBETTER, MARTHA
/ APPLICANT: THOMPSON, PETER A.
/ TITLE OF INVENTION: BINDING CONSTRUCTS AND METHODS FOR USE THEREOF
/ FILE REFERENCE: 49076.000004.CIP2
/ CURRENT APPLICATION NUMBER: US/10/627,556
/ PRIOR FILING DATE: 2003-07-26
/ PRIOR APPLICATION NUMBER: 10/053,530
/ PRIOR FILING DATE: 2002-01-17
/ PRIOR APPLICATION NUMBER: 60/367,358
/ PRIOR FILING DATE: 2002-01-16
/ PRIOR APPLICATION NUMBER: 09/765,208
/ PRIOR FILING DATE: 2001-01-17
/ PRIOR APPLICATION NUMBER: 60/385,691
/ PRIOR FILING DATE: 2002-06-03
/ NUMBER OF SEQ ID NOS: 699
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 242
/ LENGTH: 122
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-627-556-242.
```

```
Query Match      80.9%; Score 72; DB 5; Length 122;
Best Local Similarity 81.2%; Pred. No. 0.00066;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
OY      2 IYPGNDISTYNOKFXG 17
      ||||| ||||| |||||
Db      51 IYPGNGDTSYNOKFXG 66
```

```
RESULT 31
US-11-021-874-14
/ Sequence 14, Application US/11021874
/ Publication No. US20050163775A1
/ GENERAL INFORMATION:
/ APPLICANT: Qian Gong
/ APPLICANT: Andrew Chan
/ APPLICANT: Flavius Martin
/ TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS
/ FILE REFERENCE: P2040R1P1
/ CURRENT APPLICATION NUMBER: US/11/021,874
/ PRIOR FILING DATE: 2004-12-22
/ PRIOR APPLICATION NUMBER: US 10/861,049
/ PRIOR FILING DATE: 2004-06-04
/ PRIOR APPLICATION NUMBER: US 60/476,531
/ PRIOR FILING DATE: 2003-06-06
/ PRIOR APPLICATION NUMBER: US 60/476,481
/ PRIOR FILING DATE: 2003-06-05
/ PRIOR APPLICATION NUMBER: US 60/476,414
/ PRIOR FILING DATE: 2003-06-05
/ NUMBER OF SEQ ID NOS: 165
/ SEQ ID NO 14
/ LENGTH: 122
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: sequence is synthesized
US-11-021-874-14
```

```
Query Match      80.9%; Score 72; DB 6; Length 122;
Best Local Similarity 81.2%; Pred. No. 0.00066;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
OY      2 IYPGNDISTYNOKFXG 17
      ||||| ||||| |||||
Db      51 IYPGNGDTSYNOKFXG 66
```

```
RESULT 32
US-11-005-677-2
/ Sequence 2, Application US/11005677
/ Publication No. US20050186206A1
/ GENERAL INFORMATION:
/ APPLICANT: BRUNETTA, PAUL G.
/ TITLE OF INVENTION: DETECTION OF CD20 IN THERAPY OF AUTOIMMUNE DISEASES
/ FILE REFERENCE: P2061R1
/ CURRENT APPLICATION NUMBER: US/11/005,677
/ PRIOR FILING DATE: 2004-12-07
/ PRIOR APPLICATION NUMBER: US 60/531,363
/ PRIOR FILING DATE: 2003-12-19
/ NUMBER OF SEQ ID NOS: 4
/ SEQ ID NO 2
/ LENGTH: 122
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: Sequence is synthesized.
US-11-005-677-2
```

```
Query Match      80.9%; Score 72; DB 6; Length 122;
Best Local Similarity 81.2%; Pred. No. 0.00066;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
OY      2 IYPGNDISTYNOKFXG 17
      ||||| ||||| |||||
Db      51 IYPGNGDTSYNOKFXG 66
```

```
RESULT 33
US-11-006-136-2
/ Sequence 2, Application US/11006136
/ Publication No. US20050191297A1
/ GENERAL INFORMATION:
/ APPLICANT: BRUNETTA, PAUL G.
/ TITLE OF INVENTION: DETECTION OF CD20 IN TRANSPLANT REJECTION
/ FILE REFERENCE: P2062R1
/ CURRENT APPLICATION NUMBER: US/11/006,136
/ PRIOR FILING DATE: 2004-12-07
/ PRIOR APPLICATION NUMBER: US 60/531,594
/ PRIOR FILING DATE: 2003-12-19
/ NUMBER OF SEQ ID NOS: 4
/ SEQ ID NO 2
/ LENGTH: 122
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: Sequence is synthesized.
US-11-006-136-2
```

```
Query Match      80.9%; Score 72; DB 6; Length 122;
Best Local Similarity 81.2%; Pred. No. 0.00066;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
OY      2 IYPGNDISTYNOKFXG 17
      ||||| ||||| |||||
Db      51 IYPGNGDTSYNOKFXG 66
```

```
RESULT 34
US-09-892-613C-18
/ Sequence 18, Application US/09892613C
/ Publication No. US20030040606A1
/ GENERAL INFORMATION:
/ APPLICANT: Leung, Shawn Shi-on
/ TITLE OF INVENTION: REDUCING IMMUNOGENICITIES OF IMMUNOGLOBULINS BY FRAMEWORK-PATCHING
/ FILE REFERENCE: 655
/ CURRENT APPLICATION NUMBER: US/09/892,613C
/ PRIOR FILING DATE: 2001-06-27
/ NUMBER OF SEQ ID NOS: 32
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SOFTWARE: Patentin version 3.1
SEQ ID NO 18
LENGTH: 123
TYPE: PRT
ORGANISM: Chimera sp.
US-09-892-613C-18

Query Match 80.9%; Score 72; DB 3; Length 123;
Best Local Similarity 81.2%; Pred. No. 0.00066;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IYGNNDISYNQKFXG 17
|||||
Db 51 IYGNNDISYNQKFXG 66

RESULT 35
US-10-482-759-18
Sequence 18, Application US/10482759
Publication No. US20050033028A1
GENERAL INFORMATION:
APPLICANT: Leung, Shawn Shui-on
TITLE OF INVENTION: REDUCING IMMUNOGENICITIES OF IMMUNOGLOBULINS BY FRAMEWORK-PATCHING
FILE REFERENCE: 655
CURRENT APPLICATION NUMBER: US/10/482,759
CURRENT FILING DATE: 2003-12-29
PRIOR APPLICATION NUMBER: US 09/892,613
PRIOR FILING DATE: 2001-06-27
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin version 3.1
SEQ ID NO 18
LENGTH: 123
TYPE: PRT
ORGANISM: Chimera sp.
US-10-482-759-18

Query Match 80.9%; Score 72; DB 5; Length 123;
Best Local Similarity 81.2%; Pred. No. 0.00066;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IYGNNDISYNQKFXG 17
|||||
Db 51 IYGNNDISYNQKFXG 66

RESULT 36
US-09-905-928-6
Sequence 6, Application US/09905928
Publication No. US20030021781A1
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
APPLICANT: Hanna, Nabli
APPLICANT: Leonard, John E.
APPLICANT: Newman, Roland A.
APPLICANT: Reif, Mitchell E.
APPLICANT: Rastetter, William H.
TITLE OF INVENTION: Therapeutic Application of Chimeric and
TITLE OF INVENTION: Radiolabeled Antibodies to Human B Lymphocyte Restricted
TITLE OF INVENTION: Differentiation Antigens for the Treatment of B-Cell Lymphoma
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince St.
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/905,928
FILING DATE: 17-JUL-2001
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/475,813
FILING DATE: 07-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/149,099
FILING DATE: 03-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,891
FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Teekin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-158
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 140 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-905-928-6

Query Match 80.9%; Score 72; DB 3; Length 140;
Best Local Similarity 81.2%; Pred. No. 0.00076;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IYGNNDISYNQKFXG 17
|||||
Db 70 IYGNNDISYNQKFXG 85

RESULT 37
US-10-096-964-6
Sequence 6, Application US/10096964
Publication No. US20030082172A1
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
APPLICANT: Hanna, Nabli
APPLICANT: Leonard, John E.
APPLICANT: Newman, Roland A.
APPLICANT: Reif, Mitchell E.
APPLICANT: Rastetter, William H.
TITLE OF INVENTION: Therapeutic Application of Chimeric and
TITLE OF INVENTION: Radiolabeled Antibodies to Human B Lymphocyte Restricted
TITLE OF INVENTION: Differentiation Antigens for the Treatment of B-Cell Lymphoma
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince St.
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/096,964
FILING DATE: 14-Mar-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/475,813
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/149,099
FILING DATE: 03-NOV-1993

APPLICATION NUMBER: US 07/978,891
FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-158
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 140 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-096-964-6

Query Match 80.9%; Score 72; DB 4; Length 140;
Best Local Similarity 81.2%; Pred. No. 0.00076;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGNDISYNOKFXG 17
Db 70 IYPGNGDTSYNOKFXG 85

RESULT 38
US-10-238-681-11
Sequence 11, Application US/10238681
Publication No. US20030147885A1
GENERAL INFORMATION:
APPLICANT: ANDERSON, DARRELL R.
APPLICANT: HANNA, NABIL
APPLICANT: LEONARD, JOHN E.
APPLICANT: NEWMAN, ROLAND A.
APPLICANT: REEF, MITCHELL E.
APPLICANT: RASTLETER, WILLIAM H.
TITLE OF INVENTION: THERAPEUTIC APPLICATION OF CHIMERIC AND RADIOLABELLED
TITLE OF INVENTION: ANTIBODIES TO HUMAN B LYMPHOCYTE RESTRICTED
TITLE OF INVENTION: DIFFERENTIATION ANTIGEN FOR TREATMENT OF B CELL
TITLE OF INVENTION: LYMPHOMA
FILE REFERENCE: 37003/0291808
CURRENT APPLICATION NUMBER: US/10/238,681
CURRENT FILING DATE: 2002-09-11
PRIOR APPLICATION NUMBER: 08/921,060
PRIOR FILING DATE: 1997-08-23
PRIOR APPLICATION NUMBER: 08/149,099
PRIOR FILING DATE: 1993-11-03
PRIOR APPLICATION NUMBER: 07/978,891
PRIOR FILING DATE: 1992-11-13
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11
LENGTH: 140
TYPE: PRT
ORGANISM: Murine sp.
US-10-238-681-11

Query Match 80.9%; Score 72; DB 4; Length 140;
Best Local Similarity 81.2%; Pred. No. 0.00076;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGNDISYNOKFXG 17
Db 70 IYPGNGDTSYNOKFXG 85

RESULT 39
US-10-366-709-48
Sequence 48, Application US/10366709
Publication No. US20030219433A1
GENERAL INFORMATION:

APPLICANT: HANSEN, HANS
APPLICANT: OU, ZHENGXING
APPLICANT: GOLDENBERG, DAVID M.
TITLE OF INVENTION: ANTI-CD20 ANTIBODIES AND FUSION PROTEINS THEREOF AND
TITLE OF INVENTION: METHODS OF USE
FILE REFERENCE: 18733/115
CURRENT APPLICATION NUMBER: US/10/366,709
CURRENT FILING DATE: 2003-02-14
PRIOR APPLICATION NUMBER: 60/356,132
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: 60/416,232
PRIOR FILING DATE: 2002-10-07
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 48
LENGTH: 140
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: heavy chain ha20VH1 amino acid sequence
US-10-366-709-48

Query Match 80.9%; Score 72; DB 4; Length 140;
Best Local Similarity 81.2%; Pred. No. 0.00076;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGNDISYNOKFXG 17
Db 70 IYPGNGDTSYNOKFXG 85

RESULT 40
US-10-366-709-50
Sequence 50, Application US/10366709
Publication No. US20030219433A1
GENERAL INFORMATION:
APPLICANT: HANSEN, HANS
APPLICANT: OU, ZHENGXING
APPLICANT: GOLDENBERG, DAVID M.
TITLE OF INVENTION: ANTI-CD20 ANTIBODIES AND FUSION PROTEINS THEREOF AND
TITLE OF INVENTION: METHODS OF USE
FILE REFERENCE: 18733/115
CURRENT APPLICATION NUMBER: US/10/366,709
CURRENT FILING DATE: 2003-02-14
PRIOR APPLICATION NUMBER: 60/356,132
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: 60/416,232
PRIOR FILING DATE: 2002-10-07
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 50
LENGTH: 140
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: heavy chain ha20VH2 amino acid sequence
US-10-366-709-50

Query Match 80.9%; Score 72; DB 4; Length 140;
Best Local Similarity 81.2%; Pred. No. 0.00076;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGNDISYNOKFXG 17
Db 70 IYPGNGDTSYNOKFXG 85

RESULT 41
US-10-411-037-62
Sequence 62, Application US/10411037
Publication No. US20040043446A1

GENERAL INFORMATION:
APPLICANT: Neose Technologies, Inc.
APPLICANT: Defrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
APPLICANT: Chen, Xi
APPLICANT: Bowe, Caryn
TITLE OF INVENTION: ALPHA GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA
FILE REFERENCE: 040853-01-5082
CURRENT APPLICATION NUMBER: US/10/411,037
CURRENT FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/387,292
PRIOR FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn version 3.2
SEQ ID NO 62
LENGTH: 140
TYPE: PRT
ORGANISM: Mus musculus
US-10-411-037-62

Query Match 80.9%; Score 72; DB 4; Length 140;
Best Local Similarity 81.2%; Pred. No. 0.00076;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGNDISYNOKFXG 17
Db 70 IYPNGDTSYNOKFKG 85

RESULT 42
US-10-411-026-62
Sequence 62, Application US/10411026
Publication No. US20040063911A1
GENERAL INFORMATION:
APPLICANT: Neose Technologies, Inc.
APPLICANT: Defrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
APPLICANT: Chen, Xi
TITLE OF INVENTION: PROTEIN REMODELING METHODS AND PEPTIDES PRODUCED BY THE
FILE REFERENCE: 040853-01-5053
CURRENT APPLICATION NUMBER: US/10/411,026
CURRENT FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/387,292
PRIOR FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 60/407,527

PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn version 3.2
SEQ ID NO 62
LENGTH: 140
TYPE: PRT
ORGANISM: Mus musculus
US-10-411-026-62

Query Match 80.9%; Score 72; DB 4; Length 140;
Best Local Similarity 81.2%; Pred. No. 0.00076;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGNDISYNOKFXG 17
Db 70 IYPNGDTSYNOKFKG 85

RESULT 43
US-10-410-962-62
Sequence 62, Application US/10410962
Publication No. US20040077836A1
GENERAL INFORMATION:
APPLICANT: Neose Technologies, Inc.
APPLICANT: Defrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
APPLICANT: Chen, Xi
TITLE OF INVENTION: GRANULOCYTE COLONY STIMULATING FACTOR: REMODELING AND
FILE REFERENCE: 040853-01-5054
CURRENT APPLICATION NUMBER: US/10/410,962
CURRENT FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/387,292
PRIOR FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn version 3.2
SEQ ID NO 62
LENGTH: 140
TYPE: PRT
ORGANISM: Mus musculus
US-10-410-962-62

Query Match 80.9%; Score 72; DB 4; Length 140;
Best Local Similarity 81.2%; Pred. No. 0.00076;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGNDISYNOKFXG 17
Db 70 IYPNGDTSYNOKFKG 85

RESULT 44
US-10-411-049-62
Sequence 62, Application US/10411049
Publication No. US20040082026A1
GENERAL INFORMATION:
APPLICANT: Neose Technologies, Inc.
APPLICANT: Defrees, Shawn

```

APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
APPLICANT: Chen, Xi
APPLICANT: Bove, Caryn
TITLE OF INVENTION: INTERPERON ALPHA: REMODELLING AND GLYCOCONJUGATION OF INTERPERON
TITLE OF INVENTION: ALPHA
FILE REFERENCE: 040853-01-5055
CURRENT APPLICATION NUMBER: US/10/411, 049
CURRENT FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/387,292
PRIOR FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn version 3.2
SEQ ID NO 62
LENGTH: 140
TYPE: PRT
ORGANISM: Mus musculus
US-10-411-049-62

```

Query Match	80.9%	Score 72;	DB 4;	Length 140;
Best Local Similarity	81.2%	Pred. No. 0.00076;		
Matches 13; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;
QY	2	IYPGNDISYNQKEXG	17	
db	70	IYPGNGDTSYNQKFKG	85	

```

RESULT 45
US-10-327-663-14
; Sequence 14, Application US/10327663
; Publication No. US20040093621A1
; GENERAL INFORMATION:
; APPLICANT: Kenya SHITARA
; APPLICANT: Mikiko SAKURADA
; APPLICANT: Kazuhisa UCHIDA
; APPLICANT: Toyohide SHINKAWA
; APPLICANT: Mitsuo SATOH
; APPLICANT: Ryoosuke NAKANO
; TITLE OF INVENTION: ANTIBODY COMPOSITION WHICH SPECIFICALLY BINDS TO CD20
; FILE REFERENCE: 249-289
; CURRENT APPLICATION NUMBER: US/10/327,663
; CURRENT FILING DATE: 2002-12-24
; PRIOR APPLICATION NUMBER: JP 2001-392753
; PRIOR FILING DATE: 2001-12-25
; PRIOR APPLICATION NUMBER: JP 2002-106948
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: JP 2002-319975
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-327-663-14

```

Query Match	80.9%;	Score 72;	DB 4;	Length 140;
Best Local Similarity	81.2%;	Pred. No. 0.00076;		
Matches 13;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;

QY 2 IYPGNDDISYNQKFXG 17
||| | ||||| |
Db 70 IYPGNGDTSYNQKFKG 85

```

RESULT 46
US-10-410-930-62
: Sequence 62, Application US/10410930
: Publication No. US20040115168A1
: GENERAL INFORMATION:
: APPLICANT: Neosec Technologies, Inc.
: APPLICANT: Defrees, Shawn
: APPLICANT: Zopf, David
: APPLICANT: Bayer, Robert
: APPLICANT: Hakes, David
: APPLICANT: Chen, Xi
: APPLICANT: Bove, Caryn
: TITLE OF INVENTION: INTERFERON BETA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
: TITLE OF INVENTION: BETA
: FILER REFERENCE: 040853-01-5056
: CURRENT APPLICATION NUMBER: US/10/410,930
: CURRENT FILING DATE: 2003-04-09
: PRIOR APPLICATION NUMBER: US 60/328,523
: PRIOR FILING DATE: 2001-10-10
: PRIOR APPLICATION NUMBER: US 60/344,692
: PRIOR FILING DATE: 2001-10-19
: PRIOR APPLICATION NUMBER: US 60/387,292
: PRIOR FILING DATE: 2002-06-07
: PRIOR APPLICATION NUMBER: US 60/391,777
: PRIOR FILING DATE: 2002-06-25
: PRIOR APPLICATION NUMBER: US 60/396,594
: PRIOR FILING DATE: 2002-07-17
: PRIOR APPLICATION NUMBER: US 60/404,249
: PRIOR FILING DATE: 2002-08-16
: PRIOR APPLICATION NUMBER: US 60/407,527
: PRIOR FILING DATE: 2002-08-28
: NUMBER OF SEQ ID NOS: 75
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 62
: LENGTH: 140
: TYPE: PRT
: ORGANISM: Mus musculus
US-10-410-930-62

```

Query Match	80.9%	Score 72;	DB 4;	Length 140;
Best Local Similarity	81.2%	Pred. No.	0.00076;	
Matches 13; Conservative	0;	Mismatches	3;	Indels 0;
Gaps	0;			

QY	2	IYPGNDIDISTYNQKFXG	17
db	70	IYPGNDIDISTYNQKFXG	85

RESULT 47
US-10-410-997-62
Sequence 62, Application US/10410997
Publication No. US20040126838A1
GENERAL INFORMATION:
APPLICANT: Neosec Technologies, Inc.
APPLICANT: Defrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
APPLICANT: Chen, Xi
APPLICANT: Bone, Caryn
TITLE OF INVENTION: FOLLICLE STIMULATING HORMONE: REMODELLING AND GLYCOCONJUGATION OF
FILE REFERENCE: 040853-01-5059
CURRENT APPLICATION NUMBER: US/10/410,997
CURRENT FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10

PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/387,292
PRIOR FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn version 3.2
SEQ ID NO 62
LENGTH: 140
TYPE: PRT
ORGANISM: Mus musculus
US-10-410-997-62

Query Match 80.9%; Score 72; DB 4; Length 140;
Best Local Similarity 81.2%; Pred. No. 0.00076;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 IYPGNDISYNQKFXG 17
Db 70 IYPGNDISYNQKFXG 85

RESULT 48
US-10-411-012-62
Sequence 62, Application US/10411012
Publication No. US20040132640A1
GENERAL INFORMATION:
APPLICANT: Neose Technologies, Inc.
APPLICANT: Defrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
APPLICANT: Chen, Xi
APPLICANT: Bove, Caryn
TITLE OF INVENTION: GLYCOCONGUATION METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
FILE REFERENCE: 040853-01-5051
CURRENT APPLICATION NUMBER: US/10/411,012
CURRENT FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/387,292
PRIOR FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn version 3.2
SEQ ID NO 62
LENGTH: 140
TYPE: PRT
ORGANISM: Mus musculus
US-10-411-012-62

Query Match 80.9%; Score 72; DB 4; Length 140;
Best Local Similarity 81.2%; Pred. No. 0.00076;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 2 IYPGNDISYNQKFXG 17

Db 70 IYPGNDISYNQKFXG 85

RESULT 49
US-10-287-994-62
Sequence 62, Application US/10287994
Publication No. US20040137557A1
GENERAL INFORMATION:
APPLICANT: Neose Technologies, Inc.
APPLICANT: Defrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Bove, Caryn
APPLICANT: Hakes, David
APPLICANT: Chen, Xi
TITLE OF INVENTION: REMODELING AND GLYCOCONGUATION OF PEPTIDES
FILE REFERENCE: 040853-01-5052-00
CURRENT APPLICATION NUMBER: US/10/287,994
CURRENT FILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/387,292
PRIOR FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PatentIn version 3.1
SEQ ID NO 62
LENGTH: 140
TYPE: PRT
ORGANISM: Mus musculus
US-10-287-994-62

Query Match 80.9%; Score 72; DB 4; Length 140;
Best Local Similarity 81.2%; Pred. No. 0.00076;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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RESULT 50
US-10-410-913-62
Sequence 62, Application US/10410913
Publication No. US20040142856A1
GENERAL INFORMATION:
APPLICANT: Neose Technologies, Inc.
APPLICANT: Defrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
APPLICANT: Chen, Xi
TITLE OF INVENTION: GLYCOCONGUATION METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
FILE REFERENCE: 040853-01-5081
CURRENT APPLICATION NUMBER: US/10/410,913
CURRENT FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/387,292

; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
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; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 62
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-410-913-62

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OY 2 IYPGNDISYNQKXG 17
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Db 70 IYPGNDISYNQKXG 85

Search completed: May 4, 2006, 13:53:01
Job time : 129.484 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 4, 2006, 13:46:13 ; Search time 19.6984 Seconds
(without alignments)
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	73	82.0	615	9 US-10-512-184-50	Sequence 50, App1
3	72	80.9	17	10 US-11-254-182-61	Sequence 61, App1
4	72	80.9	17	11 US-11-120-338-11	Sequence 11, App1
5	72	80.9	17	11 US-11-106-820-11	Sequence 11, App1
6	72	80.9	17	11 US-11-190-364-11	Sequence 11, App1
7	72	80.9	17	11 US-11-147-780-11	Sequence 11, App1
8	72	80.9	17	11 US-11-143-386-11	Sequence 11, App1
9	72	80.9	17	11 US-11-143-386-11	Sequence 11, App1
10	72	80.9	40	11 US-11-143-077-11	Sequence 11, App1
11	72	80.9	40	11 US-11-187-364-10	Sequence 10, App1
12	72	80.9	40	11 US-11-187-364-11	Sequence 11, App1
13	72	80.9	121	11 US-11-107-028-27	Sequence 27, App1
14	72	80.9	121	11 US-11-107-028-35	Sequence 35, App1
15	72	80.9	121	11 US-11-107-028-37	Sequence 37, App1
16	72	80.9	121	11 US-11-107-028-38	Sequence 38, App1
17	72	80.9	122	10 US-11-254-182-28	Sequence 28, App1
18	72	80.9	122	10 US-11-254-182-29	Sequence 29, App1
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25	72	80.9	122	11 US-11-106-820-8	Sequence 8, App1
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27	72	80.9	122	11 US-11-143-077-8	Sequence 8, App1
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31	72	80.9	122	11 US-11-147-780-8	Sequence 8, App1
32	72	80.9	122	11 US-11-143-386-7	Sequence 7, App1
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84	64	71.9	451	11 US-11-143-077-22	Sequence 22, App1
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86	64	71.9	451	11 US-11-187-364-29	Sequence 29, App1
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ALIGNMENTS

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RESULT 1
US-10-512-184-36
; Sequence 36, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: scFv SS2 with
; OTHER INFORMATION: specificity against Sclerotinia sclerotiorum;
; OTHER INFORMATION: originates from Mus musculus.
US-10-512-184-36
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Db 53 IYPGNSDTSYNOKFXG 68
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; Publication No. US20050244901A1
; GENERAL INFORMATION:
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; APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; LENGTH: 615
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: fusion protein
; OTHER INFORMATION: comprising the leader peptide - chitinase - linker
; OTHER INFORMATION: - scFv SS2 - cmc/H186.
US-10-512-184-50
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Best Local Similarity 81.2%; Pred. No. 0.00028;
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; Sequence 61, Application US/11254182
; Publication No. US20060088523A1
; GENERAL INFORMATION:
; APPLICANT: ANDYA, JAMES
; APPLICANT: GWEE, SHIANG C.
; APPLICANT: LIU, JUN
; APPLICANT: SHEN, YE
; TITLE OF INVENTION: ANTI-BODY FORMULATIONS
; FILE REFERENCE: P2104R1
; CURRENT APPLICATION NUMBER: US/11/254,182
; CURRENT FILING DATE: 2005-10-19
; PRIOR APPLICATION NUMBER: US 60/620,413
; PRIOR FILING DATE: 2004-10-20
; NUMBER OF SEQ ID NOS: 74
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; TYPE: PRT
; ORGANISM: Artificial sequence
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; OTHER INFORMATION: Sequence is synthesized.
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; Sequence 11, Application US/11120338
; Publication No. US20050271658A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G.
; APPLICANT: GREWAL, IOBAL S.
; APPLICANT: WALICKE, PATRICIA A.
; TITLE OF INVENTION: PREVENTING AUTOIMMUNE DISEASE
; FILE REFERENCE: P2079R2
; CURRENT APPLICATION NUMBER: US/11/120,338
; CURRENT FILING DATE: 2005-05-03
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;; PRIOR APPLICATION NUMBER: US 60/568,460
;; PRIOR FILING DATE: 2004-05-05
;; NUMBER OF SEQ ID NOS: 25
;; SEQ ID NO 11
;; LENGTH: 17
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;; ORGANISM: Mus musculus
US-11-120-338-11

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Best Local Similarity 81.2%; Pred. No. 1e-05; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 3;

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Db 2 IYPGNDISYNQKFXG 17

RESULT 5
US-11-106-820-11
; Sequence 11, Application US/11106820
; Publication No. US2006002330A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G.
; APPLICANT: SEWELL, KATHRYN L.
; TITLE OF INVENTION: Treatment of Disorders
; FILE REFERENCE: P2102R1
; CURRENT APPLICATION NUMBER: US/11/106,820
; PRIOR FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/563,227
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/565,098
; PRIOR FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 45
; SEQ ID NO 11
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-106-820-11

Query Match 80.9%; Score 72; DB 11; Length 17;
Best Local Similarity 81.2%; Pred. No. 1e-05; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 3;

Qy 2 IYPGNDISYNQKFXG 17
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Db 2 IYPGNDISYNQKFXG 17

RESULT 6
US-11-190-364-11
; Sequence 11, Application US/11190364
; Publication No. US20060024300A1
; GENERAL INFORMATION:
; APPLICANT: ADAMS ET AL.
; TITLE OF INVENTION: Immunoglobulin Variants and Uses Thereof
; FILE REFERENCE: P190R3C1
; CURRENT APPLICATION NUMBER: US/11/190,364
; PRIOR FILING DATE: 2005-07-26
; PRIOR APPLICATION NUMBER: US 60/434,115
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: US 60/526,163
; PRIOR FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: PCT/US03/40426
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: US 11/147,780
; PRIOR FILING DATE: 2005-06-07
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 11
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-190-364-11

Query Match 80.9%; Score 72; DB 11; Length 17;
Best Local Similarity 81.2%; Pred. No. 1e-05; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 3;

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Db 2 IYPGNDISYNQKFXG 17

RESULT 7
US-11-147-780-11
; Sequence 11, Application US/11147780
; Publication No. US20060034835A1
; GENERAL INFORMATION:
; APPLICANT: ADAMS ET AL.
; TITLE OF INVENTION: Immunoglobulin Variants and Uses Thereof
; FILE REFERENCE: P190R3C1
; CURRENT APPLICATION NUMBER: US/11/147,780
; PRIOR FILING DATE: 2005-06-07
; PRIOR APPLICATION NUMBER: US 60/434,115
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: US 60/526,163
; PRIOR FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: PCT/US03/40426
; PRIOR FILING DATE: 2003-12-16
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; ORGANISM: Mus musculus
US-11-147-780-11

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Best Local Similarity 81.2%; Pred. No. 1e-05; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 3;

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Db 2 IYPGNDISYNQKFXG 17

RESULT 8
US-11-143-386-11
; Sequence 11, Application US/11143386
; Publication No. US20060051345A1
; GENERAL INFORMATION:
; APPLICANT: FROHNA, PAUL A.
; TITLE OF INVENTION: METHOD FOR TREATING MULTIPLE SCLEROSIS
; FILE REFERENCE: P2134R1
; CURRENT APPLICATION NUMBER: US/11/143,386
; PRIOR FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US 60/576,993
; PRIOR FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 11
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-143-386-11

Query Match 80.9%; Score 72; DB 11; Length 17;
Best Local Similarity 81.2%; Pred. No. 1e-05; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 3;

Qy 2 IYPGNDISYNQKFXG 17
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Db 2 IYPGNDISYNQKFXG 17

RESULT 9
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; Sequence 10, Application US/11143077

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; Publication No. US20060024295A1
; GENERAL INFORMATION:
; APPLICANT: Brunetta, Paul G.
; TITLE OF INVENTION: METHOD FOR TREATING LUPUS
; FILE REFERENCE: P2133R1
; CURRENT APPLICATION NUMBER: US/11/143,077
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US 60/577,235
; PRIOR FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 60/617,997
; PRIOR FILING DATE: 2004-10-11
; NUMBER OF SEQ ID NOS: 24
; SEQ ID NO 10
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-11-143-077-10

Query Match      80.9%; Score 72; DB 11; Length 40;
Best Local Similarity 81.2%; Pred. No. 2.5e-05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 IYPGNDISYNOKFXG 17
Db      12 IYPGNGDTSYNOKFKG 27

RESULT 10
US-11-143-077-11
; Sequence 11, Application US/11143077
; Publication No. US20060024295A1
; GENERAL INFORMATION:
; APPLICANT: Brunetta, Paul G.
; TITLE OF INVENTION: METHOD FOR TREATING LUPUS
; FILE REFERENCE: P2133R1
; CURRENT APPLICATION NUMBER: US/11/143,077
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US 60/577,235
; PRIOR FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 60/617,997
; PRIOR FILING DATE: 2004-10-11
; NUMBER OF SEQ ID NOS: 24
; SEQ ID NO 11
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-11-143-077-11

Query Match      80.9%; Score 72; DB 11; Length 40;
Best Local Similarity 81.2%; Pred. No. 2.5e-05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 IYPGNDISYNOKFXG 17
Db      12 IYPGNGDTSYNOKFKG 27

RESULT 11
US-11-187-364-10
; Sequence 10, Application US/11187364
; Publication No. US20060062787A1
; GENERAL INFORMATION:
; APPLICANT: Hitrava, Elena
; TITLE OF INVENTION: METHOD FOR TREATING SJOGREN'S SYNDROME
; FILE REFERENCE: P2149R1
; CURRENT APPLICATION NUMBER: US/11/187,364
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US 60/590,302
; PRIOR FILING DATE: 2004-07-22
```

```
; NUMBER OF SEQ ID NOS: 36
; SEQ ID NO 10
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-11-187-364-10

Query Match      80.9%; Score 72; DB 11; Length 40;
Best Local Similarity 81.2%; Pred. No. 2.5e-05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 IYPGNDISYNOKFXG 17
Db      12 IYPGNGDTSYNOKFKG 27

RESULT 12
US-11-187-364-11
; Sequence 11, Application US/11187364
; Publication No. US20060062787A1
; GENERAL INFORMATION:
; APPLICANT: Hitrava, Elena
; TITLE OF INVENTION: METHOD FOR TREATING SJOGREN'S SYNDROME
; FILE REFERENCE: P2149R1
; CURRENT APPLICATION NUMBER: US/11/187,364
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US 60/590,302
; PRIOR FILING DATE: 2004-07-22
; NUMBER OF SEQ ID NOS: 36
; SEQ ID NO 11
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-11-187-364-11

Query Match      80.9%; Score 72; DB 11; Length 40;
Best Local Similarity 81.2%; Pred. No. 2.5e-05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 IYPGNDISYNOKFXG 17
Db      12 IYPGNGDTSYNOKFKG 27

RESULT 13
US-11-107-028-27
; Sequence 27, Application US/11107028
; Publication No. US20050276803A1
; GENERAL INFORMATION:
; APPLICANT: CHAN, ANDREW C.
; APPLICANT: GONG, QIAN
; APPLICANT: MARTIN, FLAVIUS
; TITLE OF INVENTION: Method for Augmenting B Cell Depletion
; FILE REFERENCE: P2112R1
; CURRENT APPLICATION NUMBER: US/11/107,028
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/563,263
; PRIOR FILING DATE: 2004-04-16
; NUMBER OF SEQ ID NOS: 52
; SEQ ID NO 27
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Mus musculus
; OTHER INFORMATION:
US-11-107-028-27

Query Match      80.9%; Score 72; DB 11; Length 121;
Best Local Similarity 81.2%; Pred. No. 7.7e-05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```


QY 2 IYPGNDISYNOKFXG 17
| | | | | | | | | |
Db 51 IYPGNDISYNOKFXG 66

RESULT 14
US-11-107-028-35
; Sequence 35, Application US/11107028
; Publication No. US20050276803A1
; GENERAL INFORMATION:
; APPLICANT: CHAN, ANDREW C.
; APPLICANT: GONG, QIAN
; APPLICANT: MARTIN, FLAVIUS
; TITLE OF INVENTION: Method for Augmenting B Cell Depletion
; FILE REFERENCE: P2112R1
; CURRENT APPLICATION NUMBER: US/11/107,028
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/563,263
; PRIOR FILING DATE: 2004-04-16
; NUMBER OF SEQ ID NOS: 52
; SEQ ID NO 35
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-107-028-35

Query Match 80.9%; Score 72; DB 11; Length 121;
Best Local Similarity 81.2%; Pred. No. 7.7e-05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGNDISYNOKFXG 17
| | | | | | | | | |
Db 51 IYPGNDISYNOKFXG 66

RESULT 15
US-11-107-028-37
; Sequence 37, Application US/11107028
; Publication No. US20050276803A1
; GENERAL INFORMATION:
; APPLICANT: CHAN, ANDREW C.
; APPLICANT: GONG, QIAN
; APPLICANT: MARTIN, FLAVIUS
; TITLE OF INVENTION: Method for Augmenting B Cell Depletion
; FILE REFERENCE: P2112R1
; CURRENT APPLICATION NUMBER: US/11/107,028
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/563,263
; PRIOR FILING DATE: 2004-04-16
; NUMBER OF SEQ ID NOS: 52
; SEQ ID NO 37
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-107-028-37

Query Match 80.9%; Score 72; DB 11; Length 121;
Best Local Similarity 81.2%; Pred. No. 7.7e-05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGNDISYNOKFXG 17
| | | | | | | | | |
Db 51 IYPGNDISYNOKFXG 66

RESULT 16
US-11-107-028-38
; Sequence 38, Application US/11107028
; Publication No. US20050276803A1

; GENERAL INFORMATION:
; APPLICANT: CHAN, ANDREW C.
; APPLICANT: GONG, QIAN
; APPLICANT: MARTIN, FLAVIUS
; TITLE OF INVENTION: Method for Augmenting B Cell Depletion
; FILE REFERENCE: P2112R1
; CURRENT APPLICATION NUMBER: US/11/107,028
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/563,263
; PRIOR FILING DATE: 2004-04-16
; NUMBER OF SEQ ID NOS: 52
; SEQ ID NO 38
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-107-028-38

Query Match 80.9%; Score 72; DB 11; Length 121;
Best Local Similarity 81.2%; Pred. No. 7.7e-05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGNDISYNOKFXG 17
| | | | | | | | | |
Db 51 IYPGNDISYNOKFXG 66

RESULT 17
US-11-254-182-28
; Sequence 28, Application US/11254182
; Publication No. US20060088523A1
; GENERAL INFORMATION:
; APPLICANT: ANDYA, JAMES
; APPLICANT: GWE, SHIANG C.
; APPLICANT: LIU, JUN
; APPLICANT: SHEN, YE
; TITLE OF INVENTION: ANTIBODY FORMULATIONS
; FILE REFERENCE: P2104R1
; CURRENT APPLICATION NUMBER: US/11/254,182
; CURRENT FILING DATE: 2005-10-19
; PRIOR APPLICATION NUMBER: US 60/620,413
; PRIOR FILING DATE: 2004-10-20
; NUMBER OF SEQ ID NOS: 74
; SEQ ID NO 28
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-254-182-28

Query Match 80.9%; Score 72; DB 10; Length 122;
Best Local Similarity 81.2%; Pred. No. 7.8e-05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGNDISYNOKFXG 17
| | | | | | | | | |
Db 51 IYPGNDISYNOKFXG 66

RESULT 18
US-11-254-182-29
; Sequence 29, Application US/11254182
; Publication No. US20060088523A1
; GENERAL INFORMATION:
; APPLICANT: ANDYA, JAMES
; APPLICANT: GWE, SHIANG C.
; APPLICANT: LIU, JUN
; APPLICANT: SHEN, YE
; TITLE OF INVENTION: ANTIBODY FORMULATIONS
; FILE REFERENCE: P2104R1
; CURRENT APPLICATION NUMBER: US/11/254,182
; CURRENT FILING DATE: 2005-10-19
; PRIOR APPLICATION NUMBER: US 60/620,413

PRIOR FILING DATE: 2004-10-20
; NUMBER OF SEQ ID NOS: 74
; SEQ ID NO 29
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-254-182-29

Query Match 80.9%; Score 72; DB 10; Length 122;
Best Local Similarity 81.2%; Pred. No. 7.8e-05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IYPGNDISYNOKFXG 17
Db 51 IYPGNGDTSYNOKFXG 66

RESULT 19
US-11-120-338-7
; Sequence 7, Application US/11120338
; Publication No. US20050271658A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G.
; APPLICANT: GREWAL, IOBAL S.
; APPLICANT: MALICKE, PATRICIA A.
; TITLE OF INVENTION: PREVENTING AUTOIMMUNE DISEASE
; FILE REFERENCE: P2079R2
; CURRENT APPLICATION NUMBER: US/11/120,338
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: US 60/568,460
; PRIOR FILING DATE: 2004-05-05
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 7
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-120-338-7

Query Match 80.9%; Score 72; DB 11; Length 122;
Best Local Similarity 81.2%; Pred. No. 7.8e-05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IYPGNDISYNOKFXG 17
Db 51 IYPGNGDTSYNOKFXG 66

RESULT 20
US-11-120-338-8
; Sequence 8, Application US/11120338
; Publication No. US20050271658A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G.
; APPLICANT: GREWAL, IOBAL S.
; APPLICANT: MALICKE, PATRICIA A.
; TITLE OF INVENTION: PREVENTING AUTOIMMUNE DISEASE
; FILE REFERENCE: P2079R2
; CURRENT APPLICATION NUMBER: US/11/120,338
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: US 60/568,460
; PRIOR FILING DATE: 2004-05-05
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 8
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-120-338-8

Query Match 80.9%; Score 72; DB 11; Length 122;

Best Local Similarity 81.2%; Pred. No. 7.8e-05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IYPGNDISYNOKFXG 17
Db 51 IYPGNGDTSYNOKFXG 66

RESULT 21
US-11-107-028-30
; Sequence 30, Application US/11107028
; Publication No. US20050276803A1
; GENERAL INFORMATION:
; APPLICANT: GONG, QIAN
; APPLICANT: CHAN, ANDREW C.
; APPLICANT: MARTIN, FLAVIUS
; TITLE OF INVENTION: Method for Augmenting B Cell Depletion
; FILE REFERENCE: P2112R1
; CURRENT APPLICATION NUMBER: US/11/107,028
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/563,263
; PRIOR FILING DATE: 2004-04-16
; NUMBER OF SEQ ID NOS: 52
; SEQ ID NO 30
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-107-028-30

Query Match 80.9%; Score 72; DB 11; Length 122;
Best Local Similarity 81.2%; Pred. No. 7.8e-05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IYPGNDISYNOKFXG 17
Db 51 IYPGNGDTSYNOKFXG 66

RESULT 22
US-11-107-028-39
; Sequence 39, Application US/11107028
; Publication No. US20050276803A1
; GENERAL INFORMATION:
; APPLICANT: GONG, QIAN
; APPLICANT: CHAN, ANDREW C.
; APPLICANT: MARTIN, FLAVIUS
; TITLE OF INVENTION: Method for Augmenting B Cell Depletion
; FILE REFERENCE: P2112R1
; CURRENT APPLICATION NUMBER: US/11/107,028
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/563,263
; PRIOR FILING DATE: 2004-04-16
; NUMBER OF SEQ ID NOS: 52
; SEQ ID NO 39
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-107-028-39

Query Match 80.9%; Score 72; DB 11; Length 122;
Best Local Similarity 81.2%; Pred. No. 7.8e-05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IYPGNDISYNOKFXG 17
Db 51 IYPGNGDTSYNOKFXG 66

RESULT 23

US-11-107-028-41
; Sequence 41, Application US/11107028
; Publication No. US20050276803A1
; GENERAL INFORMATION:
; APPLICANT: CHAN, ANDREW C.
; APPLICANT: GONG, QIAN
; APPLICANT: MARTIN, FLAVIUS
; TITLE OF INVENTION: Method for Augmenting B Cell Depletion
; FILE REFERENCE: P2112R1
; CURRENT APPLICATION NUMBER: US/11/107,028
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/563,263
; PRIOR FILING DATE: 2004-04-16
; NUMBER OF SEQ ID NOS: 52
; SEQ ID NO 41
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-107-028-41

Query Match 80.9%; Score 72; DB 11; Length 122;
Best Local Similarity 81.2%; Pred. No. 7.8e-05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGNDISYNQKFXG 17
| | | | | | | | | | | | | | | | | | | | | |
Db 51 IYPGNGDTSYNQKFXG 66

RESULT 24
US-11-106-820-7
; Sequence 7, Application US/11106820
; Publication No. US2006002930A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G.
; APPLICANT: SEWELL, KATHRYN L.
; TITLE OF INVENTION: Treatment of Disorders
; FILE REFERENCE: P2102R1
; CURRENT APPLICATION NUMBER: US/11/106,820
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/563,227
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/565,098
; PRIOR FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 45
; SEQ ID NO 7
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-106-820-7

Query Match 80.9%; Score 72; DB 11; Length 122;
Best Local Similarity 81.2%; Pred. No. 7.8e-05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGNDISYNQKFXG 17
| | | | | | | | | | | | | | | | | | | | | |
Db 51 IYPGNGDTSYNQKFXG 66

RESULT 25
US-11-106-820-8
; Sequence 8, Application US/11106820
; Publication No. US2006002930A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G.
; APPLICANT: SEWELL, KATHRYN L.
; TITLE OF INVENTION: Treatment of Disorders
; FILE REFERENCE: P2102R1
; CURRENT APPLICATION NUMBER: US/11/106,820
; CURRENT FILING DATE: 2005-04-15

; PRIOR APPLICATION NUMBER: US 60/563,227
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/565,098
; PRIOR FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 45
; SEQ ID NO 8
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-106-820-8

Query Match 80.9%; Score 72; DB 11; Length 122;
Best Local Similarity 81.2%; Pred. No. 7.8e-05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGNDISYNQKFXG 17
| | | | | | | | | | | | | | | | | | | | | |
Db 51 IYPGNGDTSYNQKFXG 66

RESULT 26
US-11-143-077-7
; Sequence 7, Application US/11143077
; Publication No. US20060024295A1
; GENERAL INFORMATION:
; APPLICANT: Brunetta, Paul G.
; TITLE OF INVENTION: METHOD FOR TREATING LUPUS
; FILE REFERENCE: P2133R1
; CURRENT APPLICATION NUMBER: US/11/143,077
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US 60/577,235
; PRIOR FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 60/617,997
; PRIOR FILING DATE: 2004-10-11
; NUMBER OF SEQ ID NOS: 24
; SEQ ID NO 7
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-143-077-7

Query Match 80.9%; Score 72; DB 11; Length 122;
Best Local Similarity 81.2%; Pred. No. 7.8e-05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGNDISYNQKFXG 17
| | | | | | | | | | | | | | | | | | | | | |
Db 51 IYPGNGDTSYNQKFXG 66

RESULT 27
US-11-143-077-8
; Sequence 8, Application US/11143077
; Publication No. US20060024295A1
; GENERAL INFORMATION:
; APPLICANT: Brunetta, Paul G.
; TITLE OF INVENTION: METHOD FOR TREATING LUPUS
; FILE REFERENCE: P2133R1
; CURRENT APPLICATION NUMBER: US/11/143,077
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US 60/577,235
; PRIOR FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 60/617,997
; PRIOR FILING DATE: 2004-10-11
; NUMBER OF SEQ ID NOS: 24
; SEQ ID NO 8
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized

US-11-143-077-8

Query Match	80.9%	Score 72;	DB 11;	Length 122;
Best Local Similarity	81.2%	Pred. No. 7.8e-05;		
Matches 13; Conservative		0; Mismatches 3; Indels		

QY 2 IYPGNDDISYNQKFXG 17
||||| | ||||| |
Db 51 IYPGNGDTSYNQKFXG 66

RESULT 28

```

US-11-190-364-7
? Sequence 7, Application US/11190364
? Publication No. US20060024300A1
? GENERAL INFORMATION:
? APPLICANT: Adams ET AL.
? TITLE OF INVENTION: Immunoglobulin Variants and Uses Thereof
? FILE REFERENCE: P1950R3C1P1
? CURRENT APPLICATION NUMBER: US/11/190,364
? CURRENT FILING DATE: 2005-07-26
? PRIOR APPLICATION NUMBER: US 60/434,115
? PRIOR FILING DATE: 2002-12-16
? PRIOR APPLICATION NUMBER: US 60/526,153
? PRIOR FILING DATE: 2003-12-01
? PRIOR APPLICATION NUMBER: PCT/US03/40426
? PRIOR FILING DATE: 2003-12-16
? PRIOR APPLICATION NUMBER: US 11/147,780
? PRIOR FILING DATE: 2005-06-07
? NUMBER OF SEQ ID NOS: 38
? SEQ ID NO 7
? LENGTH: 122
? TYPE: PRT
? ORGANISM: Mus musculus
US-11-190-364-7

```

Query Match	80.9%	Score 72;	DB 11;	Length 122;
Best Local Similarity	81.2%	Pred. No. 7.8e-05;		
Matches 13; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

QY 2 IYPGNDDISYNQKFXG 17
||| ||| ||| ||| |||
Db 51 IYPGNGDTSYNQKFXG 66

RESULT 29
US-11-190

```

; Sequence 8, Application US/11190364
; Publication No. US20060024300A1
; GENERAL INFORMATION:
; APPLICANT: Adams ET AL.
; TITLE OF INVENTION: Immunoglobulin Variants and Uses thereof
; FILE REFERENCE: P1990R3C1P1
; CURRENT APPLICATION NUMBER: US/11/190,364
; CURRENT FILING DATE: 2005-07-26
; PRIOR APPLICATION NUMBER: US 60/434,115
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: US 60/526,163
; PRIOR FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: PCT/US03/40426
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: US 11/147,780
; PRIOR FILING DATE: 2005-06-07
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 8
; LENGTH: 122
; TYPE: prt
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-11-190-364-8

```

Query Match	80.9%; Score 72; DB 11; Length 122;
-------------	-------------------------------------

Best Local Similarity 81.2%; Pred. No. 7.8e-05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGNDISYNQKFXG 17
||| | ||| |
Db 51 IYPGNGDTSYNQKFXG 66

RESULT 30

```

US-11-147-780-7
Sequence 7, Application US/11147780
Publication No. US20060034835A1
GENERAL INFORMATION:
APPLICANT: Adams ET AL.
TITLE OF INVENTION: Immunoglobulin Variants and Uses Thereof
FILE REFERENCE: P1990R3C1
CURRENT APPLICATION NUMBER: US/11/147,780
CURRENT FILING DATE: 2005-06-07
PRIOR APPLICATION NUMBER: US 60/434,115
PRIOR FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: US 60/526,163
PRIOR FILING DATE: 2003-12-01
PRIOR APPLICATION NUMBER: PCT/US03/40426
PRIOR FILING DATE: 2003-12-16
NUMBER OF SEQ ID NOS: 38
SEQ ID NO 7
LENGTH: 122
TYPE: PRT
ORGANISM: Mus musculus
US-11-147-780-7

```

Query Match	80.9%	Score 72;	DB 11;	Length 122;
Best Local Similarity	81.2%	Pred. No. 7.8e-05;		
Matches 13; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

QY 2 IYPGNDISYNQKFXG 17
||| | ||| |
Db 51 IYPGNGDTSYNQKFKG 66

RESULT 31
US-11-147

```

? Sequence 8, Application US/11147780
? Publication No. US2006003483A1
?
? GENERAL INFORMATION:
?   APPLICANT: Adams ET AL.
?   TITLE OF INVENTION: Immunoglobulin Variants and Uses Thereof
?   FILE REFERENCE: P1990R3C1
?   CURRENT APPLICATION NUMBER: US/11/147,780
?   CURRENT FILING DATE: 2005-06-07
?   PRIOR APPLICATION NUMBER: US 60/434,115
?   PRIOR FILING DATE: 2002-12-16
?   PRIOR APPLICATION NUMBER: US 60/526,163
?   PRIOR FILING DATE: 2003-12-01
?   PRIOR APPLICATION NUMBER: PCT/US03/40426
?   PRIOR FILING DATE: 2003-12-16
?   NUMBER OF SEQ ID NOS: 38
?
? SEQ ID NO 8
?   LENGTH: 122
?   TYPE: PRT
?   ORGANISM: Artificial sequence
?   FEATURE:
?     OTHER INFORMATION: Sequence is synthesized
US-11-147-780-8

```

Query Match	80.9%;	Score 72;	DB 11;	Length 122;
Best Local Similarity	81.2%;	Pred. No. 7.8e-05;		
Matches 13;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0

QY	2	IYPGNDDISYNQKFXG	17
Db	51	IYPGNGDTSYNQKFXG	66

RESULT 32
US-11-143-386-7
; Sequence 7, Application US/11143386
; Publication No. US20060051345A1
; GENERAL INFORMATION:
; APPLICANT: FROHNA, PAUL A.
; TITLE OF INVENTION: METHOD FOR TREATING MULTIPLE SCLEROSIS
; FILE REFERENCE: P2134R1
; CURRENT APPLICATION NUMBER: US/11/143,386
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US 60/576,993
; PRIOR FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 7
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-143-386-7

Query Match 80.9%; Score 72; DB 11; Length 122;
Best Local Similarity 81.2%; Pred. No. 7.8e-05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGNDISYNQKFXG 17
|||||
DB 51 IYPGNGDTSYNQKFXG 66

RESULT 33
US-11-143-386-8
; Sequence 8, Application US/11143386
; Publication No. US20060051345A1
; GENERAL INFORMATION:
; APPLICANT: FROHNA, PAUL A.
; TITLE OF INVENTION: METHOD FOR TREATING MULTIPLE SCLEROSIS
; FILE REFERENCE: P2134R1
; CURRENT APPLICATION NUMBER: US/11/143,386
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US 60/576,993
; PRIOR FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 8
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized.
US-11-143-386-8

Query Match 80.9%; Score 72; DB 11; Length 122;
Best Local Similarity 81.2%; Pred. No. 7.8e-05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGNDISYNQKFXG 17
|||||
DB 51 IYPGNGDTSYNQKFXG 66

RESULT 34
US-11-187-364-7
; Sequence 7, Application US/11187364
; Publication No. US20060062787A1
; GENERAL INFORMATION:
; APPLICANT: Hiltaya, Elena
; TITLE OF INVENTION: METHOD FOR TREATING SJOGREN'S SYNDROME
; FILE REFERENCE: P2149R1
; CURRENT APPLICATION NUMBER: US/11/187,364
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US 60/590,302
; PRIOR FILING DATE: 2004-07-22
; NUMBER OF SEQ ID NOS: 36
; SEQ ID NO 7

; LENGTH: 122
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-187-364-7

Query Match 80.9%; Score 72; DB 11; Length 122;
Best Local Similarity 81.2%; Pred. No. 7.8e-05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGNDISYNQKFXG 17
|||||
DB 51 IYPGNGDTSYNQKFXG 66

RESULT 35
US-11-187-364-8
; Sequence 8, Application US/11187364
; Publication No. US20060062787A1
; GENERAL INFORMATION:
; APPLICANT: Hiltaya, Elena
; TITLE OF INVENTION: METHOD FOR TREATING SJOGREN'S SYNDROME
; FILE REFERENCE: P2149R1
; CURRENT APPLICATION NUMBER: US/11/187,364
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US 60/590,302
; PRIOR FILING DATE: 2004-07-22
; NUMBER OF SEQ ID NOS: 36
; SEQ ID NO 8
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-11-187-364-8

Query Match 80.9%; Score 72; DB 11; Length 122;
Best Local Similarity 81.2%; Pred. No. 7.8e-05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGNDISYNQKFXG 17
|||||
DB 51 IYPGNGDTSYNQKFXG 66

RESULT 36
US-11-208-422-2
; Sequence 2, Application US/11208422
; Publication No. US20060067930A1
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia W.
; APPLICANT: Liem, Samantha
; APPLICANT: Lowman, Henry B.
; APPLICANT: Marvin, Jonathan S.
; APPLICANT: Meng, Yu-Ju G.
; TITLE OF INVENTION: POLYPEPTIDE VARIANTS WITH ALTERED EFFECTOR FUNCTION
; FILE REFERENCE: P2158R1
; CURRENT APPLICATION NUMBER: US/11/208,422
; CURRENT FILING DATE: 2005-08-19
; PRIOR APPLICATION NUMBER: US 60/603,057
; PRIOR FILING DATE: 2004-08-19
; NUMBER OF SEQ ID NOS: 54
; SEQ ID NO 2
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-11-208-422-2

Query Match 80.9%; Score 72; DB 11; Length 122;
Best Local Similarity 81.2%; Pred. No. 7.8e-05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 IYPGNDISYNQKFXG 17
|||||
Db 51 IYPGNDISTYNQKFXG 66

RESULT 37

US-11-183-218-62
; Sequence 62, Application US/11183218
; Publication NO. US20060088906A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bove, Caryne
; TITLE OF INVENTION: ERYTHROPOIETIN: REMODELING AND
; TITLE OF INVENTION: GLYCOCONJUGATION OF ERYTHROPOIETIN
; FILE REFERENCE: 040853-01-5083-US02
; CURRENT APPLICATION NUMBER: US/11/183,218
; CURRENT FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: US 10/410,945
; PRIOR FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: PCT/US02/32263
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US 60/334,301
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 60/334,233
; PRIOR FILING DATE: 2001-11-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.12
; SEQ ID NO 62
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-183-218-62

Query Match 80.9%; Score 72; DB 10; Length 140;

Best Local Similarity 81.2%; Pred. No. 9e-05; 3; Indels 0; Gaps 0;

OY 2 IYPGNDISYNQKFXG 17
|||||
Db 70 IYPGNDISTYNQKFXG 85

RESULT 38

US-11-183-205-62
; Sequence 62, Application US/11183205
; Publication NO. US20060030521A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, Caryn
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; TITLE OF INVENTION: REMODELING AND GLYCOCONJUGATION OF PEPTIDES

FILE REFERENCE: 040853-01-5052-US01
; CURRENT APPLICATION NUMBER: US/11/183,205
; CURRENT FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: US 11/183,205
; PRIOR FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: US 60/334,233
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 60/334,301
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: PCT/US2002/032263
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US 10/287,994
; PRIOR FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-183-205-62

Query Match 80.9%; Score 72; DB 11; Length 140;
Best Local Similarity 81.2%; Pred. No. 9e-05; 3; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 3;

OY 2 IYPGNDISYNQKFXG 17
|||||
Db 70 IYPGNDISTYNQKFXG 85

RESULT 39
US-11-106-820-20
; Sequence 20, Application US/11106820
; Publication No. US2006002930A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G.
; APPLICANT: SEWELL, KATHRYN L.
; TITLE OF INVENTION: Treatment of Disorders
; FILE REFERENCE: P2102R1
; CURRENT APPLICATION NUMBER: US/11/106,820
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/563,227
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/565,098
; PRIOR FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 45
; SEQ ID NO 20
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-106-820-20

Query Match 80.9%; Score 72; DB 11; Length 253;
Best Local Similarity 81.2%; Pred. No. 0.00017; 3; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 3;

OY 2 IYPGNDISYNQKFXG 17
|||||
Db 74 IYPGNDISTYNQKFXG 89

RESULT 40
US-11-190-364-18
; Sequence 18, Application US/11190364
; Publication No. US20060024300A1
; GENERAL INFORMATION:
; APPLICANT: Adams ET AL.
; TITLE OF INVENTION: Immunoglobulin Variants and Uses Thereof
; FILE REFERENCE: P1990R3C1P1
; CURRENT APPLICATION NUMBER: US/11/190,364
; CURRENT FILING DATE: 2005-07-26
; PRIOR APPLICATION NUMBER: US 60/434,115
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: US 60/526,163
; PRIOR FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: PCT/US03/40426
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: US 11/147,780
; PRIOR FILING DATE: 2005-06-07
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 18
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is chimeric
US-11-190-364-18

Query Match 80.9%; Score 72; DB 11; Length 253;
Best Local Similarity 81.2%; Pred. No. 0.00017;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IYPGNDISYNOKFXG 17
Db 74 IYPGNGDTSYNOKFXG 89

RESULT 41
US-11-147-780-18
; Sequence 18, Application US/11147780
; Publication No. US20060034835A1
; GENERAL INFORMATION:
; APPLICANT: Adams ET AL.
; TITLE OF INVENTION: Immunoglobulin Variants and Uses Thereof
; FILE REFERENCE: P1990R3C1
; CURRENT APPLICATION NUMBER: US/11/147,780
; CURRENT FILING DATE: 2005-06-07
; PRIOR APPLICATION NUMBER: US 60/434,115
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: US 60/526,163
; PRIOR FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: PCT/US03/40426
; PRIOR FILING DATE: 2003-12-16
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 18
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is chimeric
US-11-147-780-18

Query Match 80.9%; Score 72; DB 11; Length 253;
Best Local Similarity 81.2%; Pred. No. 0.00017;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IYPGNDISYNOKFXG 17
Db 74 IYPGNGDTSYNOKFXG 89

RESULT 42
US-11-254-182-71
; Sequence 71, Application US/11254182

; Publication No. US20060086523A1
; GENERAL INFORMATION:
; APPLICANT: ANDYA, JAMES
; APPLICANT: GWEE, SHIANG C.
; APPLICANT: LIU, JUN
; APPLICANT: SHEN, YE
; TITLE OF INVENTION: ANTIBODY FORMULATIONS
; FILE REFERENCE: P2104R1
; CURRENT APPLICATION NUMBER: US/11/254,182
; CURRENT FILING DATE: 2005-10-19
; PRIOR APPLICATION NUMBER: US 60/620,413
; PRIOR FILING DATE: 2004-10-20
; NUMBER OF SEQ ID NOS: 74
; SEQ ID NO 71
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized.
US-11-254-182-71

Query Match 80.9%; Score 72; DB 10; Length 451;
Best Local Similarity 81.2%; Pred. No. 0.0003;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IYPGNDISYNOKFXG 17
Db 51 IYPGNGDTSYNOKFXG 66

RESULT 43
US-11-120-338-22
; Sequence 22, Application US/11120338
; Publication No. US20050271658A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G.
; APPLICANT: GREWAL, IOBAL S.
; APPLICANT: WALICKE, PATRICIA A.
; TITLE OF INVENTION: PREVENTING AUTOIMMUNE DISEASE
; FILE REFERENCE: P2079R2
; CURRENT APPLICATION NUMBER: US/11/120,338
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: US 60/568,460
; PRIOR FILING DATE: 2004-05-05
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 22
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-120-338-22

Query Match 80.9%; Score 72; DB 11; Length 451;
Best Local Similarity 81.2%; Pred. No. 0.0003;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IYPGNDISYNOKFXG 17
Db 51 IYPGNGDTSYNOKFXG 66

RESULT 44
US-11-124-620-5
; Sequence 5, Application US/11124620
; Publication No. US20060024298A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; APPLICANT: Dang, Wei
; APPLICANT: Desjarlais, John R.
; APPLICANT: Karki, Sher Bahadur
; APPLICANT: Vafa, Omid
; APPLICANT: Hayes, Robert

TITLE OF INVENTION: OPTIMIZED FC VARIANTS
FILE REFERENCE: A-71386-9
CURRENT APPLICATION NUMBER: US/11/124,620
CURRENT FILING DATE: 2005-05-05
PRIOR APPLICATION NUMBER: US 60/568,440
PRIOR FILING DATE: 2004-07-15
PRIOR APPLICATION NUMBER: US 60/589,906
PRIOR FILING DATE: 2004-07-20
PRIOR APPLICATION NUMBER: US 60/627,026
PRIOR FILING DATE: 2004-11-09
PRIOR APPLICATION NUMBER: US 60/626,991
PRIOR FILING DATE: 2004-11-10
PRIOR APPLICATION NUMBER: US 60/627,774
PRIOR FILING DATE: 2004-11-12
PRIOR APPLICATION NUMBER: US 10/822,231
PRIOR FILING DATE: 2004-03-26
PRIOR APPLICATION NUMBER: US 10/672,280
PRIOR FILING DATE: 2003-09-26
PRIOR APPLICATION NUMBER: US 10/379,392
PRIOR FILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.3
SEQ ID NO 5
LENGTH: 451
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Synthetic
NAME/KEY: misc feature
LOCATION: (243)..(243)
OTHER INFORMATION: Xaa can be Serine, Aspartic Acid, Glutamic Acid, Asparagine,
OTHER INFORMATION: Glutamine or Threonine
FEATURE:
NAME/KEY: misc feature
LOCATION: (244)..(244)
OTHER INFORMATION: Xaa can be Valine, Isoleucine or Methionine
FEATURE:
NAME/KEY: misc feature
LOCATION: (268)..(268)
OTHER INFORMATION: Xaa can be Valine, Isoleucine, Threonine or Tyrosine
FEATURE:
NAME/KEY: misc feature
LOCATION: (272)..(272)
OTHER INFORMATION: Xaa can be Histidine, Aspartic Acid or Glutamic Acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (276)..(276)
OTHER INFORMATION: Xaa can be Glutamic Acid or Tyrosine
FEATURE:
NAME/KEY: misc feature
LOCATION: (278)..(278)
OTHER INFORMATION: Xaa can be Lysine or Glutamic Acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (301)..(301)
OTHER INFORMATION: Xaa can be Asparagine or Aspartic Acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (302)..(302)
OTHER INFORMATION: Xaa can be Serine, Alanine or Aspartic Acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (330)..(330)
OTHER INFORMATION: Xaa can be Lysine, Glutamic Acid or Threonine
FEATURE:
NAME/KEY: misc feature
LOCATION: (334)..(334)
OTHER INFORMATION: Xaa can be Alanine, Tyrosine, Leucine or Isoleucine
FEATURE:
NAME/KEY: misc feature
LOCATION: (336)..(336)
OTHER INFORMATION: Xaa can be Isoleucine, Aspartic Acid, Glutamic Acid, Asparagine

OTHER INFORMATION: or Glutamine
US-11-124-620-5
Query Match 80.9%; Score 72; DB 11; Length 451;
Best Local Similarity 81.2%; Pred. No. 0.0003;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 2 IYPGNDISYNOKFXG 17
Db 51 IYPGNDISYNOKFXG 66
RESULT 45
US-11-124-620-7
Sequence 7, Application US/11/124,620
Publication No. US20060024296A1
GENERAL INFORMATION:
APPLICANT: Lazar, Gregory Alan
APPLICANT: Dang, Wei
APPLICANT: Desjarlais, John R.
APPLICANT: Karki, Sher Bahadur
APPLICANT: Vata, Omid
APPLICANT: Hayes, Robert
TITLE OF INVENTION: OPTIMIZED FC VARIANTS
FILE REFERENCE: A-71386-9
CURRENT APPLICATION NUMBER: US/11/124,620
CURRENT FILING DATE: 2005-05-05
PRIOR APPLICATION NUMBER: US 60/568,440
PRIOR FILING DATE: 2004-07-15
PRIOR APPLICATION NUMBER: US 60/589,906
PRIOR FILING DATE: 2004-07-20
PRIOR APPLICATION NUMBER: US 60/627,026
PRIOR FILING DATE: 2004-11-09
PRIOR APPLICATION NUMBER: US 60/626,991
PRIOR FILING DATE: 2004-11-10
PRIOR APPLICATION NUMBER: US 60/627,774
PRIOR FILING DATE: 2004-11-12
PRIOR APPLICATION NUMBER: US 10/822,231
PRIOR FILING DATE: 2004-03-26
PRIOR APPLICATION NUMBER: US 10/672,280
PRIOR FILING DATE: 2003-09-26
PRIOR APPLICATION NUMBER: US 10/379,392
PRIOR FILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.3
SEQ ID NO 7
LENGTH: 451
TYPE: PRT
ORGANISM: Homo sapiens
US-11-124-620-7
Query Match 80.9%; Score 72; DB 11; Length 451;
Best Local Similarity 81.2%; Pred. No. 0.0003;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 2 IYPGNDISYNOKFXG 17
Db 51 IYPGNDISYNOKFXG 66
RESULT 46
US-11-143-386-22
Sequence 22, Application US/11/143,386
Publication No. US20060051345A1
GENERAL INFORMATION:
APPLICANT: FROHNA, PAUL A.
TITLE OF INVENTION: METHOD FOR TREATING MULTIPLE SCLEROSIS
FILE REFERENCE: P2134R1
CURRENT APPLICATION NUMBER: US/11/143,386
CURRENT FILING DATE: 2005-06-02
PRIOR APPLICATION NUMBER: US 60/576,993
PRIOR FILING DATE: 2004-06-04
NUMBER OF SEQ ID NOS: 25

SEQ ID NO 22
LENGTH: 451
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Sequence is synthesized.
US-11-143-386-22

Query Match 80.9%; Score 72; DB 11; Length 451;
Best Local Similarity 81.2%; Pred. No. 0.0003;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGNDISTYNQKFXG 17
|||||
Db 51 IYPGNGDTSTYNQKFXG 66

RESULT 47
US-11-208-422-25
Sequence 25, Application US/11208422
Publication No. US20060067930A1
GENERAL INFORMATION:
APPLICANT: Adams, Camellia W.
APPLICANT: Lien, Samantha
APPLICANT: Lowman, Henry B.
APPLICANT: Marvin, Jonathan S.
APPLICANT: Meng, Yu-Ju G.
TITLE OF INVENTION: POLYPEPTIDE VARIANTS WITH ALTERED EFFECTOR FUNCTION
FILE REFERENCE: P2158R1
CURRENT APPLICATION NUMBER: US/11/208,422
CURRENT FILING DATE: 2005-08-19
PRIOR APPLICATION NUMBER: US 60/603,057
PRIOR FILING DATE: 2004-08-19
NUMBER OF SEQ ID NOS: 54
SEQ ID NO 25
LENGTH: 451
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: sequence is synthesized
US-11-208-422-25

Query Match 80.9%; Score 72; DB 11; Length 451;
Best Local Similarity 81.2%; Pred. No. 0.0003;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGNDISTYNQKFXG 17
|||||
Db 51 IYPGNGDTSTYNQKFXG 66

RESULT 48
US-11-254-182-65
Sequence 65, Application US/11254182
Publication No. US20060088523A1
GENERAL INFORMATION:
APPLICANT: ANDYA, JAMES
APPLICANT: GWEI, SHIANG C.
APPLICANT: LIU, JUN
APPLICANT: SHEN, YE
TITLE OF INVENTION: ANTIBODY FORMULATIONS
FILE REFERENCE: P2104R1
CURRENT APPLICATION NUMBER: US/11/254,182
CURRENT FILING DATE: 2005-10-19
PRIOR APPLICATION NUMBER: US 60/620,413
PRIOR FILING DATE: 2004-10-20
NUMBER OF SEQ ID NOS: 74
SEQ ID NO 65
LENGTH: 452
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Sequence is synthesized.

US-11-254-182-65

Query Match 80.9%; Score 72; DB 10; Length 452;
Best Local Similarity 81.2%; Pred. No. 0.0003;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGNDISTYNQKFXG 17
|||||
Db 51 IYPGNGDTSTYNQKFXG 66

RESULT 49
US-11-120-338-14
Sequence 14, Application US/11120338
Publication No. US20050271658A1
GENERAL INFORMATION:
APPLICANT: BRUNETTA, PAUL G.
APPLICANT: GREWAL, IOBAL S.
APPLICANT: MALICK, PATRICIA A.
TITLE OF INVENTION: PREVENTING AUTOIMMUNE DISEASE
FILE REFERENCE: P2079R2
CURRENT APPLICATION NUMBER: US/11/120,338
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: US 60/568,460
PRIOR FILING DATE: 2004-05-05
NUMBER OF SEQ ID NOS: 25
SEQ ID NO 14
LENGTH: 452
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: sequence is synthesized
US-11-120-338-14

Query Match 80.9%; Score 72; DB 11; Length 452;
Best Local Similarity 81.2%; Pred. No. 0.0003;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGNDISTYNQKFXG 17
|||||
Db 51 IYPGNGDTSTYNQKFXG 66

RESULT 50
US-11-120-338-15
Sequence 15, Application US/11120338
Publication No. US20050271658A1
GENERAL INFORMATION:
APPLICANT: BRUNETTA, PAUL G.
APPLICANT: GREWAL, IOBAL S.
APPLICANT: MALICK, PATRICIA A.
TITLE OF INVENTION: PREVENTING AUTOIMMUNE DISEASE
FILE REFERENCE: P2079R2
CURRENT APPLICATION NUMBER: US/11/120,338
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: US 60/568,460
PRIOR FILING DATE: 2004-05-05
NUMBER OF SEQ ID NOS: 25
SEQ ID NO 15
LENGTH: 452
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: sequence is synthesized
US-11-120-338-15

Query Match 80.9%; Score 72; DB 11; Length 452;
Best Local Similarity 81.2%; Pred. No. 0.0003;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGNDISTYNQKFXG 17
|||||
Db 51 IYPGNGDTSTYNQKFXG 66

Search completed: May 4, 2006, 13:54:10
Job time : 24.6984 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 4, 2006, 12:46:10 ; Search time 80 Seconds
(without alignments)
49.430 Million cell updates/sec

Title: US-10-700-632-3

Perfect score: 46

Sequence: 1 EVRLRYPDV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

1: Genesep21:.*
2: Genesep21980s:.*
3: Genesep2000s:.*
4: Genesep2001s:.*
5: Genesep2002s:.*
6: Genesep2003as:.*
7: Genesep2003bs:.*
8: Genesep2004s:.*
9: Genesep2005s:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	46	100.0	9	8	AD032087 Mouse ant
2	46	100.0	20	8	AD032137 Mouse ant
3	46	100.0	117	8	AD032157 Mouse ant
4	46	100.0	118	8	AD032091 Mouse ant
5	46	100.0	118	8	AD032093 Humanised
6	38	82.6	306	9	ADX58064 A single
7	38	82.6	816	5	AB889783 Human pol
8	38	82.6	897	4	AAW93422 Human pro
9	38	82.6	897	4	ADL31011 Human pro
10	38	82.6	933	2	AAW26349 Human sec
11	38	82.6	933	3	AAW73400 Human sec
12	38	82.6	1152	3	AAW94920 Human sec
13	38	82.6	1217	6	AB052996 Human spl
14	38	82.6	1217	6	AB053071 Human put
15	38	82.6	1217	9	ADY91632 Human pro
16	38	82.6	1276	7	ADP60175 Human con
17	37	80.4	470	8	ADJ46275 Arabaena
18	36	78.3	358	8	ADN47011 Arabaena
19	35	76.1	13	8	ADP70132 Anti-Idio
20	35	76.1	59	6	AAE31554 Rice prot
21	35	76.1	96	5	ABU51223 Helicobac
22	35	76.1	143	3	AAW43855 Heavy cha
23	35	76.1	206	6	AAE31534 Rice prot
24	35	76.1	224	2	AAW98281 H. pylori

25	35	76.1	356	5	AAW47339 Vibrio vu
26	35	76.1	491	8	ADX89679 Plant ful
27	35	76.1	868	6	AAE31527 Rice cap
28	35	76.1	1169	4	ABE68757 Bacteri
29	35	73.9	233	8	ADN21239 Bacteri
30	34	73.9	433	7	ADCC01102 Enteroc
31	34	73.9	661	6	ABU20820 Protein e
32	34	73.9	705	8	ADX71265 Plant ful
33	34	73.9	780	2	AAW72798 Phosphol
34	34	73.9	780	8	ADX77858 Plant ful
35	34	73.9	809	6	ADA20755 Soybean p
36	34	73.9	812	2	AAW72797 Phosphol
37	34	73.9	812	2	AAW06134 Phosphol
38	34	73.9	812	2	AAW25675 Phosphol
39	34	73.9	813	8	ADY22319 Plant ful
40	34	73.9	817	8	ADX77899 Plant ful
41	34	73.9	820	8	ADY22413 Plant ful
42	34	73.9	820	8	ADX91040 Plant ful
43	34	73.9	821	8	ADX95175 Plant ful
44	34	73.9	849	8	ADX77856 Plant ful
45	33	71.7	151	7	ADH86225 Enterococ
46	33	71.7	202	4	ABE63459 Drosophi
47	33	71.7	304	9	ABE44584 Sleep dis
48	33	71.7	311	7	ABO80046 Pseudomon
49	33	71.7	345	4	ABE65205 Drosophi
50	33	71.7	359	8	ADT58054 Plant pol
51	33	71.7	419	9	ABE44585 Sleep dis
52	33	71.7	452	5	ABE07641 Mouse mit
53	33	71.7	452	7	ADSE9639 Rat Prote
54	33	71.7	452	7	ADSE9635 Rat Prote
55	33	71.7	536	7	ADB70203 C. neofo
56	33	71.7	563	3	ABE28406 Thermotog
57	33	71.7	563	8	ADN20342 Bacteri
58	33	71.7	571	9	ABE18198 Thermotog
59	33	71.7	571	9	ABE44583 Sleep dis
60	33	71.7	616	2	AAW32013 Drosophi
61	33	71.7	616	8	AD138326 Drosophi
62	33	71.7	616	8	ADSE96452 Drosophi
63	33	71.7	641	4	ABE58034 Drosophi
64	33	71.7	643	9	ABE44582 Sleep dis
65	33	71.7	655	9	ABE44586 Sleep dis
66	33	71.7	656	8	ADSE16292 Fruit fly
67	33	71.7	2085	8	ADP04339 Potential
68	33	71.7	2196	8	ADP04337 Squid pot
69	32	69.6	114	5	AAE17793 Escherich
70	32	69.6	137	2	ADY72665 Hepaticis
71	32	69.6	137	2	AAW33310 MAB15 hea
72	32	69.6	137	3	AAW85198 Heavy cha
73	32	69.6	192	3	AAW828186 Human iso
74	32	69.6	250	6	ABU48833 Protein e
75	32	69.6	279	6	ABU50637 Protein e
76	32	69.6	309	8	ADX65734 Plant ful
77	32	69.6	348	8	ADW48126 Polypept
78	32	69.6	367	9	ADW16539 E. faecal
79	32	69.6	385	7	ADH87274 Enterococ
80	32	69.6	392	8	ADP84522 Human bre
81	32	69.6	411	2	AAW11586 Streptomy
82	32	69.6	436	8	ADW77601 Plant ful
83	32	69.6	438	8	ADP84523 Human bre
84	32	69.6	452	7	ADSE9641 Human pro
85	32	69.6	452	7	ADSE9637 Human pro
86	32	69.6	452	7	ADJ70661 Human hea
87	32	69.6	452	7	ADJ71208 Human hea
88	32	69.6	452	8	ADL14803 Human iso
89	32	69.6	452	8	ABW81661 Tumour-as
90	32	69.6	452	9	ADW08790 Human pro
91	32	69.6	452	9	ADY16357 PRO polyp
92	32	69.6	452	9	ABE69238 Human mod
93	32	69.6	484	3	AAW31977 Human can
94	32	69.6	523	5	ADK36976 Novel hum
95	32	69.6	610	9	ABE40276 L. pneumo
96	32	69.6	628	8	ADSE24965 Bacteri
97	32	69.6	667	9	ABE36913 L. pneumo

98	32	69.6	1662	8	AD016889	Ad016889 Tobacco b	171	31	67.4	433	7	ADJ69554	AdJ69554 Human hea
99	32	69.6	1764	8	AD016893	Ad016893 Tobacco b	172	31	67.4	433	8	ADH09633	AdH09633 Human hos
100	31	67.4	179	8	AB055655	Ab055655 Human gen	173	31	67.4	433	8	AD049107	Ad049107 Human ded
101	31	67.4	150	7	AD28060	Ad28060 Human Ieu	174	31	67.4	433	8	ADU20919	AdU20919 Human gly
102	31	67.4	166	9	ABM96941	M. xanthu	175	31	67.4	433	8	ADU06409	AdU06409 Novel bro
103	31	67.4	198	4	ABG07306	Novel hum	176	31	67.4	433	9	ABE25735	ABe25735 Human and
104	31	67.4	206	6	AAE31535	Novel pro	177	31	67.4	438	4	ABB62946	ABb62946 Drosophi
105	31	67.4	229	9	ABE40084	L. pneumo	178	31	67.4	439	8	ADRe6057	ADr66057 Human pro
106	31	67.4	237	9	ABE36692	L. pneumo	179	31	67.4	439	8	ADRe6399	ADr66399 Human pro
107	31	67.4	238	4	ABG07040	Novel hum	180	31	67.4	447	5	ABB07581	ABb07581 Human tru
108	31	67.4	264	6	ABU16972	Novel e	181	31	67.4	474	4	ABB96247	ABb96247 Putative
109	31	67.4	269	6	ADA34562	Actinotoba	182	31	67.4	478	4	ABB69816	ABb69816 Drosophi
110	31	67.4	279	5	ABP39862	Staphyloc	183	31	67.4	483	4	AAE06521	AAe06521 Human gly
111	31	67.4	279	8	ADSO6901	Staphyloc	184	31	67.4	483	5	ABB07580	ABb07580 Human gly
112	31	67.4	290	7	ABO65618	Klebsiell	185	31	67.4	483	5	ABB77874	ABb77874 Amino aci
113	31	67.4	314	7	ABO69853	Pseudomon	186	31	67.4	483	5	AAO22557	AAo22557 KC3A_huma
114	31	67.4	327	2	AAy43031	Human pro	187	31	67.4	483	7	ABR44292	ABr44292 Human gly
115	31	67.4	327	2	AAy41679	Human H-b	188	31	67.4	483	7	ABR44296	ABr44296 Human gly
116	31	67.4	327	2	AAy41679	Human H-b	189	31	67.4	483	7	ABR44290	ABr44290 Human gly
117	31	67.4	341	6	ABU19721	Protein e	190	31	67.4	483	7	ABR44297	ABr44297 Human gly
118	31	67.4	350	8	ADRO6329	Human pro	191	31	67.4	483	7	ABR44291	ABr44291 Human gly
119	31	67.4	351	5	ABB07583	Human tru	192	31	67.4	483	8	ADH09631	ADh09631 Human hos
120	31	67.4	351	8	ADH09635	Human hos	193	31	67.4	483	8	ADH09632	ADh09632 Human hos
121	31	67.4	352	8	ADH09636	Human hos	194	31	67.4	483	8	ADU18809	ADu18809 Human sof
122	31	67.4	352	8	ADRO6319	Gsk-3 bet	195	31	67.4	483	8	ADU18031	ADu18031 Human can
123	31	67.4	352	8	ADRO6318	Gsk-3 bet	196	31	67.4	483	9	AEA39563	AEa39563 Human gly
124	31	67.4	352	9	ADY85459	Catalytic	197	31	67.4	483	9	AEA39563	AEa39563 Human gly
125	31	67.4	361	3	AAE53264	Human col	198	31	67.4	484	7	ADD22903	ADD22903 T. reesei
126	31	67.4	361	5	ABB07579	Human tru	199	31	67.4	495	2	AAy32014	AAy32014 Human cat
127	31	67.4	361	5	AAE47983	Human tru	200	31	67.4	495	2	ABBS7250	ABb57250 Mouse lsc
128	31	67.4	361	7	ADC37107	Human GSK	201	31	67.4	495	6	ABE44215	ABr44215 Human pot
129	31	67.4	367	8	ADRO6334	Gsk-3 bet	202	31	67.4	495	7	ADE57673	ADe57673 Rat Prote
130	31	67.4	375	4	ABG22460	Novel hum	203	31	67.4	495	7	ADE57677	ADe57677 Rat Prote
131	31	67.4	378	5	ABB77877	Sequence	204	31	67.4	495	7	ADE57679	ADe57679 Human pro
132	31	67.4	383	5	ABB07582	Human tru	205	31	67.4	495	7	ADE57675	ADe57675 Human pro
133	31	67.4	385	6	ABU3517	Catalytic	206	31	67.4	495	8	AD138327	AD138327 Human can
134	31	67.4	389	9	ABU3517	Protein e	207	31	67.4	495	6	ABR42416	ABr42416 Human pot
135	31	67.4	390	6	ABU3517	Protein e	208	31	67.4	499	8	ABO85019	ABo85019 Human can
136	31	67.4	394	5	ABB07578	Human tru	209	31	67.4	499	8	ABO85018	ABo85018 Human can
137	31	67.4	398	4	ABG28865	Novel hum	210	31	67.4	499	9	ADZ13412	ADz13412 Human can
138	31	67.4	402	7	ADN26182	Hypether	211	31	67.4	499	9	ADZ13414	ADz13414 Human can
139	31	67.4	407	7	ABO64354	Klebsiell	212	31	67.4	499	9	ADZ13406	ADz13406 Murine ca
140	31	67.4	414	8	ADRO6333	p38-alpha	213	31	67.4	505	8	ADX74631	ADx74631 Plant ful
141	31	67.4	420	2	AAE61326	Tau-prote	214	31	67.4	507	3	AAE58794	AAe58794 Breast an
142	31	67.4	420	4	AAE61327	Tau-prote	215	31	67.4	514	7	ADD46353	ADD46353 Human pro
143	31	67.4	420	4	AAE05398	Human gly	216	31	67.4	514	9	ADM06695	ADm06695 Human pro
144	31	67.4	420	5	ABB07577	Human gly	217	31	67.4	514	9	AEA21027	AEa21027 Novel hum
145	31	67.4	420	5	ABE77875	Amino aci	218	31	67.4	515	9	AEA21028	AEa21028 Novel hum
146	31	67.4	420	6	ABP70714	Human gly	219	31	67.4	515	7	ADF61834	ADf61834 Human glu
147	31	67.4	420	6	ABR82106	Human gly	220	31	67.4	515	8	ADQ18219	ADq18219 Human sof
148	31	67.4	420	7	ABR44289	Human gly	221	31	67.4	515	8	ADP25366	ADp25366 PRO polyp
149	31	67.4	420	7	ABR44293	Human gly	222	31	67.4	517	4	ABB66825	ABb66825 Drosophi
150	31	67.4	420	7	ABR44294	Human gly	223	31	67.4	523	6	ABR42417	ABr42417 Human pot
151	31	67.4	420	7	ADD68742	Rat lau p	224	31	67.4	523	7	ADU70209	ADu70209 Human hea
152	31	67.4	420	7	ADDE64051	Human pro	225	31	67.4	523	8	ABO840129	ABo840129 Human vol
153	31	67.4	420	7	ADDE64051	Rat Prote	226	31	67.4	523	8	ABO84782	ABo84782 Human can
154	31	67.4	420	8	ADK11467	Human gly	227	31	67.4	523	9	ADZ13401	ADz13401 Human can
155	31	67.4	420	8	ADH09634	Human hos	228	31	67.4	523	9	ADZ13399	ADz13399 Human can
156	31	67.4	420	8	ADH09637	Human hos	229	31	67.4	523	9	ADZ13403	ADz13403 Human can
157	31	67.4	420	8	AD128893	Mouse gly	230	31	67.4	524	4	ABB69124	ABb69124 Drosophi
158	31	67.4	420	8	ADRO6320	Gsk-3 bet	231	31	67.4	528	4	ABO84781	ABo84781 Murine ca
159	31	67.4	420	8	ADRO6317	Gsk-3 bet	232	31	67.4	528	9	ADZ13396	ADz13396 Murine ca
160	31	67.4	420	8	ADR40191	Gsk-3 bet	233	31	67.4	532	4	AAU15060	AAu15060 Protein e
161	31	67.4	420	8	ADG92965	Glycogen	234	31	67.4	532	5	ABP73206	ABp73206 Candida a
162	31	67.4	420	8	ADT92555	Human gly	235	31	67.4	608	9	ABE42257	ABe42257 L. pneumo
163	31	67.4	420	8	ADY64106	Human gly	236	31	67.4	608	9	ABE35122	ABe35122 Rice abio
164	31	67.4	420	9	AEA39562	Human gly	237	31	67.4	641	7	ABM87741	ABm87741 Staphyloc
165	31	67.4	420	9	AEA39564	Mouse gly	238	31	67.4	687	5	AAE80307	AAe80307 Protein e
166	31	67.4	420	9	ABE28124	Human gly	239	31	67.4	693	6	ABU19700	ABu19700 Protein e
167	31	67.4	428	7	ADG92960	Human KPP	240	31	67.4	729	2	ABU23550	ABu23550 Protein e
168	31	67.4	428	7	ADG92960	Human KPP	241	31	67.4	729	2	ADDE61340	ADe61340 Rat Prote
169	31	67.4	433	7	ABR44295	Human gly	242	31	67.4	764	2	ABR84345	ABr84345 Weilon aco
170	31	67.4	433	7	ABR44298	Human gly	243	31	67.4	848	5	ABB05429	ABb05429 Atrialdops

244	31	67.4	848	6	AAE31528	AAE31528	Arabidops
245	31	67.4	898	8	ADQ26200	ADQ26200	Arabidops
246	31	67.4	919	2	AAR84337	AAR84337	Arabidops
247	31	67.4	927	2	ABO23611	ABO23611	Leishmani
248	31	67.4	927	2	AAR85598	AAR85598	Arabidops
249	31	67.4	1010	6	AAOI5926	AAOI5926	Zea mays
250	31	67.4	1010	6	ADL00226	ADL00226	Corn tecti
251	31	67.4	1033	9	AEA20178	AEA20178	Novel hum
252	31	67.4	1050	4	ABG04174	ABG04174	Novel hum
253	31	67.4	1108	9	AEA20179	AEA20179	Novel hum
254	31	67.4	1211	4	ABAI1434	ABAI1434	P. pastor
255	31	67.4	1449	4	ABG15729	ABG15729	Novel hum
256	31	67.4	1769	8	ADN21581	ADN21581	Bacterial
257	31	67.4	2835	5	ABR98574	ABR98574	Dextran s
258	31	67.4	2835	5	ABR55594	ABR55594	Amino aci
259	30	65.2	9	2	AAW27423	AAW27423	CDR3 from
260	30	65.2	9	9	ADZ69234	ADZ69234	IL-5R alp
261	30	65.2	15	8	ADO36531	ADO36531	Human ant
262	30	65.2	19	5	ABP46809	ABP46809	Human Bly
263	30	65.2	19	7	ADG97636	ADG97636	scFV VHCD
264	30	65.2	84	8	ADH87486	ADH87486	Enterococ
265	30	65.2	91	8	ADV89253	ADV89253	Streptoco
266	30	65.2	91	8	ADV80506	ADV80506	Streptoco
267	30	65.2	126	4	ABG12131	ABG12131	Novel hum
268	30	65.2	128	4	ABBI1074	ABBI1074	Human GPI
269	30	65.2	137	2	AAW21845	AAW21845	Heavy cha
270	30	65.2	149	4	AAE10437	AAE10437	Novel hum
271	30	65.2	156	8	ADX80374	ADX80374	Plant ful
272	30	65.2	158	7	ABO76364	ABO76364	Pseudomon
273	30	65.2	158	7	ABO74327	ABO74327	Pseudomon
274	30	65.2	158	7	ABO64946	ABO64946	Klebsiell
275	30	65.2	176	7	ADC96995	ADC96995	E. faeciu
276	30	65.2	220	8	ADR95582	ADR95582	Novel S.
277	30	65.2	220	8	AEA59452	AEA59452	Streptoco
278	30	65.2	226	7	ADF03904	ADF03904	Bacterial
279	30	65.2	236	6	AAR38305	AAR38305	Sequence
280	30	65.2	236	6	ABU02307	ABU02307	S. pneumo
281	30	65.2	236	6	ADL71362	ADL71362	Delta pro
282	30	65.2	236	8	ADK46514	ADK46514	Streptoco
283	30	65.2	239	4	AAE10438	AAE10438	Novel hum
284	30	65.2	241	8	ADR96180	ADR96180	Novel S.
285	30	65.2	241	8	AEA60050	AEA60050	Streptoco
286	30	65.2	244	5	ABBA48557	ABBA48557	Listeria
287	30	65.2	244	5	ABG25664	ABG25664	Novel hum
288	30	65.2	249	5	ABP45245	ABP45245	Human Bly
289	30	65.2	257	7	ADG96072	ADG96072	Single ch
290	30	65.2	261	4	AAE10439	AAE10439	Novel hum
291	30	65.2	262	4	AAW01111	AAW01111	CFE 114 P
292	30	65.2	262	4	ADK46692	ADK46692	Streptoco
293	30	65.2	262	8	ADT50131	ADT50131	S. pneumo
294	30	65.2	266	4	AAU37887	AAU37887	Streptoco
295	30	65.2	266	4	AAU38072	AAU38072	Streptoco
296	30	65.2	266	6	ABU02131	ABU02131	S. pneumo
297	30	65.2	266	6	ABU46186	ABU46186	Protein e
298	30	65.2	275	4	AAU28046	AAU28046	Novel hum
299	30	65.2	275	4	ADN18328	ADN18328	Bacterial
300	30	65.2	280	5	ABU51982	ABU51982	Helicobac
301	30	65.2	290	5	ABH08002	ABH08002	Human lip
302	30	65.2	290	5	ADT58969	ADT58969	Plant pol
303	30	65.2	298	4	ABB72041	ABB72041	Drosophi
304	30	65.2	298	4	ADAS4826	ADAS4826	Human pro
305	30	65.2	304	8	ADRS9001	ADRS9001	Human Blk
306	30	65.2	304	8	ADRS9001	ADRS9001	Human Blk
307	30	65.2	307	8	ADS22104	ADS22104	Bacterial
308	30	65.2	308	6	ABU41449	ABU41449	Protein e
309	30	65.2	308	6	ADN46641	ADN46641	Thermoco
310	30	65.2	313	7	ABG75167	ABG75167	M. acetiv
311	30	65.2	315	8	ADRO6324	ADRO6324	Protein k
312	30	65.2	315	8	ADRO6325	ADRO6325	Protein k
313	30	65.2	317	4	ABR99832	ABR99832	AGC prote
314	30	65.2	317	4	ADJ38880	ADJ38880	PXBbeta a
315	30	65.2	322	6	ABM69551	ABM69551	Phototrab
316	30	65.2	323	6	ABM68961	ABM68961	Phototrab
317	30	65.2	325	6	ABR44778	ABR44778	Human TGF
318	30	65.2	325	8	ADQ30612	ADQ30612	Pancreas
319	30	65.2	325	8	ABM80054	ABM80054	Tumour -as
320	30	65.2	325	5	ABE13359	ABE13359	TGF -beta
321	30	65.2	326	5	ABBS5332	ABBS5332	Lactococ
322	30	65.2	327	3	ABG06776	ABG06776	Arabidops
323	30	65.2	327	5	ABBA4967	ABBA4967	Listeria
324	30	65.2	329	4	AAE10435	AAE10435	Novel hum
325	30	65.2	329	4	ADH88353	ADH88353	Enterococ
326	30	65.2	329	5	ADP28882	ADP28882	Streptoco
327	30	65.2	331	8	ADV88375	ADV88375	Streptoco
328	30	65.2	331	8	ADV79628	ADV79628	Streptoco
329	30	65.2	331	8	ADV81793	ADV81793	Streptoco
330	30	65.2	335	8	ADRO6326	ADRO6326	Protein k
331	30	65.2	335	8	ADRO6339	ADRO6339	Atk1 prot
332	30	65.2	336	6	ABR57469	ABR57469	AGC famil
333	30	65.2	341	7	ADC14232	ADC14232	Human enz
334	30	65.2	341	7	ADH87639	ADH87639	Enterococ
335	30	65.2	341	8	ADRS8999	ADRS8999	Human Elk
336	30	65.2	351	4	AAE10436	AAE10436	Novel hum
337	30	65.2	352	3	AAAG4904	AAAG4904	Arabidops
338	30	65.2	352	3	AAAG4916	AAAG4916	Arabidops
339	30	65.2	357	3	AAAG4915	AAAG4915	Arabidops
340	30	65.2	357	3	AAAG4903	AAAG4903	Arabidops
341	30	65.2	359	8	ADX89099	ADX89099	Plant ful
342	30	65.2	359	2	AAW96600	AAW96600	Putative
343	30	65.2	378	4	AAAG14902	AAAG14902	Arabidops
344	30	65.2	383	3	AAAG49914	AAAG49914	Arabidops
345	30	65.2	383	3	ADT55681	ADT55681	Plant pol
346	30	65.2	391	2	AAAY34444	AAAY34444	Porphyrom
347	30	65.2	391	2	AAAY34423	AAAY34423	Porphyrom
348	30	65.2	397	8	ADN21067	ADN21067	Bacterial
349	30	65.2	397	8	ADN21068	ADN21068	Bacterial
350	30	65.2	402	4	AAU35757	AAU35757	Helicobac
351	30	65.2	402	6	AAU30833	AAU30833	Protein e
352	30	65.2	415	4	AAU35491	AAU35491	Haemophil
353	30	65.2	415	5	ABBS3587	ABBS3587	Herbicide
354	30	65.2	418	7	ABO66638	ABO66638	Klebsiell
355	30	65.2	430	8	ABM84606	ABM84606	Human dia
356	30	65.2	430	8	ABM84605	ABM84605	Human dia
357	30	65.2	430	8	ABM84602	ABM84602	Human dia
358	30	65.2	430	8	ADX89864	ADX89864	Plant ful
359	30	65.2	436	8	ABM84603	ABM84603	Human dia
360	30	65.2	436	8	ABM84604	ABM84604	Human dia
361	30	65.2	436	8	ABM84609	ABM84609	Human dia
362	30	65.2	436	8	ABM84605	ABM84605	Human dia
363	30	65.2	436	8	ABM84605	ABM84605	Human dia
364	30	65.2	436	8	ABM84607	ABM84607	Human dia
365	30	65.2	436	8	ABM84599	ABM84599	Human dia
366	30	65.2	436	8	ABM84610	ABM84610	Human dia
367	30	65.2	436	8	ABM84601	ABM84601	Human dia
368	30	65.2	438	7	ADG74658	ADG74658	Human kin
369	30	65.2	442	8	ABM84608	ABM84608	Human dia
370	30	65.2	442	8	ADK66334	ADK66334	Plant ful
371	30	65.2	445	4	ABBS69957	ABBS69957	Drosophi
372	30	65.2	447	8	ADN18341	ADN18341	Bacterial
373	30	65.2	469	7	ADC96309	ADC96309	E. faeciu
374	30	65.2	480	4	AAAG78019	AAAG78019	Human Act
375	30	65.2	480	4	AAAB19997	AAAB19997	Human ser
376	30	65.2	480	8	ADG85254	ADG85254	Human Chr
377	30	65.2	480	8	ADK67022	ADK67022	Plant ful
378	30	65.2	481	5	AAAY3246	AAAY3246	Human pro
379	30	65.2	481	5	AAU79419	AAU79419	Human pro
380	30	65.2	481	5	ABBO6997	ABBO6997	Human Akt
381	30	65.2	481	5	ABRS7473	ABRS7473	Human PKB
382	30	65.2	481	7	ADBS6091	ADBS6091	Human pro
383	30	65.2	481	7	ADBS6089	ADBS6089	Rat Prote
384	30	65.2	481	7	ADFA5033	ADFA5033	Human kin
385	30	65.2	481	8	ADN71938	ADN71938	Human pro
386	30	65.2	488	8	ABO84895	ABO84895	Murine ca
387	30	65.2	489	4	AAU32453	AAU32453	Novel hum
388	30	65.2	489	4	ABM84613	ABM84613	Human dia
389	30	65.2	498	8	ADS28858	ADS28858	Bacterial

390	30	65.2	503	4	ABG20305	ABG20305	Novel hum	463	29	63.0	17	6	ADA90854	Ada90854	MS-Roche
391	30	65.2	506	8	ADM17713	ADM17713	Pinus rad	464	29	63.0	17	6	ADA91088	Ada91088	MS-R Fab/
392	30	65.2	512	8	ABM84611	ABM84611	Human dia	465	29	63.0	17	6	ADA91332	Ada91332	MS-R Fab/
393	30	65.2	540	8	ABM84612	ABM84612	Human dia	466	29	63.0	17	6	ADA89958	Ada89958	Anti-I -Abet
394	30	65.2	542	8	ADG42229	ADG42229	Bacterial	467	29	63.0	17	6	ADA90260	Ada90260	MS-R Fab/
395	30	65.2	548	8	ADOG1981	ADOG1981	Transcrip	468	29	63.0	17	6	ADA90725	Ada90725	MS-Roche
396	30	65.2	557	6	ABU36175	ABU36175	Protein e	469	29	63.0	17	6	ADA90726	Ada90726	MS-Roche
397	30	65.2	564	8	ABO84896	ABO84896	Human can	470	29	63.0	17	6	ADA90732	Ada90732	MS-Roche
398	30	65.2	570	5	ABP26646	ABP26646	Streptococ	471	29	63.0	17	6	ADA90736	Ada90736	MS-Roche
399	30	65.2	586	7	ABO82265	ABO82265	Pseudomon	472	29	63.0	17	6	ADA90741	Ada90741	MS-Roche
400	30	65.2	587	6	AAO30104	AAO30104	Yersinia	473	29	63.0	17	6	ADA90844	Ada90844	MS-Roche
401	30	65.2	594	7	ABO63852	ABO63852	Klebsiell	474	29	63.0	17	6	ADA90845	Ada90845	MS-Roche
402	30	65.2	613	4	AAU32452	AAU32452	Novel hum	475	29	63.0	17	6	ADA90853	Ada90853	MS-Roche
403	30	65.2	615	8	ADN26551	ADN26551	Bacterial	476	29	63.0	17	6	ADA90859	Ada90859	MS-Roche
404	30	65.2	634	6	ABU39078	ABU39078	Protein e	477	29	63.0	17	6	ADA91203	Ada91203	MS-R Fab/
405	30	65.2	636	7	ABO61684	ABO61684	Klebsiell	478	29	63.0	17	6	ADA91205	Ada91205	MS-R Fab/
406	30	65.2	645	8	ADS28458	ADS28458	Bacterial	479	29	63.0	17	6	ADA91329	Ada91329	MS-R Fab/
407	30	65.2	648	7	ADF06702	ADF06702	Bacterial	480	29	63.0	17	6	ADA89909	Ada89909	MSR -7 VH
408	30	65.2	668	9	ABM95045	ABM95045	M. xanthu	481	29	63.0	17	6	ADA90256	Ada90256	Anti-I -Abet
409	30	65.2	681	4	ABB69493	ABB69493	Drosophil	482	29	63.0	17	6	ADA90613	Ada90613	MS-Roche
410	30	65.2	703	8	ABU70687	ABU70687	Pyrococcu	483	29	63.0	17	6	ADA90738	Ada90738	MS-Roche
411	30	65.2	712	8	ADS26675	ADS26675	Bacterial	484	29	63.0	17	6	ADA90742	Ada90742	MS-Roche
412	30	65.2	717	7	ADB70241	ADB70241	C. neoFor	485	29	63.0	17	6	ADA90855	Ada90855	MS-Roche
413	30	65.2	722	8	AAH70686	AAH70686	Pyrococcu	486	29	63.0	17	6	ADA90863	Ada90863	MS-Roche
414	30	65.2	743	8	ADP47748	ADP47748	Human inf	487	29	63.0	17	6	ADA91094	Ada91094	MS-R Fab/
415	30	65.2	789	4	ABB64840	ABB64840	Drosophil	488	29	63.0	17	6	ADA91324	Ada91324	MS-R Fab/
416	30	65.2	808	2	AAW32911	AAW32911	Castor be	489	29	63.0	17	6	ADA91326	Ada91326	MS-R Fab/
417	30	65.2	833	2	AAH28960	AAH28960	Delta D11	490	29	63.0	17	6	ADA91393	Ada91393	MS-R Fab/
418	30	65.2	833	2	AAO27056	AAO27056	Delta pro	491	29	63.0	17	6	ADA91394	Ada91394	MS-R Fab/
419	30	65.2	833	4	ABH71247	ABH71247	Drosophil	492	29	63.0	17	6	ADA90862	Ada90862	MS-Roche
420	30	65.2	834	3	AAV79031	AAV79031	Drosophil	493	29	63.0	17	6	ADA91206	Ada91206	MS-R Fab/
421	30	65.2	842	4	ABH65111	ABH65111	Drosophil	494	29	63.0	17	6	ADA89954	Ada89954	MS-R Fab/
422	30	65.2	858	6	ABH53197	ABH53197	Protein s	495	29	63.0	17	6	ADA90731	Ada90731	MS-Roche
423	30	65.2	858	7	ADG63242	ADG63242	Disease t	496	29	63.0	17	6	ADA90734	Ada90734	MS-Roche
424	30	65.2	860	4	ABG20300	ABG20300	Novel hum	497	29	63.0	17	6	ADA90860	Ada90860	MS-Roche
425	30	65.2	860	7	ADI60448	ADI60448	Secreted	498	29	63.0	17	6	ADA90727	Ada90727	MS-Roche
426	30	65.2	928	7	ABM93849	ABM93849	M. xanthu	499	29	63.0	17	6	ADA90740	Ada90740	MS-Roche
427	30	65.2	973	2	AAH75707	AAH75707	Eph-relat	500	29	63.0	17	6	ADA90966	Ada90966	MS-R Fab/
428	30	65.2	996	3	AAH25558	AAH25558	Pinus rad	501	29	63.0	17	6	ADA91091	Ada91091	MS-R Fab/
429	30	65.2	996	3	AAH25514	AAH25514	Pinus rad	502	29	63.0	17	6	ADA90621	Ada90621	MS-Roche
430	30	65.2	1063	5	ABP35715	ABP35715	Fungal ZB	503	29	63.0	17	6	ADA90846	Ada90846	MS-Roche
431	30	65.2	1068	5	ABP35714	ABP35714	Fungal ZB	504	29	63.0	17	6	ADA90968	Ada90968	MS-R Fab/
432	30	65.2	1068	7	ADG63116	ADG63116	Disease t	505	29	63.0	17	6	ADA91092	Ada91092	MS-R Fab/
433	30	65.2	1088	5	ABH91044	ABH91044	Herbicida	506	29	63.0	17	6	ADA90618	Ada90618	MS-Roche
434	30	65.2	1088	8	ADN72213	ADN72213	Thale cre	507	29	63.0	17	6	ADA90623	Ada90623	MS-Roche
435	30	65.2	1354	4	ABH64256	ABH64256	Drosophil	508	29	63.0	17	6	ADA90730	Ada90730	MS-Roche
436	30	65.2	1375	5	AAU96028	AAU96028	S. mutans	509	29	63.0	17	6	ADA90852	Ada90852	MS-Roche
437	30	65.2	1375	5	AAU79288	AAU79288	Streptococ	510	29	63.0	17	6	ADA91089	Ada91089	MS-R Fab/
438	30	65.2	1375	7	ADD93655	ADD93655	Streptococ	511	29	63.0	17	6	ADA91330	Ada91330	MS-R Fab/
439	30	65.2	1375	9	ADX37278	ADX37278	Streptococ	512	29	63.0	17	6	ADA91336	Ada91336	MS-R Fab/
440	30	65.2	1469	8	ADR66889	ADR66889	Human pro	513	29	63.0	17	6	ADA91401	Ada91401	MS-R Fab/
441	30	65.2	1469	8	ADR65991	ADR65991	Human pro	514	29	63.0	17	6	ADA90262	Ada90262	Anti -Abet
442	30	65.2	1477	6	AAH37177	AAH37177	Human LRR	515	29	63.0	17	6	ADA90264	Ada90264	Anti-I -Abet
443	30	65.2	1479	8	ADL35717	ADL35717	Human per	516	29	63.0	17	6	ADA90614	Ada90614	MS-Roche
444	30	65.2	1483	4	ABG16336	ABG16336	Novel hum	517	29	63.0	17	6	ADA90915	Ada90915	MS-Roche
445	30	65.2	1496	2	AAW81030	AAW81030	Melanoma	518	29	63.0	17	6	ADA90915	Ada90915	MS-Roche
446	30	65.2	1496	3	AAV70469	AAV70469	Human p53	519	29	63.0	17	6	ADA90969	Ada90969	MS-R Fab/
447	30	65.2	1496	6	ABU03498	ABU03498	Angiogene	520	29	63.0	17	6	ADA91327	Ada91327	MS-R Fab/
448	30	65.2	1496	7	ADD89024	ADD89024	TAT264. 1	521	29	63.0	17	6	ADA91333	Ada91333	MS-R Fab/
449	30	65.2	1496	7	ADF28706	ADF28706	Human per	522	29	63.0	17	6	ADA91334	Ada91334	MS-R Fab/
450	30	65.2	1496	8	ADQ18902	ADQ18902	Human sof	523	29	63.0	17	6	ADA91400	Ada91400	MS-R Fab/
451	30	65.2	1496	8	ADO89920	ADO89920	Antagonis	524	29	63.0	17	6	ADA89978	Ada89978	Anti-I -Abet
452	30	65.2	1496	8	ADO89914	ADO89914	Antagonis	525	29	63.0	17	6	ADA90050	Ada90050	Anti -Abet
453	30	65.2	1496	8	ADR66092	ADR66092	Human pro	526	29	63.0	17	6	ADA90724	Ada90724	MS-Roche
454	30	65.2	1496	8	ADR66434	ADR66434	Human pro	527	29	63.0	17	6	ADA90999	Ada90999	MS-R Fab/
455	30	65.2	1498	4	ABH11587	ABH11587	Human per	528	29	63.0	17	6	ADA91000	Ada91000	MS-R Fab/
456	30	65.2	1498	7	ABO00762	ABO00762	Polypepti	529	29	63.0	17	6	ADA91093	Ada91093	MS-R Fab/
457	30	65.2	1499	7	ADC54806	ADC54806	Protein S	530	29	63.0	17	6	ADA91095	Ada91095	MS-R Fab/
458	30	65.2	1543	4	ABH69373	ABH69373	Drosophil	531	29	63.0	17	6	ADA91096	Ada91096	MS-R Fab/
459	30	65.2	1873	4	ABH59270	ABH59270	Drosophil	532	29	63.0	17	6	ADA91204	Ada91204	MS-R Fab/
460	30	65.2	1988	8	ADU49639	ADU49639	Oil -aseoc	533	29	63.0	17	6	ADA91395	Ada91395	MS-R Fab/
461	30	65.2	2263	4	ABH66793	ABH66793	Drosophil	534	29	63.0	17	6	ADA91396	Ada91396	MS-R Fab/
462	30	65.2	3242	4	ABH58857	ABH58857	Drosophil	535	29	63.0	17	6	ADA90266	Ada90266	Anti-I -Abet

536	29	63.0	17	6	ADA90615	ADA90615 MS-Roche	609	29	63.0	124	6	ADA89924	ADA89924 Anti-Abet
537	29	63.0	17	6	ADA90622	ADA90622 MS-Roche	610	29	63.0	126	5	AAH50861	AAH50861 Mouse ren
538	29	63.0	17	6	ADA90733	ADA90733 MS-Roche	611	29	63.0	126	6	ADA89974	ADA89974 Anti-Abet
539	29	63.0	17	6	ADA90857	ADA90857 MS-Roche	612	29	63.0	126	6	ADA89891	ADA89891 MS-Roche
540	29	63.0	17	6	ADA90988	ADA90988 MS-R Fab/	613	29	63.0	133	5	ABG97829	ABG97829 Mouse 12E
541	29	63.0	17	6	ADA91006	ADA91006 MS-R Fab/	614	29	63.0	133	5	ABG35331	ABG35331 Thrombopo
542	29	63.0	17	6	ADA91402	ADA91402 MS-R Fab/	615	29	63.0	137	5	ABP08572	ABP08572 Human ORF
543	29	63.0	17	6	ADA90254	ADA90254 Anti-Abet	616	29	63.0	140	2	AAH55556	AAH55556 DRG-200
544	29	63.0	17	6	ADA90617	ADA90617 MS-Roche	617	29	63.0	140	2	AAH55554	AAH55554 DRG-200
545	29	63.0	17	6	ADA90850	ADA90850 MS-Roche	618	29	63.0	151	3	AAH11005	AAH11005 Arabidops
546	29	63.0	17	6	ADA90987	ADA90987 MS-R Fab/	619	29	63.0	151	3	AAH51938	AAH51938 Arabidops
547	29	63.0	17	6	ADA91202	ADA91202 MS-R Fab/	620	29	63.0	153	3	AAH11004	AAH11004 Arabidops
548	29	63.0	17	6	ADA91331	ADA91331 MS-R Fab/	621	29	63.0	159	3	AAH51937	AAH51937 Arabidops
549	29	63.0	17	6	ADA90033	ADA90033 Anti-Abet	622	29	63.0	161	4	ABG16934	ABG16934 Novel hum
550	29	63.0	17	6	ADA90258	ADA90258 Anti-Abet	623	29	63.0	164	5	ABP26585	ABP26585 Streptoco
551	29	63.0	17	6	ADA90737	ADA90737 MS-Roche	624	29	63.0	164	8	ADH87876	ADH87876 Streptoco
552	29	63.0	17	6	ADA90743	ADA90743 MS-Roche	625	29	63.0	164	8	ADH81327	ADH81327 Streptoco
553	29	63.0	17	6	ADA90849	ADA90849 MS-Roche	626	29	63.0	164	8	ADH79129	ADH79129 Streptoco
554	29	63.0	17	6	ADA90970	ADA90970 MS-R Fab/	627	29	63.0	167	8	ADH06666	ADH06666 Plant ful
555	29	63.0	17	6	ADA91090	ADA91090 MS-R Fab/	628	29	63.0	172	8	ADR95315	ADR95315 Novel S.
556	29	63.0	17	6	ADA91207	ADA91207 MS-R Fab/	629	29	63.0	172	8	AEA59185	AEA59185 Streptoco
557	29	63.0	17	6	ADA90616	ADA90616 MS-Roche	630	29	63.0	173	8	ADL04769	ADL04769 M. catarr
558	29	63.0	17	6	ADA90620	ADA90620 MS-Roche	631	29	63.0	176	4	ABG09282	ABG09282 Novel hum
559	29	63.0	17	6	ADA90729	ADA90729 MS-Roche	632	29	63.0	181	9	ADY78796	ADY78796 Phospholi
560	29	63.0	17	6	ADA90856	ADA90856 MS-Roche	633	29	63.0	192	9	ADH40538	ADH40538 HIV Vif p
561	29	63.0	17	6	ADA90914	ADA90914 MS-Roche	634	29	63.0	207	6	ABM70872	ABM70872 Staphyloc
562	29	63.0	17	6	ADA91335	ADA91335 MS-R Fab/	635	29	63.0	215	5	ABH90590	ABH90590 Chlamydia
563	29	63.0	17	6	ADA89950	ADA89950 Anti-Abet	636	29	63.0	215	7	ADD43780	ADD43780 Chlamydia
564	29	63.0	17	6	ADA89952	ADA89952 Anti-Abet	637	29	63.0	215	9	AEA19072	AEA19072 Chlamydia
565	29	63.0	17	6	ADA90847	ADA90847 MS-Roche	638	29	63.0	219	4	AAH96109	AAH96109 Putative
566	29	63.0	17	6	ADA90861	ADA90861 MS-Roche	639	29	63.0	228	2	AAH36936	AAH36936 Chlamydia
567	29	63.0	17	6	ADA91328	ADA91328 MS-R Fab/	640	29	63.0	231	6	ABM71291	ABM71291 Staphyloc
568	29	63.0	17	6	ADA91392	ADA91392 MS-R Fab/	641	29	63.0	232	2	AAH00374	AAH00374 Anti-CD18
569	29	63.0	17	6	ADA89956	ADA89956 Anti-Abet	642	29	63.0	232	2	AAH34503	AAH34503 Heavy ch
570	29	63.0	17	6	ADA90612	ADA90612 MS-Roche	643	29	63.0	232	2	AAH08753	AAH08753 Human ant
571	29	63.0	17	6	ADA90851	ADA90851 MS-Roche	644	29	63.0	232	5	ABG31888	ABG31888 Humanised
572	29	63.0	17	6	ADA91325	ADA91325 MS-R Fab/	645	29	63.0	232	8	ADK18341	ADK18341 Amino aci
573	29	63.0	33	6	ABO32577	ABO32577 Secreted	646	29	63.0	233	6	ABM69599	ABM69599 Porcinarb
574	29	63.0	33	6	ABO10206	ABO10206 Human pol	647	29	63.0	233	7	ADF07929	ADF07929 Bacterial
575	29	63.0	54	4	AAH92669	AAH92669 Human dig	648	29	63.0	236	6	ADA91414	ADA91414 Anti-Abet
576	29	63.0	54	4	AAU22663	AAU22663 Novel hum	649	29	63.0	241	2	AAH95614	AAH95614 Humanized
577	29	63.0	54	7	ABH32503	ABH32503 Human nov	650	29	63.0	241	4	AAH66776	AAH66776 Thymab CD
578	29	63.0	57	5	ABP63745	ABP63745 Human ORF	651	29	63.0	241	9	ABE27967	ABE27967 Humanized
579	29	63.0	62	5	ABG62092	ABG62092 Human pro	652	29	63.0	244	2	AAH06718	AAH06718 Antibody
580	29	63.0	70	8	ADK48341	ADK48341 Streptoco	653	29	63.0	244	8	ADO39737	ADO39737 Human c-m
581	29	63.0	70	8	ADR95225	ADR95225 Novel S.	654	29	63.0	246	8	ADT57218	ADT57218 Plant pol
582	29	63.0	70	9	AEA59095	AEA59095 Streptoco	655	29	63.0	255	2	AAH35000	AAH35000 Chlamydia
583	29	63.0	80	4	ABG20832	ABG20832 Novel hum	656	29	63.0	256	5	ABG97834	ABG97834 Single ch
584	29	63.0	85	5	ABH75708	ABH75708 Human LPI	657	29	63.0	256	5	ABG35335	ABG35335 Thrombopo
585	29	63.0	89	4	AAU60443	AAU60443 Propionib	658	29	63.0	266	5	ABG97835	ABG97835 Single ch
586	29	63.0	89	6	ABM56962	ABM56962 Propionib	659	29	63.0	266	5	ABG35336	ABG35336 Thrombopo
587	29	63.0	93	6	ABO32572	ABO32572 Secreted	660	29	63.0	271	9	ADY52578	ADY52578 Human onc
588	29	63.0	93	8	ADM68865	ADM68865 Insect sp	661	29	63.0	275	8	ADS27366	ADS27366 Bacterial
589	29	63.0	93	8	ADQ10201	ADQ10201 Human pol	662	29	63.0	277	2	AAH30631	AAH30631 Recombina
590	29	63.0	112	5	ABM95948	ABM95948 M. xanthu	663	29	63.0	277	9	ABE27978	ABE27978 Humanized
591	29	63.0	114	5	ABG97827	ABG97827 Human MPL	664	29	63.0	280	8	ADK46718	ADK46718 Streptoco
592	29	63.0	114	5	ABG35304	ABG35304 Thrombopo	665	29	63.0	280	8	ADQ38231	ADQ38231 Pig SYKCD
593	29	63.0	115	4	AAU00680	AAU00680 Human INT	666	29	63.0	280	8	ADQ38234	ADQ38234 Mouse SYK
594	29	63.0	115	4	AAE29298	AAE29298 S. aureus	667	29	63.0	280	8	ADQ38230	ADQ38230 Human SYK
595	29	63.0	115	6	ABO32570	ABO32570 Secreted	668	29	63.0	280	8	ADQ38232	ADQ38232 Rat SYKCD
596	29	63.0	115	6	ADQ10199	ADQ10199 Human pol	669	29	63.0	280	8	ADQ38233	ADQ38233 Rat SYKCD
597	29	63.0	121	2	AAH77874	AAH77874 Humanised	670	29	63.0	280	8	ADO38229	ADO38229 SYKCD ami
598	29	63.0	124	6	ADA90194	ADA90194 Anti-Abet	671	29	63.0	282	6	ABU02103	ABU02103 S. pneumo
599	29	63.0	124	6	ADA89926	ADA89926 Anti-Abet	672	29	63.0	285	8	ADR96250	ADR96250 Novel S.
600	29	63.0	124	6	ADA90200	ADA90200 Anti-Abet	673	29	63.0	285	9	AEA60120	AEA60120 Streptoco
601	29	63.0	124	6	ADA90202	ADA90202 Anti-Abet	674	29	63.0	286	6	ABU21997	ABU21997 Protein e
602	29	63.0	124	6	ADA90204	ADA90204 Anti-Abet	675	29	63.0	291	7	ADM27061	ADM27061 Hyperther
603	29	63.0	124	6	ADA89922	ADA89922 Anti-Abet	676	29	63.0	291	8	ADQ38228	ADQ38228 SYKCD ami
604	29	63.0	124	6	ADA89928	ADA89928 Anti-Abet	677	29	63.0	293	2	ABM71755	ABM71755 Staphyloc
605	29	63.0	124	6	ADA89930	ADA89930 Anti-Abet	678	29	63.0	300	2	AAH95623	AAH95623 pS1130 ex
606	29	63.0	124	6	ADA90196	ADA90196 Anti-Abet	679	29	63.0	300	2	AAH30635	AAH30635 Recombina
607	29	63.0	124	6	ADA90198	ADA90198 Anti-Abet	680	29	63.0	300	4	AAH66785	AAH66785 Protein e
608	29	63.0	124	6	ADA90206	ADA90206 Anti-Abet	681	29	63.0	300	6	ABP72746	ABP72746 Anti-CD18

682	29	63.0	300	9	AEb27977	STII-huma	755	29	63.0	461	8	ADR95301	Adt95301	Novel S.
683	29	63.0	301	6	ABP57449	Mycobacte	756	29	63.0	461	9	AEA59171	AAe59171	Streptococ
684	29	63.0	312	4	AAM93471	Human pol	757	29	63.0	464	2	AAW95054	AAw95054	Campyloba
685	29	63.0	312	8	ADL31112	Human pro	758	29	63.0	473	7	ADH87555	ADh87555	Enterococ
686	29	63.0	312	9	ADW86786	Human pro	759	29	63.0	482	7	ADM26487	ADM26487	Hypertner
687	29	63.0	315	9	ADY85532	Catalytic	760	29	63.0	494	7	ABO69405	ABO69405	Pseudomon
688	29	63.0	322	5	ABB32476	Staphyloc	761	29	63.0	501	4	AAU38496	AAu38496	Salmonell
689	29	63.0	322	5	ABB32475	Staphyloc	762	29	63.0	505	8	ADS44333	ADS44333	Bacterial
690	29	63.0	322	6	ABM72558	Staphyloc	763	29	63.0	509	8	ADG22649	ADg22649	Cyanophag
691	29	63.0	322	7	ADC21328	Staphyloc	764	29	63.0	512	7	ABM88905	ABm88905	Rice abio
692	29	63.0	322	7	ADC25014	S. aureus	765	29	63.0	512	8	ADI45293	ADI45293	Rice isop
693	29	63.0	322	7	ADD52516	Staphyloc	766	29	63.0	514	4	AAAB9692	AAb9692	A. gyzae
694	29	63.0	325	8	ADY05678	Plant ful	767	29	63.0	514	7	ADD46351	ADD46351	Rat Prote
695	29	63.0	331	5	ABB32488	Staphyloc	768	29	63.0	515	5	ABB57349	ABB57349	Mouse isc
696	29	63.0	331	5	ABB32487	Staphyloc	769	29	63.0	519	8	ABO65074	ABO65074	Klebsiell
697	29	63.0	331	7	ADC21394	Staphyloc	770	29	63.0	521	6	ABU35972	ABU35972	Protein e
698	29	63.0	331	7	ADC25080	S. aureus	771	29	63.0	521	9	ADY52577	ADY52577	Human onc
699	29	63.0	331	7	ADD52582	Staphyloc	772	29	63.0	525	6	ABU34661	ABU34661	Protein e
700	29	63.0	334	5	ABP41920	Human ova	773	29	63.0	525	6	ABU36878	ABU36878	Protein e
701	29	63.0	343	3	AAAG20817	Arabidops	774	29	63.0	530	8	ADS30132	ADS30132	Bacterial
702	29	63.0	349	8	ADS26592	Bacterial	775	29	63.0	531	4	ABB63846	ABB63846	Drosophi
703	29	63.0	349	8	ADS27320	Bacterial	776	29	63.0	532	5	ABB77631	ABB77631	AMPV NAD
704	29	63.0	349	8	ADS26967	Bacterial	777	29	63.0	537	3	AAAB03664	AAb03664	Anti-CD18
705	29	63.0	350	6	ABU43908	Protein e	778	29	63.0	552	2	AAAR30775	AAAR30775	pH52-8.0
706	29	63.0	351	6	ADA33765	Actinoba	779	29	63.0	554	6	ABM73512	ABM73512	Staphyloc
707	29	63.0	353	6	ABU45126	Protein e	780	29	63.0	559	4	ABG28803	ABG28803	Novel hum
708	29	63.0	354	8	ADS21522	Bacterial	781	29	63.0	565	2	AAAG23299	AAg23299	Penicilli
709	29	63.0	355	6	ABU30926	Protein e	782	29	63.0	571	3	AAAG09371	AAg09371	Arabidops
710	29	63.0	357	5	AAAM47340	Pseudomon	783	29	63.0	575	9	AEBO6259	AEBO6259	Amino aci
711	29	63.0	357	6	ABM68389	Photornab	784	29	63.0	576	3	AAAG09370	AAg09370	Arabidops
712	29	63.0	358	5	ABB82010	Pseudomon	785	29	63.0	603	2	AAAY05277	AAy05277	P. roquet
713	29	63.0	358	8	ADRO0548	Pseudomon	786	29	63.0	611	4	ABB67239	ABB67239	Drosophi
714	29	63.0	358	8	ADS25049	Bacterial	787	29	63.0	611	4	ABB70054	ABB70054	Drosophi
715	29	63.0	367	9	ABM90918	M. xanthu	788	29	63.0	612	4	AAW09321	AAW09321	Human mas
716	29	63.0	371	6	ABU26701	Protein e	789	29	63.0	614	7	ADB65122	ADB65122	Human pro
717	29	63.0	371	9	ADZ75757	Xanthomon	790	29	63.0	619	8	ADN17997	ADN17997	Bacterial
718	29	63.0	372	3	AAAY95654	Arabidops	791	29	63.0	628	2	AAAR64979	AAAR64979	Pig Syk.
719	29	63.0	372	3	AAAG13721	Arabidops	792	29	63.0	630	2	AAAR62688	AAAR62688	Tyrosine-
720	29	63.0	372	6	ABU27477	Protein e	793	29	63.0	630	2	AAAR64978	AAAR64978	Human Syk
721	29	63.0	372	7	ABO69210	Pseudomon	794	29	63.0	635	2	AAAY27123	AAy27123	Amino aci
722	29	63.0	374	6	ABU31524	Protein e	795	29	63.0	635	6	ABRS5692	ABRS5692	Human pro
723	29	63.0	377	6	ABP97601	Amino aci	796	29	63.0	635	7	ADD18782	ADD18782	Human dls
724	29	63.0	382	7	ABO80950	Pseudomon	797	29	63.0	635	7	ADPF45090	ADPF45090	Human kin
725	29	63.0	388	3	AAAY67237	Barnacle	798	29	63.0	635	8	ADO07540	ADO07540	Human Syk
726	29	63.0	391	7	ADC94792	E. faeciu	799	29	63.0	635	8	ADOQ88282	ADOQ88282	Human PRO
727	29	63.0	402	8	ADS41993	Bacterial	800	29	63.0	635	8	ADP56066	ADP56066	Human PRO
728	29	63.0	404	9	AEAN43202	Penthytol	801	29	63.0	635	9	ADY97105	ADY97105	Human Syk
729	29	63.0	405	4	AAU35898	Helicobac	802	29	63.0	636	6	ABU11827	ABU11827	Human MD
730	29	63.0	406	3	AAAG13720	Arabidops	803	29	63.0	669	4	ABBS52905	ABBS52905	Escherich
731	29	63.0	407	3	AAAG13719	Arabidops	804	29	63.0	680	4	ADY52644	ADY52644	Human tita
732	29	63.0	409	8	ADM57191	A thailan	805	29	63.0	687	4	ABB71407	ABB71407	Drosophi
733	29	63.0	427	3	AAAG20816	Arabidops	806	29	63.0	687	7	ADFO5554	ADFO5554	Bacterial
734	29	63.0	430	9	ADY52645	Human tita	807	29	63.0	690	7	ABM90802	ABM90802	M. xanthu
735	29	63.0	434	3	ABBS8798	Breast an	808	29	63.0	695	8	ADS43903	ADS43903	Bacterial
736	29	63.0	440	9	ABM95216	Abm95216	809	29	63.0	699	8	ADSS44536	ADSS44536	Bacterial
737	29	63.0	448	3	AAAG20815	Arabidops	810	29	63.0	725	7	ABO72466	ABO72466	Pseudomon
738	29	63.0	450	2	AAAM34505	Heavy cha	811	29	63.0	729	5	ABGB61839	ABGB61839	Prostate
739	29	63.0	450	2	AAAY08755	Human Igg	812	29	63.0	729	6	ABUS6741	ABUS6741	Lung can
740	29	63.0	450	5	ABG31890	Full leng	813	29	63.0	729	7	ADBR75543	ADBR75543	Prostate
741	29	63.0	450	8	ADK18943	Amino aci	814	29	63.0	729	7	ADBE61342	ADBE61342	Human Pro
742	29	63.0	453	4	AAU34670	E. coli c	815	29	63.0	729	7	ADDA45073	ADDA45073	Human Pro
743	29	63.0	453	3	AAAG98879	Protein e	816	29	63.0	729	7	ADN33264	ADN33264	Cancer/an
744	29	63.0	453	6	ABU14674	Protein e	817	29	63.0	729	8	ADQ089068	ADQ089068	Human uro
745	29	63.0	453	6	ABU47894	Protein e	818	29	63.0	729	8	ADU33741	ADU33741	Human sol
746	29	63.0	454	2	AAAR30774	H52H4-160	819	29	63.0	749	6	ABRA41749	ABRA41749	Human DIT
747	29	63.0	457	4	AAU36355	Pseudomon	820	29	63.0	788	8	ADN19995	ADN19995	Bacterial
748	29	63.0	457	6	ABU38615	Protein e	821	29	63.0	826	7	ABO73397	ABO73397	Pseudomon
749	29	63.0	458	6	ABU39289	Protein e	822	29	63.0	829	7	ABO78404	ABO78404	Pseudomon
750	29	63.0	458	6	ABU41759	Protein e	823	29	63.0	868	8	ADSS44035	ADSS44035	Bacterial
751	29	63.0	461	6	ABU01104	S. pneumo	824	29	63.0	878	4	ABBS7761	ABBS7761	Drosophi
752	29	63.0	461	6	ABP81358	Streptoco	825	29	63.0	1041	5	ABR93910	ABR93910	Herbicida
753	29	63.0	461	8	ADK46311	Streptoco	826	29	63.0	1068	5	ADN20534	ADN20534	Bacterial
754	29	63.0	461	8	ADM92124	S pneumon	827	29	63.0	1099	7	ADJ80154	ADJ80154	Novel hum

828	29	63.0	1101	3	ABO7036	Abb07036	Mouse	SRG	901	29	63.0	2339	8	ADM57741	Adm57741	Human	cal
829	29	63.0	1104	6	ABU04703	Abu04703	Human	exp	902	29	63.0	2339	8	ADR43910	Adr43910	Human	N-t
830	29	63.0	1104	6	ABU04704	Abu04704	Human	exp	903	29	63.0	2339	8	ADT98518	Adt98518	Human	N-t
831	29	63.0	1104	6	ABU04701	Abu04701	Human	exp	904	29	63.0	2343	2	AAV31809	Aav31809	N-type	ca
832	29	63.0	1104	8	ADQ19455	Adq19455	Human	sof	905	29	63.0	2343	8	ADR43932	Adr43932	Human	N-t
833	29	63.0	1105	4	AAE09325	Aae09325	Human	int	906	29	63.0	2392	6	ADAI3410	Ada13410	Human	tira
834	29	63.0	1105	6	ABU04702	Abu04702	Human	exp	907	29	63.0	2519	7	ABM88218	Abm88218	Rice	abio
835	29	63.0	1147	9	ADU13771	Adu13771	Human	can	908	29	63.0	3115	4	ABM59485	Abm59485	Drosophill	
836	29	63.0	1228	4	ABE71296	Abb71296	Drosophill		909	29	63.0	3457	2	AAW62504	Aaw62504	Large pol	
837	29	63.0	1274	8	ADO59445	Ado59445	Human	can	910	29	63.0	3457	2	AAW62504	Aaw62504	Large pol	
838	29	63.0	1274	8	ADO59445	Ado59445	Human	can	911	29	63.0	3781	4	ABB71980	Abb71980	Drosophill	
839	29	63.0	1275	6	ABU25467	Abj25467	Murine	ca	912	29	63.0	4067	8	ADU73542	Adu73542	Glycopept	
840	29	63.0	1321	6	ADN23549	Adn23549	Bacterial		913	29	63.0	4868	8	ADM68813	Adm68813	Mosquito	
841	29	63.0	1342	4	ABB64632	Abb64632	Drosophill		914	29	63.0	5100	8	ADM68902	Adm68902	Heliothis	
842	29	63.0	1362	9	ADZ13767	Adz13767	Human	can	915	29	63.0	5101	8	ADM68760	Adm68760	Myzus per	
843	29	63.0	1381	9	ADZ13769	Adz13769	Human	can	916	29	63.0	5104	8	ADM68762	Adm68762	Periplane	
844	29	63.0	1381	9	ADZ13761	Adz13761	Human	can	917	29	63.0	5107	4	ABB65257	Abb65257	Drosophill	
845	29	63.0	1432	9	ADQ62813	Adq62813	Pseudomon		918	29	63.0	5109	8	ADM68766	Adm68766	Drosophill	
846	29	63.0	1435	6	ABJ26067	Abj26067	Aspergill		919	29	63.0	5112	8	ADM68881	Adm68881	Drosophill	
847	29	63.0	1441	9	ADY99946	Ady99946	Banana	RG	920	29	63.0	5112	8	ADM68882	Adm68882	Drosophill	
848	29	63.0	1443	7	ADM05159	Adm05159	Human	pro	921	29	63.0	5113	8	ADM68877	Adm68877	Drosophill	
849	29	63.0	1478	7	ADK40911	Adk40911	Novel	hum	922	29	63.0	5126	8	ADM68879	Adm68879	Drosophill	
850	29	63.0	1478	7	ADK15634	Adk15634	Kinase	40	923	29	63.0	5126	8	ADM68880	Adm68880	Drosophill	
851	29	63.0	1493	2	AAZ27640	Aaz27640	Human	cal	924	29	63.0	5126	8	ADM68812	Adm68812	Drosophill	
852	29	63.0	1564	8	ADO96162	Ado96162	T cell	ac	925	29	63.0	5127	8	ADM68878	Adm68878	Drosophill	
853	29	63.0	1586	8	ADK60181	Adk60181	Angiogene		926	29	63.0	5127	8	ADM68764	Adm68764	Peregrinu	
854	29	63.0	1586	8	ADK60482	Adk60482	Angiogene		927	29	63.0	5127	8	ADM68876	Adm68876	Drosophill	
855	29	63.0	1586	8	ADP73105	Adp73105	Angiogene		928	29	63.0	5128	8	ADM68884	Adm68884	Heliothis	
856	29	63.0	1592	6	ABR52599	Abv52599	Protein	s	929	29	63.0	5134	8	ADM68886	Adm68886	Heliothis	
857	29	63.0	1592	6	ABP59619	Abp59619	Saccharom		930	29	63.0	5142	8	ADM68758	Adm68758	Heliothis	
858	29	63.0	1592	7	ADK63890	Adk63890	Disease	t	931	29	63.0	5142	8	ADM68900	Adm68900	Heliothis	
859	29	63.0	1668	7	ADI21172	Adi21172	Novel	hum	932	29	63.0	7094	8	ABY03145	Abv03145	Bovine	col
860	29	63.0	1745	8	ADM31028	Adm31028	Human	cal	933	29	63.0	7176	8	ABY03151	Abv03151	Murine	he
861	29	63.0	1748	7	ADJ70162	Adj70162	Human	hea	934	29	63.0	7771	9	ADZ51730	Adz51730	PKS	FACE
862	29	63.0	1880	9	ADZ13759	Adz13759	Human	can	935	29	60.9		6	AAV06709	Aav06709	Abv	varia
863	29	63.0	1899	9	ADZ13765	Adz13765	Human	can	936	29	60.9		6	AAE17799	Aae17799	E. coli	m
864	29	63.0	1931	2	AAZ27649	Aaz27649	Human	cal	937	29	60.9		8	ADO39707	Ado39707	Human	12E
865	29	63.0	1942	9	ADZ13763	Adz13763	Human	can	938	29	60.9	10	9	ADY75364	Ady75364	Peptide	e
866	29	63.0	2222	7	ADD47000	Add47000	Rat	Prote	939	29	60.9	12	7	ABR63058	Abv63058	Pathogen	
867	29	63.0	2237	2	AAK33550	Aak33550	Sequence		940	29	60.9		5	AAU69669	Aau69669	Cell	deat
868	29	63.0	2237	2	AAK71006	Aak71006	Human	neu	941	29	60.9		6	ADA90240	Ada90240	Anti-Abet	
869	29	63.0	2237	2	AAW63142	Aaw63142	Human	cal	942	29	60.9		6	ADA90463	Ada90463	MS-Roch	
870	29	63.0	2237	3	AAI10573	Aai10573	Human	cal	943	29	60.9		13	ADA91083	Ada91083	MS-R	Fab/
871	29	63.0	2237	5	AAE24786	Aae24786	Human	cal	944	29	60.9		6	ADA91214	Ada91214	MS-R	Fab/
872	29	63.0	2237	6	ABP72256	Abp72256	Human	N-t	945	29	60.9		6	ADA91320	Ada91320	MS-R	Fab/
873	29	63.0	2237	8	ADJ38319	Adj38319	Human	cal	946	29	60.9		6	ADA90446	Ada90446	MS-Roch	
874	29	63.0	2237	8	ADM57742	Adm57742	Human	cal	947	29	60.9		6	ADA91087	Ada91087	MS-R	Fab/
875	29	63.0	2237	8	ADT98520	Adt98520	Human	N-t	948	29	60.9		6	ADA91210	Ada91210	MS-R	Fab/
876	29	63.0	2251	2	AAK71009	Aak71009	Human	neu	949	29	60.9		6	ADA90449	Ada90449	MS-Roch	
877	29	63.0	2251	5	AAI10581	Aai10581	Human	cal	950	29	60.9		6	ADA90453	Ada90453	MS-Roch	
878	29	63.0	2251	5	AAE24794	Aae24794	Human	cal	951	29	60.9		6	ADA90466	Ada90466	MS-Roch	
879	29	63.0	2251	6	ADA13412	Ada13412	Human	cal	952	29	60.9		6	ADA91322	Ada91322	MS-R	Fab/
880	29	63.0	2251	8	ADJ38343	Adj38343	Human	cal	953	29	60.9		6	ADA91323	Ada91323	MS-R	Fab/
881	29	63.0	2251	8	ADM57750	Adm57750	Human	cal	954	29	60.9		6	ADA90244	Ada90244	Anti-Abet	
882	29	63.0	2251	8	ADO59448	Ado59448	Human	can	955	29	60.9		6	ADA90457	Ada90457	MS-Roch	
883	29	63.0	2264	8	ADM31026	Adm31026	Human	can	956	29	60.9		6	ADA90601	Ada90601	MS-Roch	
884	29	63.0	2270	2	AAK71010	Aak71010	Human	neu	957	29	60.9		6	ADA91211	Ada91211	MS-R	Fab/
885	29	63.0	2270	2	AAK69604	Aak69604	Calcium	c	958	29	60.9		6	ADA91217	Ada91217	MS-R	Fab/
886	29	63.0	2270	3	AAI10582	Aai10582	Human	cal	959	29	60.9		6	ADA91220	Ada91220	MS-R	Fab/
887	29	63.0	2270	5	AAE24795	Aae24795	Human	cal	960	29	60.9		6	ADA90445	Ada90445	MS-Roch	
888	29	63.0	2270	8	ADJ38345	Adj38345	Human	cal	961	29	60.9		6	ADA90459	Ada90459	MS-Roch	
889	29	63.0	2270	8	ADM57751	Adm57751	Human	cal	962	29	60.9		6	ADA90461	Ada90461	MS-Roch	
890	29	63.0	2270	8	ADO59540	Ado59540	Human	can	963	29	60.9		6	ADA90470	Ada90470	MS-Roch	
891	29	63.0	2313	8	ADO59542	Ado59542	Human	can	964	29	60.9		6	ADA90472	Ada90472	MS-Roch	
892	29	63.0	2337	2	AAW37878	Aaw37878	Human	cal	965	29	60.9		6	ADA90599	Ada90599	MS-Roch	
893	29	63.0	2339	2	AAK33549	Aak33549	Human	cal	966	29	60.9		6	ADA90602	Ada90602	MS-Roch	
894	29	63.0	2339	2	AAK71005	Aak71005	Sequence		967	29	60.9		6	ADA90611	Ada90611	MS-Roch	
895	29	63.0	2339	2	AAW63141	Aaw63141	Human	neu	968	29	60.9		6	ADA89907	Ada89907	MSR-3	VH
896	29	63.0	2339	3	AAI10572	Aai10572	Human	cal	969	29	60.9		6	ADA90455	Ada90455	MS-Roch	
897	29	63.0	2339	5	AAE24785	Aae24785	Human	cal	970	29	60.9		6	ADA90464	Ada90464	MS-Roch	
898	29	63.0	2339	5	ABP72255	Abp72255	Human	N-t	971	29	60.9		6	ADA91209	Ada91209	MS-R	Fab/
899	29	63.0	2339	7	ADM45859	Adm45859	Human	N-t	972	29	60.9		6	ADA91221	Ada91221	MS-R	Fab/
900	29	63.0	2339	8	ADJ38317	Adj38317	Human	cal	973	29	60.9		6	ADA90250	Ada90250	Anti-Abet	

974	28	60.9	13	6	ADA90448
975	28	60.9	13	6	ADA90473
976	28	60.9	13	6	ADA90607
977	28	60.9	13	6	ADA91212
978	28	60.9	13	6	ADA91215
979	28	60.9	13	6	ADA91222
980	28	60.9	13	6	ADA90242
981	28	60.9	13	6	ADA90452
982	28	60.9	13	6	ADA90468
983	28	60.9	13	6	ADA90471
984	28	60.9	13	6	ADA91213
985	28	60.9	13	6	ADA91219
986	28	60.9	13	6	ADA90454
987	28	60.9	13	6	ADA90458
988	28	60.9	13	6	ADA91086
989	28	60.9	13	6	ADA91208
990	28	60.9	13	6	ADA90246
991	28	60.9	13	6	ADA90248
992	28	60.9	13	6	ADA90603
993	28	60.9	13	6	ADA90608
994	28	60.9	13	6	ADA91082
995	28	60.9	13	6	ADA91319
996	28	60.9	13	6	ADA91321
997	28	60.9	13	6	ADA89946
998	28	60.9	13	6	ADA90252
999	28	60.9	13	6	ADA90467
1000	28	60.9	13	6	ADA90610

ALIGNMENTS

RESULT 1

ADO32087 standard; peptide; 9 AA.

ADO32087;

12-AUG-2004 (first entry)

Mouse anti-CD33 antibody My9-6 heavy chain CDR3 SEQ ID NO:3.

anti-CD33 antibody; epitope-binding fragment;

complementarity-determining region; CDR; immunoglobulin; cytosolic;

antibody; myelodysplastic syndrome; acute myeloid leukaemia;

chronic myeloid leukaemia; pro-myelocytic leukaemia; mouse; My9-6;

heavy chain.

Mus musculus

WO2004043344-A2.

27-MAY-2004.

05-NOV-2003; 2003WO-US032737.

07-NOV-2002; 2002US-0424332P.

(IMMU-) IMMUNOGEN INC.

Hoffee MG, Tavares D, Lutz RJ;

WPI; 2004-411619/38.

New antibodies that bind to CD33, useful for treating a disease

associated with CD33 expression, such as myelodysplastic syndrome, acute

or chronic myeloid leukemia.

Claim 1; SEQ ID NO 3; 124pp: English.

The present invention describes an isolated anti-CD33 antibody or its

epitope-binding fragment comprising: (a) at least one complementarity-

determining region (CDR); or (b) at least heavy chain variable region

comprising 3 CDRs, and at least one light chain variable region, where the CDR has the ability to bind CD33. Also described: (1) an immunoglobulin comprising the antibody or its epitope-binding fragment linked to a drug or prodrug; (2) a composition comprising the antibody or epitope-binding fragment and a drug or prodrug; (3) a pharmaceutical composition comprising the immunoglobulin, composition or the antibody defined above, or its epitope-binding fragment, and a pharmaceutical agent; (4) a diagnostic reagent comprising the antibody defined above, where the antibody or antibody fragment is labelled; (5) inhibiting the growth of a cell expressing CD33 by contacting the cell with the above defined antibody or its epitope-binding fragment, immunoglobulin, or (pharmaceutical) composition; (6) determining whether a biological sample contains a myelogenous cancer cell; (7) an improved antibody or its epitope-binding fragment that specifically binds to CD33; (8) an isolated polynucleotide encoding the antibody or its epitope-binding fragment defined above; (9) an isolated polynucleotide encoding a light or heavy chain of the antibody defined above or its epitope-binding fragment; (10) a recombinant vector comprising the polynucleotide; (11) a host cell transformed with the recombinant vector; (12) producing an antibody or its epitope-binding fragment having the ability to bind CD33; and (13) obtaining CD33 from a biological material. The anti-CD33 antibody has cytosolic activity. The antibody or its epitope-binding fragment, immunoglobulin, composition can be used for treating a subject having a disease where CD33 is expressed, such as myelodysplastic syndrome, acute myeloid leukaemia, chronic myeloid leukaemia or pro-myelocytic leukaemia. It can also be used for inhibiting the growth of cells expressing CD33, and for in vivo imaging or as affinity purification agents. The present sequence represents the mouse anti-CD33 antibody My9-6 heavy chain CDR3, which is used in an example from the present invention.

Sequence 9 AA;

SQ

Query Match 100.0%; Score 46; DB 8; Length 9;

Best local similarity 100.0%; Pred. No. 2e-06; Mismatches 0; Gaps 0;

Matches 9; Conservative 0; Indels 0;

1 EVRLRYFDV 9

1 EVRLRYFDV 9

Db

RESULT 2

ADO32137 standard; peptide; 20 AA.

ADO32137;

12-AUG-2004 (first entry)

Mouse anti-CD33 antibody My9-6 heavy chain peptide SEQ ID NO:53.

anti-CD33 antibody; epitope-binding fragment;

complementarity-determining region; CDR; immunoglobulin; cytosolic;

antibody; myelodysplastic syndrome; acute myeloid leukaemia;

chronic myeloid leukaemia; pro-myelocytic leukaemia; mouse; My9-6.

Mus musculus.

WO2004043344-A2.

27-MAY-2004.

05-NOV-2003; 2003WO-US032737.

07-NOV-2002; 2002US-0424332P.

(IMMU-) IMMUNOGEN INC.

Hoffee MG, Tavares D, Lutz RJ;

WPI; 2004-411619/38.

New antibodies that bind to CD33, useful for treating a disease

associated with CD33 expression, such as myelodysplastic syndrome, acute

or chronic myeloid leukemia.

Claim 1; SEQ ID NO 3; 124pp: English.

The present invention describes an isolated anti-CD33 antibody or its

epitope-binding fragment comprising: (a) at least one complementarity-

determining region (CDR); or (b) at least heavy chain variable region

comprising 3 CDRs, and at least one light chain variable region, where

the CDR has the ability to bind CD33. Also described: (1) an

immunoglobulin comprising the antibody or its epitope-binding fragment

linked to a drug or prodrug; (2) a composition comprising the antibody or

epitope-binding fragment and a drug or prodrug; (3) a pharmaceutical

composition comprising the immunoglobulin, composition or the antibody

defined above, or its epitope-binding fragment, and a pharmaceutical

agent; (4) a diagnostic reagent comprising the antibody defined above,

PT associated with CD33 expression, such as myelodysplastic syndrome, acute
PT or chronic myeloid leukemia.

PS Example 3; SEQ ID NO 53; 124pp; English.

XX The present invention describes an isolated anti-CD33 antibody or its
CC epitope-binding fragment comprising: (a) at least one complementarity-
CC determining region (CDR); or (b) at least heavy chain variable region
CC comprising 3 CDRs, and at least one light chain variable region, where
CC the CDR has the ability to bind CD33. Also described: (1) an
CC immunocjugate comprising the antibody or its epitope-binding fragment
CC linked to a drug or prodrug; (2) a composition comprising the antibody or
CC epitope-binding fragment and a drug or prodrug; (3) a pharmaceutical
CC composition comprising the immunocjugate, composition or the antibody
CC defined above, or its epitope-binding fragment, and a pharmaceutical
CC agent; (4) a diagnostic reagent comprising the antibody defined above,
CC where the antibody or antibody fragment is labelled; (5) inhibiting the
CC growth of a cell expressing CD33 by contacting the cell with the above
CC defined antibody or its epitope-binding fragment, immunocjugate, or
CC (pharmaceutical) composition; (6) determining whether a biological sample
CC contains a myelogenous cancer cell; (7) an improved antibody or its
CC epitope-binding fragment that specifically binds to CD33; (8) an isolated
CC polynucleotide encoding the antibody or its epitope-binding fragment
CC defined above; (9) an isolated polynucleotide encoding a light or heavy
CC chain of the antibody defined above or its epitope-binding fragment; (10)
CC a recombinant vector comprising the polynucleotide; (11) a host cell
CC transformed with the recombinant vector; (12) producing an antibody or
CC its epitope-binding fragment having the ability to bind CD33; and (13)
CC obtaining CD33 from a biological material. The anti-CD33 antibody has
CC cytostatic activity. The antibody or its epitope-binding fragment,
CC immunocjugate, composition can be used for treating a subject having a
CC disease where CD33 is expressed, such as myelodysplastic syndrome, acute
CC myeloid leukemia, chronic myeloid leukemia or pro-myelocytic leukemia.
CC It can also be used for inhibiting the growth of cells expressing CD33,
CC and for in vivo imaging or as affinity purification agents. The present
CC sequence represents a mouse anti-CD33 antibody My9-6 heavy chain peptide,
CC which is used in an example from the present invention.

XX Sequence 20 AA;

SO Query Match 100.0%; Score 46; DB 8; Length 20;

Best Local Similarity 100.0%; Pred. No. 0.046;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVRLRYPDV 9
1 EVRLRYPDV 9

Db 1 EVRLRYPDV 9

RESULT 3

AD032157
ID AD032157 standard; protein; 117 AA.

XX ADO32157;

DT 12-AUG-2004 (first entry)

XX Mouse anti-CD33 antibody heavy chain homologous protein SEQ ID NO:73.

XX anti-CD33 antibody; epitope-binding fragment;
KW complementarity-determining region; CDR; immunocjugate; cytostatic;
KW antibody; myelodysplastic syndrome; acute myeloid leukemia;
KW chronic myeloid leukemia; pro-myelocytic leukemia; mouse; heavy chain.
XX
OS Mus musculus.

PN WO2004043344-A2.

XX 27-MAY-2004.

PF 05-NOV-2003; 2003WO-US032737.

XX 07-NOV-2002; 2002US-0424332P.

XX (IMMU-) IMMUNOGEN INC.

PI Hoffee MG, Tavares D, Lutz RJ;

DR WPI; 2004-411619/38.

XX New antibodies that bind to CD33, useful for treating a disease
PT associated with CD33 expression, such as myelodysplastic syndrome, acute
PT or chronic myeloid leukemia.

PS Example 3; SEQ ID NO 73; 124pp; English.

XX The present invention describes an isolated anti-CD33 antibody or its
CC epitope-binding fragment comprising: (a) at least one complementarity-
CC determining region (CDR); or (b) at least heavy chain variable region
CC comprising 3 CDRs, and at least one light chain variable region, where
CC the CDR has the ability to bind CD33. Also described: (1) an
CC immunocjugate comprising the antibody or its epitope-binding fragment
CC linked to a drug or prodrug; (2) a composition comprising the antibody or
CC epitope-binding fragment and a drug or prodrug; (3) a pharmaceutical
CC composition comprising the immunocjugate, composition or the antibody
CC defined above, or its epitope-binding fragment, and a pharmaceutical
CC agent; (4) a diagnostic reagent comprising the antibody defined above,
CC where the antibody or antibody fragment is labelled; (5) inhibiting the
CC growth of a cell expressing CD33 by contacting the cell with the above
CC defined antibody or its epitope-binding fragment, immunocjugate, or
CC (pharmaceutical) composition; (6) determining whether a biological sample
CC contains a myelogenous cancer cell; (7) an improved antibody or its
CC epitope-binding fragment that specifically binds to CD33; (8) an isolated
CC polynucleotide encoding the antibody or its epitope-binding fragment
CC defined above; (9) an isolated polynucleotide encoding a light or heavy
CC chain of the antibody defined above or its epitope-binding fragment; (10)
CC a recombinant vector comprising the polynucleotide; (11) a host cell
CC transformed with the recombinant vector; (12) producing an antibody or
CC its epitope-binding fragment having the ability to bind CD33; and (13)
CC obtaining CD33 from a biological material. The anti-CD33 antibody has
CC cytostatic activity. The antibody or its epitope-binding fragment,
CC immunocjugate, composition can be used for treating a subject having a
CC disease where CD33 is expressed, such as myelodysplastic syndrome, acute
CC myeloid leukemia, chronic myeloid leukemia or pro-myelocytic leukemia.
CC It can also be used for inhibiting the growth of cells expressing CD33,
CC and for in vivo imaging or as affinity purification agents. The present
CC sequence represents a mouse anti-CD33 antibody heavy chain homologous
CC amino acid sequence, which is used in an example from the present
CC invention.

XX Sequence 117 AA;

SO Query Match 100.0%; Score 46; DB 8; Length 117;

Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVRLRYPDV 9
99 EVRLRYPDV 107

Db 99 EVRLRYPDV 107

RESULT 4

AD032091
ID AD032091 standard; protein; 118 AA.

XX ADO32091;

DT 12-AUG-2004 (first entry)

XX Mouse anti-CD33 antibody My9-6 heavy chain variable region SEQ ID NO:7.

XX anti-CD33 antibody; epitope-binding fragment;
KW complementarity-determining region; CDR; immunocjugate; cytostatic;
KW antibody; myelodysplastic syndrome; acute myeloid leukemia;
KW chronic myeloid leukemia; pro-myelocytic leukemia; mouse; My9-6;
KW heavy chain.

XX OS Mus musculus.
 XX PN WO2004043344-A2.
 XX PD 27-MAY-2004.
 XX PF 05-NOV-2003; 2003WO-US032737.
 XX PR 07-NOV-2002; 2002US-0424332P.
 XX PA (IMMU-) IMMUNOGEN INC.
 XX PI Hoffee MG, Tavares D, Lutz RJ;
 XX DR WPI; 2004-411619/38.
 XX DR N-PSDB; ADO32140.
 XX PT New antibodies that bind to CD33, useful for treating a disease
 PT associated with CD33 expression, such as myelodysplastic syndrome, acute
 PT or chronic myeloid leukemia.
 XX PS Claim 5; SEQ ID NO 7; 124pp; English.
 XX XX
 CC The present invention describes an isolated anti-CD33 antibody or its
 CC epitope-binding fragment comprising: (a) at least one complementarity-
 CC determining region (CDR); or (b) at least heavy chain variable region
 CC comprising 3 CDRs, and at least one light chain variable region, where
 CC the CDR has the ability to bind CD33. Also described: (1) an
 CC immunocjugate comprising the antibody or its epitope-binding fragment
 CC linked to a drug or prodrug; (2) a composition comprising the antibody or
 CC epitope-binding fragment and a drug or prodrug; (3) a pharmaceutical
 CC composition comprising the immunocjugate, composition or the antibody
 CC defined above, or its epitope-binding fragment, and a pharmaceutical
 CC agent; (4) a diagnostic reagent comprising the antibody defined above,
 CC where the antibody or antibody fragment is labelled; (5) inhibiting the
 CC growth of a cell expressing CD33 by contacting the cell with the above
 CC defined antibody or its epitope-binding fragment, immunocjugate, or
 CC (pharmaceutical) composition; (6) determining whether a biological sample
 CC contains a myelogenous cancer cell; (7) an improved antibody or its
 CC epitope-binding fragment that specifically binds to CD33; (8) an isolated
 CC polynucleotide encoding the antibody or its epitope-binding fragment
 CC defined above; (9) an isolated polynucleotide encoding a light or heavy
 CC chain of the antibody defined above or its epitope-binding fragment; (10)
 CC a recombinant vector comprising the polynucleotide; (11) a host cell
 CC transformed with the recombinant vector; (12) producing an antibody or
 CC its epitope-binding fragment having the ability to bind CD33; and (13)
 CC obtaining CD33 from a biological material. The anti-CD33 antibody has
 CC cytostatic activity. The antibody or its epitope-binding fragment,
 CC immunocjugate, composition can be used for treating a subject having a
 CC disease where CD33 is expressed, such as myelodysplastic syndrome, acute
 CC myeloid leukemia, chronic myeloid leukemia or pro-myelocytic leukemia.
 CC It can also be used for inhibiting the growth of cells expressing CD33,
 CC and for in vivo imaging or as affinity purification agents. The present
 CC sequence represents the mouse anti-CD33 antibody My9-6 heavy chain
 CC variable region, which is used in an example from the present invention.
 XX XX
 SQ Sequence 118 AA;
 Query Match 100.0%; Score 46; DB 8; Length 118;
 Best Local Similarity 100.0%; Pred. No. 0.3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EVRLRYFDV 9
 |||||
 DB 99 EVRLRYFDV 107
 |||||
 RESULT 5
 ADO32093 standard; protein; 118 AA.
 XX ADO32093;
 AC ADO32093;

XX DT 12-AUG-2004 (first entry)
 XX DE Humanised mouse anti-CD33 antibody My9-6 heavy chain SEQ ID NO:9.
 XX XX anti-CD33 antibody; epitope-binding fragment;
 KW complementarity-determining region; CDR; immunocjugate; cytostatic;
 KW antibody; myelodysplastic syndrome; acute myeloid leukemia;
 KW chronic myeloid leukemia; pro-myelocytic leukemia; mouse; humanised;
 KW My9-6; heavy chain.
 XX XX Mus musculus.
 OS Homo sapiens.
 OS Synthetic.
 XX XX WO2004043344-A2.
 XX PD 27-MAY-2004.
 XX PF 05-NOV-2003; 2003WO-US032737.
 XX PR 07-NOV-2002; 2002US-0424332P.
 XX PA (IMMU-) IMMUNOGEN INC.
 XX PI Hoffee MG, Tavares D, Lutz RJ;
 XX DR WPI; 2004-411619/38.
 XX PT New antibodies that bind to CD33, useful for treating a disease
 PT associated with CD33 expression, such as myelodysplastic syndrome, acute
 PT or chronic myeloid leukemia.
 XX PS Claim 11; SEQ ID NO 9; 124pp; English.
 XX XX
 CC The present invention describes an isolated anti-CD33 antibody or its
 CC epitope-binding fragment comprising: (a) at least one complementarity-
 CC determining region (CDR); or (b) at least heavy chain variable region
 CC comprising 3 CDRs, and at least one light chain variable region, where
 CC the CDR has the ability to bind CD33. Also described: (1) an
 CC immunocjugate comprising the antibody or its epitope-binding fragment
 CC linked to a drug or prodrug; (2) a composition comprising the antibody or
 CC epitope-binding fragment and a drug or prodrug; (3) a pharmaceutical
 CC composition comprising the immunocjugate, composition or the antibody
 CC defined above, or its epitope-binding fragment, and a pharmaceutical
 CC agent; (4) a diagnostic reagent comprising the antibody defined above,
 CC where the antibody or antibody fragment is labelled; (5) inhibiting the
 CC growth of a cell expressing CD33 by contacting the cell with the above
 CC defined antibody or its epitope-binding fragment, immunocjugate, or
 CC (pharmaceutical) composition; (6) determining whether a biological sample
 CC contains a myelogenous cancer cell; (7) an improved antibody or its
 CC epitope-binding fragment that specifically binds to CD33; (8) an isolated
 CC polynucleotide encoding the antibody or its epitope-binding fragment
 CC defined above; (9) an isolated polynucleotide encoding a light or heavy
 CC chain of the antibody defined above or its epitope-binding fragment; (10)
 CC a recombinant vector comprising the polynucleotide; (11) a host cell
 CC transformed with the recombinant vector; (12) producing an antibody or
 CC its epitope-binding fragment having the ability to bind CD33; and (13)
 CC obtaining CD33 from a biological material. The anti-CD33 antibody has
 CC cytostatic activity. The antibody or its epitope-binding fragment,
 CC immunocjugate, composition can be used for treating a subject having a
 CC disease where CD33 is expressed, such as myelodysplastic syndrome, acute
 CC myeloid leukemia, chronic myeloid leukemia or pro-myelocytic leukemia.
 CC It can also be used for inhibiting the growth of cells expressing CD33,
 CC and for in vivo imaging or as affinity purification agents. The present
 CC sequence represents a humanised mouse anti-CD33 antibody My9-6 heavy
 CC chain variable region, which is used in an example from the present
 CC invention.
 XX XX
 SQ Sequence 118 AA;
 Query Match 100.0%; Score 46; DB 8; Length 118;
 Best Local Similarity 100.0%; Pred. No. 0.3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EVRLRYFDV 9
 |||||
 DB 99 EVRLRYFDV 107
 |||||

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EVRLRYFDV 9
 DB 99 EVRLRYFDV 107

RESULT 6
 ADX58064
 ID ADX58064 standard; protein; 306 AA.

AC ADX58064;
 DT 21-APR-2005 (first entry)
 DE A single chain antibody light chain for glycoprotein D.
 KM virucide; vaccine; single chain antibody; HSV; glycoprotein;
 KM glycoprotein D; herpes simplex virus; HSV infection.
 OS Synthetic.
 PN WO2005011580-A2.
 PD 10-FEB-2005.
 PF 26-JUL-2004; 2004WO-US024013.
 PR 25-JUL-2003; 2003US-0489984P.
 PA (TEXA) UNIV TEXAS SYSTEM.
 PI Simmons A, Chen J;
 DR WPI; 2005-142827/15.
 DR N-PSDB; ADX58063.
 PT New single chain antibody that specifically binds to a Herpes Simplex
 PT virus (HSV) glycoprotein, useful in preparing a composition for
 PT preventing or treating a HSV infection.
 PS Disclosure; SEQ ID NO 2; 99p; English.
 CC The specification describes a single chain antibody that specifically
 CC binds to a herpes simplex virus (HSV) glycoprotein, e.g. glycoprotein D.
 CC The single chain antibody of the invention is useful for preparing a
 CC composition for preventing or treating a HSV infection. The present
 CC sequence represents a single chain antibody of the invention.
 SQ Sequence 306 AA;

Query Match 82.6%; Score 38; DB 9; Length 306;
 Best Local Similarity 88.9%; Pred. No. 32;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 EVRLRYFDV 9
 DB 260 EVRLRYFDV 268

RESULT 7
 ABB89783
 ID ABB89783 standard; protein; 816 AA.

AC ABB89783;
 DT 24-MAY-2002 (first entry)
 DE Human polypeptide SEQ ID NO 2159.

KM Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
 KM antiallergic; hepatocytic; antidiabetic; antiinflammatory; antitumor;
 KM vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;

KM cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
 KM neurological disease; infection; human; secreted protein.

OS Homo sapiens.
 PN WO200190304-A2.
 PD 29-NOV-2001.
 PF 18-MAY-2001; 2001WO-US016450.
 PR 19-MAY-2000; 2000US-0205515P.
 PA (HUMA-) HUMAN GENOME SCI INC.

PI Birse CE, Rosen CA;
 DR WPI; 2002-122018/16.
 DR N-PSDB; ABL90192.

PT Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
 PT prevention of neural, immune system, muscular, reproductive,
 PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative
 PT disorders.

PS Claim 11; SEQ ID NO 2159; 2081pp + Sequence listing; English.

CC The invention relates to novel genes (ABL89449-ABL90853) and proteins
 CC (ABB89040-ABB90444) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
 CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
 CC ovarian cancer, and other cancers of the adrenal gland, bone, bone marrow,
 CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
 CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
 CC anemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
 CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
 CC cardiovascular disorders such as myocardial ischemias; (d) wound healing
 CC; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
 CC infectious diseases such as viral, bacterial, fungal and parasitic
 CC infections. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 SQ Sequence 816 AA;

Query Match 82.6%; Score 38; DB 5; Length 816;
 Best Local Similarity 75.0%; Pred. No. 91;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EVRLRYFD 8
 DB 40 EIRLRYFD 47

RESULT 8
 AAM93422
 ID AAM93422 standard; protein; 897 AA.

AC AAM93422;
 DT 06-NOV-2001 (first entry)
 DE Human polypeptide, SEQ ID NO: 3044.
 KM Human, full length cDNA; cDNA synthesis; oligo-capping.

OS Homo sapiens.
 PN EP1130094-A2.
 PD 05-SEP-2001.

XX 07-JUL-2000; 2000EP-00114089.
PF
XX 08-JUL-1999; 99JP-00194486.
PR
XX 11-JAN-2000; 2000JP-00118774.
PR
XX 02-MAY-2000; 2000JP-00183765.
PR
XX (HELI-) HELIX RES INST.
PA
XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
PI
XX Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
PI
XX WPI: 2001-524255/58.
DR
XX N-PSDB; AAK94343.
DR
XX 830 Primers useful for synthesizing full length cDNA clones and their use
PT
XX in genetic manipulation.
PT
XX
PS Disclosure; SEQ ID NO 3044; 1380bp + Sequence Listing; English.
PS
XX The invention relates to primers for synthesizing full length cDNA
CC
XX clones. 830 cDNA molecules encoding a human protein have been isolated
CC
XX and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
CC
XX been determined. Primers for synthesizing the full length cDNA are useful
CC
XX for clarifying the function of the protein encoded by the cDNA. The full
CC
XX length clones were obtained by construction of full length enriched cDNA
CC
XX libraries that were synthesised by the oligo-capping method. The primers
CC
XX enable the production of the full length cDNA easily without any special
CC
XX methods. The present sequence is a polypeptide provided in the
CC
XX specification. Note: The sequence data for this patent did not form part
CC
XX of the printed specification, but was obtained in CD-ROM format directly
CC
XX from EPO
SQ
XX Sequence 897 AA;

Query Match 82.6%; Score 38; DB 4; Length 897;
Best Local Similarity 75.0%; Pred. No. 1e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVRLRYPD 8
|:|:|:|
Db 4 EIRLKYPD 11

RESULT 9
ADL31011
ID ADL31011 standard; protein; 897 AA.
XX
XX ADL31011;
AC
XX
XX 20-MAY-2004 (first entry)
DT
XX
XX Human protein encoded by a full length cDNA clone SegID 3044.
DE
XX
XX human; medicine; signal transduction; glycoprotein; transcription;
KW
XX oligo-capping method.
KW
XX Homo sapiens.
OS
XX
XX EP1396543-A2;
PN
XX
XX 10-MAR-2004.
PD
XX
XX 07-JUL-2000; 2003EP-00025638.
PF
XX
XX 08-JUL-1999; 99JP-00194486.
PR
XX 11-JAN-2000; 2000JP-00118774.
PR
XX 02-MAY-2000; 2000JP-00183865.
PR
XX 07-JUL-2000; 2000EP-00114089.
PR
XX (REAS-) RES ASSOC BIOTECHNOLOGY.
PA
XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
PI

PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX
XX WPI: 2004-204755/20.
DR
XX N-PSDB; ADL31010.
DR
XX
XX New oligonucleotide primers (830 cDNAs) useful for synthesizing full
PT
XX length human cDNAs.
PT
XX
XX Example 1; SEQ ID NO 3044; 1340bp; English.
PS
XX
XX This invention relates to a novel primers useful for synthesizing full
CC
XX length cDNA molecules that encode human proteins. Specifically, it refers
CC
XX to secretory or membrane proteins that are potential therapeutic agents/
CC
XX target molecules in the field of medicine, and in particular genes
CC
XX encoding proteins that are associated with signal transduction.
CC
XX glycoproteins and transcription. The present invention describes a method
CC
XX for efficiently cloning a full length human cDNA from both the 5' and 3'
CC
XX ends using the oligo-capping method. This polypeptide sequence is a full
CC
XX length human protein of the invention.
CC
XX

SQ Sequence 897 AA;

Query Match 82.6%; Score 38; DB 8; Length 897;
Best Local Similarity 75.0%; Pred. No. 1e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVRLRYPD 8
|:|:|:|
Db 4 EIRLKYPD 11

RESULT 10
AAV26349
ID AAV26349 standard; protein; 933 AA.
XX
XX AAV26349;
AC
XX
XX 13-JAN-2000 (first entry)
DT
XX
XX Human secreted protein ycl4_1.
DE

XX clone ycl4_1; human; secreted protein; ycl4_1 protein; ATCC 98724;
XX cytokine; cell proliferation; cell differentiation; anti-inflammatory;
KW immune stimulation/suppression; haematopoiesis regulation; haemostatic;
KW thrombolytic; tumour inhibition; activin; inhibin activity; treatment;
KW prevention; medical condition; transmembrane domain.
KW
XX Homo sapiens.
OS
XX

XX Key Location/Qualifiers
FH 388..400
FT Peptide /label= leader/signal sequence
FT /note="Acts as a transmembrane domain due to its
FT hydrophobic nature"
FT 401..933
FT Protein /label= Mature_ycl4_1
FT
XX

XX W09951732-A1.

XX 14-OCT-1999.

XX 07-APR-1999; 99WO-US007643.
PF

XX 07-APR-1998; 98US-0080669P.
PR

XX 06-APR-1999; 99US-00287150.
PR

XX (GENY) GENETICS INST INC.
PA

XX Wong GG, Clark HF, Fechel K, Agostino MJ;
PI

XX WPI: 1999-611039/52.
DR

XX N-PSDB; AAX90833.
DR

XX

PT New polynucleotides encoding secreted human proteins, derived from human
PT adult testes, human fetal brain and human fetal kidney CDNA libraries.
XX
PS Claim 19; Page 74-77; 82pp; English.
XX
CC The present sequence is a secreted protein ycl4_1 derived from a human
CC foetal kidney (293 cell line) CDNA library. The sequence shows homology
CC to AA013642 and AA247816 sequences. It contains immunoglobulin and major
CC histocompatibility complex at its N-terminus. The clone ycl4_1 is
CC deposited under accession number ATCC 98724. The protein is predicted to
CC exhibit various activities including nutritional, cytokine and cell
CC proliferation/differentiation, immune stimulating or suppressing,
CC haematopoiesis regulating, haemostatic and thrombolytic, anti-
CC inflammatory, tumour inhibition, activin/inhibin activity etc. These
CC biological activities make the protein suitable for treating, preventing
CC or ameliorating medical conditions in humans and animals
XX
SQ Sequence 933 AA;
XX
Query Match 82.6%; Score 38; DB 2; Length 933;
Best Local Similarity 75.0%; Pred. No. 1e+02; Mismatches 0; Gaps 0;
Matches 6; Conservative 2; Indels 0; Gaps 0;
QY 1 EVRLRYFD 8
|:|:|:|
Db 40 EIRLKYFD 47
XX
AC AA073400;
XX
DT 29-FEB-2000 (first entry)
XX
DE Human secreted protein clone ycl4_1 protein sequence SEQ ID NO:22.
XX
KW Human; secreted protein; immunostimulatory; haemostatic; cytokine;
KW proliferative; differentiative; chemotactic; chemokinetic; vaccine;
KW thrombolytic; antiinflammatory; cyostatic; immunosuppressive;
KW gene therapy.
XX
OS Homo sapiens.
XX
PN WO9558642-A2.
XX
PD 18-NOV-1999.
XX
PF 14-MAY-1999; 99WO-US010643.
XX
PR 14-MAY-1998; 98US-0085472P.
PR 17-AUG-1998; 98US-0096824P.
PR 11-SEP-1998; 98US-0099843P.
PR 11-SEP-1998; 98US-0099950P.
PR 15-SEP-1998; 98US-0100424P.
PR 29-SEP-1998; 98US-0102329P.
PR 09-OCT-1998; 98US-0103615P.
PR 11-DEC-1998; 98US-0111799P.
PR 14-DEC-1998; 98US-0112159P.
PR 31-DEC-1998; 98US-0114415P.
PR 10-FEB-1999; 99US-0024805P.
PR 06-APR-1999; 99US-00287150.
PR 13-MAY-1999; 99US-00311021.
XX
XX (GENEY) GENETICS INST INC.
XX
PA Wong GG, Clark HF, Fecthel K, Agostino MJ;
XX
DR WPI; 2000-053095/04.
XX
DR N-PSDB; AA252485.
XX
PT Novel polynucleotides and proteins having biological activities which

PT make them suitable for treating, preventing or ameliorating medical
PT conditions in humans or animals.
XX
PS Claim 31; Page 595-598; 730pp; English;
XX
CC The present invention describes human secreted proteins encoded by
CC polynucleotides obtained from adult testes, foetal brain, adult brain,
CC brain (foetal and adult), foetal kidney, adult spleen, and adult thymus
CC CDNA libraries. The polynucleotides and proteins are predicted to have
CC biological activities which would make them suitable for treating,
CC preventing or ameliorating medical conditions in humans and animals.
CC Suggested activities include nutritional activity, cytokine and cell
CC proliferation/differentiation activity; immune stimulating (e.g. as
CC vaccines) or suppressing activity; haematopoiesis regulating activity,
CC tissue growth activity; activin/inhibin activity; chemotactic/
CC chemokinetic activity; haemostatic and thrombolytic activity; receptor/
CC ligand activity; anti-inflammatory activity; cadherin/tumour invasion
CC suppressor activity; and tumour inhibition activity. The polynucleotides
CC are also stated to be useful for gene therapy. Therapeutic compositions
CC are also presently valuable for veterinary applications. AA252475 to
CC AA252581 encode human secreted proteins, and AA073390 to AA073500
CC represent human secreted proteins, given in the present invention
XX
SQ Sequence 933 AA;
XX
Query Match 82.6%; Score 38; DB 3; Length 933;
Best Local Similarity 75.0%; Pred. No. 1e+02; Mismatches 0; Gaps 0;
Matches 6; Conservative 2; Indels 0; Gaps 0;
QY 1 EVRLRYFD 8
|:|:|:|
Db 40 EIRLKYFD 47
XX
AC AA094920;
XX
DT 16-JUN-2000 (first entry)
XX
DE Human secreted protein clone pm412_12 protein sequence SEQ ID NO:46.
XX
KW Human; secreted protein; immunostimulant; immunosuppressant; virucide;
KW antibacterial; antifungal; cyostatic; antiinflammatory; dermatologic;
KW antidiabetic; antistimulant; antitachytic; antineumatic; protozoacide;
KW antithyroid; immune deficiency; severe combined immunodeficiency; SCID;
KW infection; HIV; hepatitis; malaria; autoimmune disorder; systemic lupus;
KW connective tissue disease; multiple sclerosis; erythematosis;
KW rheumatoid arthritis; autoimmune pulmonary inflammation; asthma;
KW Guillain-Barre syndrome; autoimmune thyroiditis; myasthenia gravis;
KW insulin dependent diabetes mellitus; graft-versus-host-disease;
KW autoimmune inflammatory eye disease; allergy.
XX
OS Homo sapiens.
XX
PN WO200009552-A1.
XX
PD 24-FEB-2000.
XX
PF 13-AUG-1999; 99WO-US018298.
XX
PR 14-AUG-1998; 98US-0096622P.
PR 17-AUG-1998; 98US-0096815P.
PR 04-SEP-1998; 98US-0099229P.
PR 23-OCT-1998; 98US-0105368P.
PR 08-JAN-1999; 99US-0115234P.
PR 12-FEB-1999; 99US-0119931P.
PR 18-FEB-1999; 99US-0120575P.
PR 30-APR-1999; 99US-0132020P.
PR 11-AUG-1999; 99US-0148424P.
XX

PA (GENY) GENETICS INST INC.
 XX
 PI Jacobs K, McCoy JM, Lavallic ER, Collins-Racie LA, Evans C;
 PI Merberg D, Treacy M, Agostino MO, Steininger RO, Spaulding V;
 PI Wong GG, Clark HF, Fectel K;
 XX
 DR WPI; 2000-205979/18.
 XX
 PT New polynucleotides encoding secreted proteins, which may have e.g.
 PT nutritional, chemokine, immune stimulating or suppressing, hematopoiesis
 PT regulating, tissue growth, activin/inhibin antiinflammatory or tumor
 PT inhibition activity.
 XX
 PS Claim 55; Page 513-517; 641pp; English.
 XX
 CC AAA16618 to AAA16697 encode the human secreted proteins given in AA94898
 CC to AA94980, isolated from human adult brain, adult thyroid, adult
 CC retina, foetal carcinoma, adult blood, adult neural, foetal kidney, adult
 CC placenta, adult testis, whole embryo, adult cartilage, kidney, foetal
 CC brain, adult thymus, foetal placenta, adult uterus, adult tumour, and
 CC adult bladder, cDNA libraries. The polynucleotides and proteins are
 CC predicted to have biological activities which would make them suitable
 CC for treating, preventing or ameliorating medical conditions in humans and
 CC animals. The polynucleotides can be used as markers for tissues in which
 CC the protein is preferentially expressed, as molecular weight markers on
 CC Southern gels, and as chromosome markers or tags to identify chromosomes
 CC or to map gene positions. The proteins can be used in the treatment of
 CC immune deficiencies and disorders, such as severe combined
 CC immunodeficiency (SCID), as well as viral, bacterial, fungal and other
 CC infections. These infections include human immunodeficiency virus (HIV),
 CC hepatitis, herpesviruses, mycobacteria, Leishmania spp., malaria and
 CC candidiasis. The proteins can be used to treat autoimmune disorders such
 CC as connective tissue disease, multiple sclerosis, systemic lupus
 CC erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation,
 CC Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent
 CC diabetes mellitus, myasthenia gravis, graft-versus-host-disease and
 CC autoimmune inflammatory eye disease. The proteins can also be used to
 CC treat allergic conditions, such as asthma. AAA16698 to AAA16774 represent
 CC probes for the human secreted proteins from the present invention
 XX
 SQ Sequence 1152 AA;
 XX
 Query Match 82.6%; Score 38; DB 3; Length 1152;
 Best Local Similarity 75.0%; Pred. No. 1.3e+02;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EVRLRYFD 8
 Db 259 EIRLRKYPD 266
 XX
 RESULT 13
 ABOS2996
 ID ABOS2996 standard; protein; 1217 AA.
 XX
 AC ABOS2996;
 XX
 DT 09-OCT-2003 (first entry)
 XX
 DE Human spliceosome associated protein (SAP) #21.
 XX
 KW Human; SAP; spliceosome associated protein; ribonucleoprotein;
 KW RNP complex; RNA affinity substrate; RNP assembly sequence;
 KW spliceosomal complex; hnRNP complex; mRNA export complex;
 KW mRNA localisation complex; RNA editing complex; intron complex;
 KW H complex; telomerase complex; fragile X protein complex;
 KW reverse transcriptase complex; gene splicing complex.
 XX
 OS Homo sapiens.
 XX
 PN US2003068603-A1.
 XX
 PD 10-APR-2003.

XX
 PF 14-JAN-2002; 2002US-00047991.
 XX
 PR 12-JAN-2001; 2001US-0261521P.
 XX
 PA (REED/) REED R.
 PA (ZHOU/) ZHOU Z.
 XX
 PI Reed R, Zhou Z;
 XX
 DR WPI; 2003-540885/51.
 XX
 PT Isolating ribonucleoprotein complex, by contacting RNA affinity substrate
 PT having ribonucleoprotein assembly sequence and affinity tag, with protein
 PT mixture, subjecting complex formed to chromatography, affinity selection.
 XX
 PS Claim 24; Page; 39pp; English.
 XX
 CC The invention relates to forming (M1) an isolated ribonucleoprotein (RNP)
 CC complex (C), involves contacting an RNA affinity substrate (S) comprising
 CC an RNP assembly sequence (AS) and an affinity tag, with a protein mixture
 CC to permit formation of (C) on AS, subjecting (C) to chromatographic
 CC separation, and subjecting (C) to affinity selection, where the affinity
 CC tag (e.g. bacteriophage MS2 coat protein in a fusion protein with E. coli
 CC maltose binding protein) binds to an affinity matrix. Also included are
 CC an isolated spliceosome preparation (isolated by (M1)), a RNA comprising
 CC an RNP complex binding site and at least one phage coat protein
 CC recognition site, a nucleic acid encoding the RNA, and treating (M2) a
 CC subject having a disorder associated with abnormal RNP complexes (by
 CC obtaining a sample of cells from a subject, purifying RNP complexes from
 CC the cells of the subject by (M1), determining the presence in the
 CC purified RNP complexes of one or more proteins, and normalising the
 CC amount of RNPs in the subject. (M1) is useful for forming an isolated RNP
 CC complex selected from a spliceosomal complex (selected from E, A, B and C
 CC complex), an hnRNP complex, an mRNA export complex, an mRNA localisation
 CC complex, an RNA editing complex, an intron complex, or an H complex. (M1)
 CC is useful in a diagnostic assay for determining whether a subject has
 CC abnormal RNP complexes. (M2) is useful for treating a subject having a
 CC disorder associated with abnormal RNP complexes. (M1) is useful for
 CC forming an isolated RNP complex such as a telomerase complex, a fragile X
 CC protein complex, a reverse transcriptase complex or a gene splicing
 CC complex. The present sequence represents a known human spliceosome
 CC associated protein (SAP) isolated by the methods of the invention. Note:
 CC The present sequence is not shown in the specification but was obtained
 CC from Genbank or Swissprot using the information provided in table 1 of
 CC the specification
 XX
 SQ Sequence 1217 AA;
 XX
 Query Match 82.6%; Score 38; DB 6; Length 1217;
 Best Local Similarity 75.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EVRLRYFD 8
 Db 324 EIRLRKYPD 331
 XX
 RESULT 14
 ABOS3071
 ID ABOS3071 standard; protein; 1217 AA.
 XX
 AC ABOS3071;
 XX
 DT 10-OCT-2003 (first entry)
 XX
 DE Human putative spliceosome associated protein (SAP) #53.
 XX
 KW Human; SAP; spliceosome associated protein; ribonucleoprotein;
 KW RNP complex; RNA affinity substrate; RNP assembly sequence;
 KW spliceosomal complex; hnRNP complex; mRNA export complex;
 KW mRNA localisation complex; RNA editing complex; intron complex;
 KW H complex; telomerase complex; fragile X protein complex;

KW reverse transcriptase complex; gene splicing complex.
 OS Homo sapiens.
 XX US2003068803-A1.
 XX 10-APR-2003.
 PD 14-JAN-2002; 2002US-00047991.
 PF 12-JAN-2001; 2001US-0261521P.
 PR (REED/) REED R.
 PA (ZHOU/) ZHOU Z.
 XX
 PI Reed R, Zhou Z;
 DR WPI; 2003-540885/51.
 PT Isolating ribonucleoprotein complex, by contacting RNA affinity substrate
 PT having ribonucleoprotein assembly sequence and affinity tag, with protein
 PT mixture, subjecting complex formed to chromatography, affinity selection.
 XX
 PS Claim 24; Page: 39pp; English.
 XX
 CC The invention relates to forming (M1) an isolated ribonucleoprotein (RNP)
 CC complex (C), involves contacting an RNA affinity substrate (S) comprising
 CC an RNP assembly sequence (AS) and an affinity tag, with a protein mixture
 CC to permit formation of (C) on AS, subjecting (C) to chromatographic
 CC separation, and subjecting (C) to affinity selection, where the affinity
 CC tag (e.g. bacteriophage MS2 coat protein in a fusion protein with B. coli
 CC maltose binding protein) binds to an affinity matrix. Also included are
 CC an isolated spliceosome preparation (isolated by (M1)), a RNA comprising
 CC an RNP complex binding site and at least one phage coat protein
 CC recognition site, a nucleic acid encoding the RNA, and treating (M2) a
 CC subject having a disorder associated with abnormal RNP complexes (by
 CC obtaining a sample of cells from a subject, purifying RNP complexes from
 CC the cells of the subject by (M1), determining the presence in the
 CC purified RNP complexes of one or more proteins, and normalising the
 CC amount of RNPs in the subject. (M1) is useful for forming an isolated RNP
 CC complex selected from a spliceosomal complex (selected from E, A, B and C
 CC complex), an hnRNP complex, an mRNA export complex, an mRNA localisation
 CC complex, an RNA editing complex, an intron complex, or an H complex. (M1)
 CC is useful in a diagnostic assay for determining whether a subject has
 CC abnormal RNP complexes. (M2) is useful for treating a subject having a
 CC disorder associated with abnormal RNP complexes. (M1) is useful for
 CC forming an isolated RNP complex such as a telomerase complex, a fragile X
 CC protein complex, a reverse transcriptase complex or a gene splicing
 CC complex. The present sequence represents a putative novel human
 CC spliceosome associated protein (SAP) isolated by the methods of the
 CC invention. Note: The present sequence is not shown in the specification
 CC but was obtained from Genbank or Swissprot using the information provided
 CC in table 2 of the specification
 XX
 SQ Sequence 1217 AA;
 XX
 QY Query Match 82.6%; Score 38; DB 6; Length 1217;
 Db Best Local Similarity 75.0%; Pred. No. 1.4e+02; Indels 0; Gaps 0;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 1 EVRLRYPD 8
 324 EIRLKYFD 331
 RESULT 15
 ID ADY91632 standard; protein; 1217 AA.
 XX
 AC ADY91632;
 XX 16-JUN-2005 (first entry)
 DT
 XX

DE Human prostatic cancer marker, spliceosome-associated protein 130.
 XX tumor marker; cytostatic; prostate tumor; andrology;
 KW genitourinary disease; neoplasm; immunotherapy;
 KW spliceosome-associated protein 130.
 XX
 OS Homo sapiens.
 XX JP2005080524-A.
 PN 31-MAR-2005.
 PD 05-SEP-2003; 2003JP-00313565.
 PF 05-SEP-2003; 2003JP-00313565.
 PR (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
 XX
 PA WPI; 2005-266555/28.
 DR N-PSDB; ADY91667.
 XX
 PT Novel prostatic-cancer marker polypeptide, useful for diagnosing
 PT prostatic-cancer or androgen independent prostatic-cancer.
 XX
 PS Claim 1; SEQ ID NO 31; 43pp; Japanese.
 XX
 CC The invention relates to a novel prostatic cancer marker polypeptide
 CC comprising any one of 35 fully defined amino acid sequences (SEQ ID Nos:1
 CC -35) as given in specification. Prostate-specific antigen (PSA) is
 CC currently widely used as a prostatic tumor marker. Certain problems are
 CC associated with diagnosis using PSA, however, such as false positives and
 CC ambiguity between benign and malignant results. The polypeptides of the
 CC invention demonstrate cytostatic activity and may be useful for
 CC diagnosing and treating prostatic cancer or androgen-independent
 CC prostatic cancer. The polypeptides may be utilized for immunotherapy. The
 CC current sequence is that of the human prostatic cancer marker,
 CC spliceosome-associated protein 130 of the invention.
 XX
 SQ Sequence 1217 AA;
 XX
 QY Query Match 82.6%; Score 38; DB 9; Length 1217;
 Db Best Local Similarity 75.0%; Pred. No. 1.4e+02; Indels 0; Gaps 0;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 1 EVRLRYPD 8
 324 EIRLKYFD 331
 RESULT 16
 ID ADF60175 standard; protein; 1276 AA.
 XX
 AC ADF60175;
 XX 12-FEB-2004 (first entry)
 DT Human contig polypeptide sequence SEQ ID NO:2542.
 DE biological activity; genetic engineering; hybridisation probe; oligomer;
 KW primer; chromosome mapping; gene mapping; recombinant protein production;
 KW human.
 XX
 OS Homo sapiens.
 XX WO2003080795-A2.
 PN 02-OCT-2003.
 PD 09-AUG-2002; 2002WO-US025485.
 PF 09-AUG-2001; 2001US-0311261P.
 PR
 XX

PA (HYSEQ-) HYSEQ INC.
XX
PI Tang YT, Yang Y, Wang Z, Wang G, Ma Y;
XX
DR WPI; 2003-876918/81.
DR N-PSDB; ADF59723.
XX
XX New polynucleotides, useful as hybridization probes, oligomers or
PT primers, for chromosome or gene mapping, for the recombinant production
PT of proteins, and for generating antisense DNA or RNA.
XX
XX Example 3; SEQ ID NO 2542; 571pp; English.
XX
CC The present invention describes isolated polynucleotide sequences (I),
CC which encode polypeptides (II) with biological activity. Also described:
CC (1) a vector comprising (I); (2) an expression vector comprising (I); (3)
CC a host cell genetically engineered to comprise (I) which is operatively
CC associated with a regulatory sequence that modulates expression of (I) in
CC the host cell; (4) a polypeptide (II) encoded by (I); (5) a composition
CC comprising the polypeptide of (4) and a carrier; (6) an antibody directed
CC against the polypeptide of (4); (7) detecting (I) or the polypeptide of
CC (4) in a sample; (8) identifying a compound that binds to the polypeptide
CC of (4); (9) producing the polypeptide of (4); and (10) a collection of
CC polynucleotides comprising at least one of the polynucleotide sequences
CC (I). The polynucleotides (I) can be used as hybridisation probes,
CC oligomers or primers, for chromosome or gene mapping, for the recombinant
CC production of proteins, and for generating antisense DNA or RNA. The
CC present sequence represents a human contig polypeptide sequence, which is
CC used in an example from the present invention.
XX
SQ Sequence 1276 AA;

Query Match 82.6%; Score 38; DB 7; Length 1276;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVRLRYFD 8
|:|:|:|:|
Db 360 EIRLRYFD 367

RESULT 17
ADJ46275
ID ADJ46275 standard; protein; 470 AA.
XX
AC ADJ46275;
XX
DT 06-MAY-2004 (first entry)
XX
DE Anabaena sp. PCC7120 alr0436 protein.
XX
KW vitamin E; Tocen-2; tocopherol synthesis enhancing protein-2;
KW oil-producing plant; transgenic; food; animal feed; seed; pharmaceutical;
KW fine chemicals; nitrilase-1; rbcS transalt peptide; slr1263;
KW octopine synthase terminator; tocopherol; tocotrienol; alr0436.
XX
OS Anabaena sp.
XX
FN WO2004007733-A1.
XX
PD 22-JAN-2004.
XX
PF 09-JUL-2003; 2003WO-EP007358.
XX
PR 17-JUL-2002; 2002DE-01032483.
XX
PA (SUNG-) SUNGENE GMBH & CO KGAA.
XX
PI Badur R, Geijger M, Herbers K, Tropic S, Lemke R, Salchert K;
XX
XX Schulz-Friedrich R;
XX
XX WPI; 2004-122961/12.
DR
DR N-PSDB; ADJ46274.

XX
PT Increasing vitamin E content of plants, useful e.g. for preparing foods
PT or pharmaceuticals, by transgenic expression of an algal tocopherol
PT synthesis enhancing protein-2.
XX
XX
PS Claim 2; SEQ ID NO 25; 92pp; German.
XX

CC This invention describes a novel method for increasing the vitamin E
CC content in a plant (or its tissue, organs, parts, cells or replicative
CC material) comprising the transgenic expression of *Synechocystis* sp. PCC
CC 6803 Tocen-2 (tocopherol synthesis enhancing protein-2), a key factor in
CC vitamin E synthesis. The plant transfected is an oil-producing plant,
CC e.g. *Brassica napus*, *Cocos nucifera*, *Glycine max*, *Gossypium hirsutum*,
CC *Olea europaea*, *zea mays* or almond. The expression construct includes a
CC constitutive or seed-specific promoter; it may also include a promoter
CC that allows expression in organisms other than plants, e.g. *Escherichia*
CC *coli*. Transgenic plants that contain Tocen-2 are used for production of
CC vitamin E (particularly), oils, fats, free fatty acids and their
CC derivatives, also for preparation of foods, animal feeds, seeds,
CC pharmaceuticals and fine chemicals. The invention also describes an
CC expression vector, pSUN2/Nitp/slrl263/ocs which comprises, in pSUN2, a
CC cassette containing (i) the constitutive nitrilase-1 promoter of
CC *Arbidiopsis thaliana*; (ii) sequence encoding the rbcS transalt peptide;
CC (iii) the amplified *Synechocystis* PCC6803 open reading frame slr1263, and
CC (iv) the octopine synthase terminator. It was used to transform
CC *Agrobacterium tumefaciens* and the cells used to inoculate tobacco leaf
CC segments. These were regenerated to plants, all of which had tocopherol
CC and tocotrienol content greater than in wild-type plants. This sequence
CC represents an analogue of the *Synechocystis* sp. PCC 6803 Tocen-2 protein
CC isolated from *Anabaena* sp. PCC7120 described as alr0436 in the disclosure
CC of the invention.
XX
SQ Sequence 470 AA;

Query Match 80.4%; Score 37; DB 8; Length 470;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VRLRYFD 8
|:|:|:|:|
Db 407 VRLRYFD 413

RESULT 18
ADN47011
ID ADN47011 standard; protein; 358 AA.
XX
AC ADN47011;
XX
DT 01-JUL-2004 (first entry)
XX
DE *Thermococcus kodakaraensis* KOD1 protein sequence SeqID889.
XX
KW gene disruption; gene targeting; marker gene; transformation;
KW homologous recombination; hyperthermostable archaeobacterium; KOD1;
KW gene structure; gene function; enzyme activity; medicine;
KW forensic science; food; drug inspection; molecular biology; immunology.
XX
OS *Thermococcus kodakaraensis*.
XX
FN WO2004022736-A1.
XX
PD 18-MAR-2004.
XX
PF 29-AUG-2003; 2003WO-IB003597.
XX
PR 30-AUG-2002; 2002JP-00319011.
XX
PA (NIS-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI Imanaka T, Atomi H;
XX
XX WPI; 2004-257583/24.
DR

XX Method for disrupting targeted gene in genome of organism particularly
PT thermostable bacterium and with genome chips for analysis, applicable in
PT studying gene structure and functions.
XX
PS Claim 9; SEQ ID NO 889; 598bp; Japanese.
XX
CC This invention relates to a novel method for targeting disruption of an
CC arbitrary gene in a genome of an organism which comprises providing the
CC whole sequential data of the genome of such organism, selecting at least
CC 1 arbitrary region in the sequence, providing a vector that contains a
CC sequence homologous with the selected region and a marker gene,
CC transformation, and homologous recombination. The genome is preferably
CC the genome of a hyperthermostable archaeobacterium, particularly
CC Thermococcus kodakarensis KOD1. The method is for targeting the
CC disruption of a gene in the genome of an organism, which is applicable in
CC studying gene structure and functions as well as enzyme activities of
CC encoded proteins and useful in medicine, forensic science, food or drug
CC inspection, molecular biology and immunology. With this method, the
CC efficiency and reliability. The present sequence is that of a protein
CC encoded by the genome of Thermococcus kodakarensis which was derived
CC using the method of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 358 AA;
XX
Query Match 78.3%; Score 36; DB 8; Length 358;
Best Local Similarity 85.7%; Pred. No. 96;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
QY 2 VRLRYFD 8
Db 166 IRLRYFD 172
XX
RESULT 19
ADF70132
ID ADF70132 standard; peptide; 13 AA.
XX
AC ADF70132;
XX
DT 26-FEB-2004 (first entry)
XX
DE Anti-idiotype antibody related peptide.
XX
KW autoimmune disease-associated autoantibody; autoantibody;
KW autoimmune disease; immunoglobulin; anti-idiotypic antibody;
KW immunosuppressive; antiinflammatory; dermatological; muscular;
KW neuroprotective; CNS; anti-HIV; neurotropic; neuropilic; antithyroid;
KW thyromimetic; antidiabetic; anabolic; hypertensive; endocrine;
KW antipneumatic; hepatotropic; virucide; antianaemic; haemostatic;
KW gastroenteric; antitumor; antinfertility; antirheumatic;
KW antiarthritic; nephrotropic; antiarteriosclerotic; cardiac;
KW ophthalmological; uropathic; antipyretic; vaccine.
XX
OS Synthetic.
XX
PN WO2003099868-A2.
XX
PD 04-DEC-2003.
XX
PE 22-MAY-2003; 2003WO-IL000424.
XX
PR 28-MAY-2002; 2002US-0383136P.
XX
PA (OMRI-) OMRIX BIOPHARMACEUTICALS INC.
XX
PI Nur I, Shoenfeld Y;
XX
DR WPI; 2004-042771/04.

XX Identifying molecules, which mimic an idiotype of an autoimmune disease-
PT associated autoantibody, useful for treating an autoimmune disease, e.g.
PT myasthenia gravis, comprises the use of immunoglobulins purified from
PT pooled plasma.
XX
PS Example 3; Page 11; 43bp; English.
XX
CC The present invention describes a method (M1) for identifying molecules
CC (I) which mimic an idiotype of an autoimmune disease-associated
CC autoantibody (autoantibodies). M1 comprises purifying autoantibodies from
CC sera of one or more patients afflicted with the autoimmune disease,
CC binding the autoantibodies to a solid phase to form an affinity matrix,
CC contacting pooled plasma or B cells comprising immunoglobulins with the
CC affinity matrix followed by removal of unbound plasma components, eluting
CC bound immunoglobulins, being anti-idiotypic antibodies (anti-Id) to
CC autoantibodies, from the matrix, providing a molecular library comprising
CC several molecule members, and contacting the anti-Id with the molecular
CC library and isolating the bound molecules, which are bound by the anti-
CC Id, the bound molecules being molecules that mimic an idiotype of
CC autoantibodies. (I) have immunosuppressive, antiinflammatory,
CC dermatological, muscular, neuroprotective, CNS, anti-HIV, neurotropic,
CC neuroleptic, antithyroid, thyromimetic, antidiabetic, anabolic,
CC hypertensive, endocrine, antipneumatic, hepatotropic, virucide,
CC antianaemic, haemostatic, gastroenteric, antitumor, antinfertility,
CC antipneumatic, antiarthritic, nephrotropic, antiarteriosclerotic,
CC cardiac, ophthalmological, uropathic and antipyretic activities, and can
CC be used in vaccines. The molecules (I), anti-Id and pharmaceutical
CC compositions of the present invention can be used for treating a patient
CC afflicted with an autoimmune disease. The molecules (I) are also useful
CC for screening chemical compounds for their potential use in treating an
CC autoimmune disease. The present sequence is given in the exemplification
CC of the present invention.
XX
SQ Sequence 13 AA;
XX
Query Match 76.1%; Score 35; DB 8; Length 13;
Best Local Similarity 75.0%; Pred. No. 4.7;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 EVRLRYFD 8
Db 3 IRLRYFD 10
XX
RESULT 20
AAE31554
ID AAE31554 standard; protein; 59 AA.
XX
AC AAE31554;
XX
DT 24-FEB-2003 (first entry)
XX
DE Rice protein #11 used to isolate rice CBP80 orthologues.
XX
KW Cap binding protein 80; CBP80; drought tolerance; transgenic plant;
KW transgenic; abscisic acid signalling; stomatal pore opening; water loss;
KW senescence; herbicide; peptidase; water deficit resistance; animal feed;
KW pest resistance; food; rice.
XX
OS Oryza sativa.
XX
PN WO200281696-A2.
XX
PD 17-OCT-2002.
XX
PE 05-APR-2002; 2002WO-EP003809.
XX
PR 06-APR-2001; 2001US-0282370P.
XX
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
PI Kreps J, Nero PS;

XX WPI; 2003-046866/04.
DR Novel polynucleotide encoding cap binding protein useful for altering
XX abscisic acid signaling, stomatal pore opening or closing, water loss,
PT senescence, anion channel activity and/or drought tolerance, in a plant.
XX Example 1; Page 146-147; 150pp; English.
XX The present invention relates to novel cap binding protein 80 (CBP80) and
CC polynucleotides encoding such proteins. CBP80 sequences are useful for
CC producing drought tolerant plants and for altering abscisic acid
CC signaling, stomatal pore opening or closing, water loss, senescence,
CC anion channel activity and/or drought tolerance, in a plant by over- or
CC under- or knock out of expression of CBP80. Transgenic plant of the
CC invention are useful for breeding of improved plant lines that for
CC example increase the effectiveness such as conventional methods such as
CC herbicide or pesticide treatment or allow to dispense with the methods
CC due to their modified genetic properties. The transgenic plants produced
CC are useful in traditional agriculture to possess traits beneficial to the
CC grower (e.g., agronomic traits such as resistance to water deficit, pest
CC resistance, herbicide resistance or increased yield) or beneficial to the
CC consumer of the grain harvested from the plant (e.g. improved nutritive
CC content in human food or animal feed, increased vitamin, the production
CC of antibodies) or beneficial to the food processor (e.g., improved
CC processing traits). The present sequence is a rice protein used to
CC isolate rice CBP80 orthologues. This sequence is used in the
CC exemplification of the invention
XX Sequence 59 AA;
SQ
Query Match 76.1%; Score 35; DB 6; Length 59;
Best Local Similarity 75.0%; Pred. No. 23;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 EVRLRYFD 8
Db 27 EIRLSYFD 34
RESULT 21
ABUS1223
ID ABUS1223 standard; protein; 96 AA.
XX
XX ABUS1223;
XX
XX 07-MAY-2003 (first entry)
XX
XX Helicobacter pylori selected interacting domain (SID) protein #567.
XX
XX Protein-protein interaction; ulcer; selected interacting domain; SID.
XX
XX Helicobacter pylori.
XX
XX WO200266501-A2.
XX
XX 29-AUG-2002.
XX
XX 28-DEC-2001; 2001WO-EP015428.
XX
XX 02-JAN-2001; 2001US-0259302P.
XX
XX (HYBR-) HYBRIGENICS.
XX
XX (INSP) INST PASTEUR.
XX
XX Legrain P, Rain J, Colland F, De Reuse H, Labigne A;
XX
XX WPI; 2002-674910/72.
XX
XX N-PSDB; ABX65968.
XX
XX New complexes of protein-protein interactions in Helicobacter pylori,
PT useful for identifying modulating compounds for treating or preventing
PT ulcers in mammals.

XX Claim 6; Page 223; 642pp; English.
PS
XX The invention describes a complex of protein-protein interactions in
XX Helicobacter pylori selected from 421 complexes given in the
CC description.
CC The complex of protein-protein interactions are useful for
CC screening for agents which modulate the interaction of proteins.
CC Modulating compounds which binds to a targeted bacterial protein may be
CC used for treating or preventing ulcers in a human or animal. This is the
CC amino acid sequence of a selected interacting domain (SID), identified
CC via protein-protein interactions. Note: Where the patent number printed
CC at the top of the pages in the specification has obscured areas of
CC protein sequence, the indexer has replaced the residue with an X to
CC represent an illegible residue
XX Sequence 96 AA;
SQ
Query Match 76.1%; Score 35; DB 5; Length 96;
Best Local Similarity 66.7%; Pred. No. 38;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 EVRLRYFDV 9
Db 38 EVRLRYFDI 46
RESULT 22
AAAY3855
ID AAAY3855 standard; peptide; 143 AA.
XX
XX AAAY3855;
XX
XX 11-FEB-2000 (first entry)
XX
XX Heavy chain framework 3 region of antibodies from hybridoma a07.
XX
XX Heavy chain; VH; IgG; monoclonal antibody; spore; Bacillus;
XX
XX VH gene usage; anthrax; framework 3.
XX
XX Mus sp.
XX
XX WO9955842-A1.
XX
XX 04-NOV-1999.
XX
XX 27-APR-1999; 99WO-US009122.
XX
XX 29-APR-1998; 98US-00069628.
XX
XX (UABR-) UAB RES FOUND.
XX
XX Kearney JF;
XX
XX WPI; 2000-013435/01.
XX
XX Monoclonal antibody specific for Bacillus spores, used to detect anthrax.
XX
XX Example 10; Page 45; 64pp; English.
PS
XX AAAY3851-61 represent the amino acid sequences of the framework 3 (FR3)
XX region of heavy chains from antibodies against Bacillus subtilis spores.
XX The antibodies are produced by different hybridomas. The specification
XX describes monoclonal antibodies (especially IgG antibodies) which are
XX highly specific and can discriminate between the spores of the Bacillus
XX family. The antibodies are produced by exposing mice to Bacillus spores.
XX The humoral immune response to Bacillus spores shows a conservation of VH
XX gene usage which is distinct for each spore. Peptide fragments derived
XX from the antibodies are also capable of binding spores. The monoclonal
XX antibody, and peptide fragments of it, can be used to detect Bacillus
XX spores in a field sample. It is particularly uses for detecting anthrax
XX in a field sample
XX Sequence 143 AA;
SQ

KW Triaryl cationic antibiotic; antibacterial; antifungal; infection;
KM fungicide; anti-HIV; haemolysin; Vllly.
XX
OS Vibrio vulnificus.
XX
PN WO200181307-A2.
XX
PD 01-NOV-2001.
XX
PE 25-APR-2001; 2001WO-US013312.
XX
PR 26-APR-2000; 2000US-00558712.
PR 23-FEB-2001; 2001US-00791961.
XX
PA (WISC) WISCONSIN ALUMNI RES FOUND.
XX
PI Handelsman JE, Goodman RM, Gillespie DE, Bettermann AD, Clardy JC,
PI Brady SF;
XX
DR WPI; 2002-066425/09.
XX
XX New triaryl methane cationic compounds, identified using a bacterial
PT artificial chromosome library of DNA from soil, are useful for treating
PT bacterial and fungal infections.
XX
PS Example; Fig 2; 49pp; English.
XX
CC The present invention relates to novel triaryl methane cationic compounds
CC which are capable of acting as antibiotics. They can be used in the
CC treatment of bacterial and fungal infections. The present sequence is the
CC Vibrio vulnificus haemolysin (Vllly) protein, which shares homology with
CC an antibiotic protein identified from a cDNA from environmental samples
XX
SQ Sequence 356 AA:

Query Match 76.1%; Score 35; DB 5; Length 356;
Best Local Similarity 62.5%; Pred. No. 1.5e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 VRLRYFPDV 9
Db 188 VKIRYFDI 195

RESULT 26
ADX89679
ID ADX89679 standard; protein; 491 AA.
XX
AC ADX89679;
XX
DT 21-APR-2005 (first entry)
XX
DE Plant full length insert polypeptide seqid 52343.
XX
XX plant protectant; plant growth regulant; gene therapy; plant;
KM recombinant DNA construct; physical array; plant breeding marker;
KM cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KM extreme osmotic condition; pathogen tolerance; pest tolerance;
KM growth rate; cell cycle pathway; disease resistance;
KM galactomannan production; lignin production; plant growth regulator;
KM yield; plant growth; plant development; seed oil; protein yield;
KM protein content.
XX
OS Unidentified.
XX
PN US2004034888-A1.
XX
PD 19-FEB-2004.
XX
PE 28-APR-2003; 2003US-00425114.
XX
PR 06-MAY-1999; 99US-00304517.
PR 05-NOV-2001; 2001US-00985678.

XX (LITU/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
XX
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX
DR WPI; 2004-180133/17.
XX
XX New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX
PS Claim 1; SEQ ID NO 52343; 15pp; English.
XX
CC The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?docid:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This is the amino acid sequence of a plant full length insert
CC polypeptide that can be used in the recombinant DNA construct of the
CC invention.
XX
SQ Sequence 491 AA:

Query Match 76.1%; Score 35; DB 8; Length 491;
Best Local Similarity 66.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVRLRYFPDV 9
Db 303 KVRMRFPDV 311

RESULT 27
AAE31527
ID AAE31527 standard; protein; 868 AA.
XX
AC AAE31527;
XX
DT 24-FEB-2003 (first entry)
XX
DE Rice cap binding protein 80 (CBP80) protein.
XX
XX Rice; cap binding protein 80, CBP80; drought tolerance; transgenic plant;
KM transgenic; abscisic acid signalling; stomatal pore opening; water loss;
KM senescence; herbicide; pesticide; water deficit resistance; animal feed;
KM pest resistance; food.
XX
OS Oryza sativa.
XX
PN WO200281696-A2.
XX
PD 17-OCT-2002.
XX
PE 05-APR-2002; 2002WO-EP003809.
XX
PR 06-APR-2001; 2001US-0282370P.

XX (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX
 XX Kreps J, Nero PS;
 PI
 XX WPI; 2003-046866/04.
 DR N-PSDB; AAD48471.
 XX
 PT Novel polynucleotide encoding cap binding protein useful for altering
 PT abscisic acid signaling; stomatal pore opening or closing; water loss,
 PT senescence; anion channel activity and/or drought tolerance, in a plant.
 XX
 XX Claim 12; Page 124-127; 150pp; English.
 PS
 XX The present invention relates to novel cap binding protein 80 (CBP80) and
 CC polynucleotides encoding such proteins. CBP80 sequences are useful for
 CC producing drought tolerant plants and for altering abscisic acid
 CC signaling, stomatal pore opening or closing, water loss, senescence,
 CC anion channel activity and/or drought tolerance, in a plant by over- or
 CC under- or knock out of expression of CBP80. Transgenic plant of the
 CC invention are useful for breeding of improved plant lines that for
 CC example increase the effectiveness such as conventional methods such as
 CC herbicide or pesticide treatment or allow to dispense with the methods
 CC due to their modified genetic properties. The transgenic plants produced
 CC are useful in traditional agriculture to possess traits beneficial to the
 CC grower (e.g., agronomic traits such as resistance to water deficit, pest
 CC resistance, herbicide resistance or increased yield) or beneficial to the
 CC consumer of the grain harvested from the plant (e.g. improved nutritive
 CC content in human food or animal feed, increased vitamin, the production
 CC of antibodies) or beneficial to the food processor (e.g., improved
 CC processing traits). The present sequence is rice CBP80 protein
 XX
 SQ Sequence 868 AA;
 QY
 DB 1 EVRLRYFD 8
 452 EIRLSYFD 459
 Query Match 76.1%; Score 35; DB 6; Length 868;
 Best Local Similarity 75.0%; Pred. No. 3.9e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

RESULT 28
 ABB68757
 ID ABB68757 standard; protein; 1169 AA.
 XX
 AC ABB68757;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster polypeptide SEQ ID NO 33063.
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 XX
 OS Drosophila melanogaster.
 XX
 FN WO200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US009231.
 XX
 PR 23-MAR-2000; 2000US-0191637P.
 PR 11-JUL-2000; 2000US-00614150.
 XX
 PA (PEXE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX
 DR WPI; 2001-656860/75.
 DR N-PSDB; ABL12860.

XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signaling and cell-cell
 PT interactions.
 PT
 XX
 PS Disclosure; SEQ ID NO 33063; 21pp + Sequence listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB116176-AB130511), expressed DNA
 CC sequences (AB101840-AB16175) and the encoded proteins (AB57737-
 CC AB572072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WPIO at ftp:wpiointc/pub/published_pcc_sequences
 XX
 SQ Sequence 1169 AA;
 QY
 DB 1 EVRLRYFD 8
 324 EIKLRYFD 331
 Query Match 76.1%; Score 35; DB 4; Length 1169;
 Best Local Similarity 62.5%; Pred. No. 5.3e+02;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

RESULT 29
 ADN21239
 ID ADN21239 standard; protein; 233 AA.
 XX
 AC ADN21239;
 XX
 DT 02-DEC-2004 (first entry)
 XX
 DE Bacterial polypeptide #3892.
 XX
 KW Recombinant DNA construct; transformed plant; improved plant property;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
 KW pathogen tolerance; pest tolerance; plant disease resistance;
 KW cell cycle pathway modification; plant growth regulator;
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 KW bacterial polypeptide.
 XX
 OS Bacteria.
 XX
 PN US2003233675-A1.
 XX
 PD 18-DEC-2003.
 XX
 PF 20-FEB-2003; 2003US-00369493.
 XX
 PR 21-FEB-2002; 2002US-0360039P.
 XX
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 XX
 PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
 XX
 DR WPI; 2004-061375/06.
 XX
 PT New recombinant DNA construct comprising a promoter positioned to provide
 PT for expression of a polynucleotide encoding a polypeptide from a
 PT microbial source, useful for producing plants with improved properties.
 XX
 PS Claim 1; SEQ ID NO 3892; 122pp; English.

CC The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX
CC
XX
SQ Sequence 233 AA;

Query Match 73.9%; Score 34; DB 8; Length 233;
Best Local Similarity 77.8%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EVRLRYFDV 9
| |||||
Db 51 EDNLRYPDV 59

RESULT 30
ADCO1102

ID ADCO1102 standard; protein; 433 AA.

XX
AC ADCO1102;

XX
DT 04-DEC-2003 (first entry)

XX
DE Enterohaemorrhagic E. coli O157:H7-specific protein SEQ ID NO: 1146.

XX
KW enterohaemorrhagic; anti-bacterial.

XX
OS Escherichia coli; O157:H7.

XX
PN JP2002355074-A.

XX
PD 10-DEC-2002.

XX
PF 24-JAN-2002; 2002JP-00015959.

XX
PR 24-JAN-2001; 2001JP-00112010.

XX
PA (UYTS-) UNIV TSUKUBA.

XX
DR WPI; 2003-451640/43.

XX
PT Enterohaemorrhagic Escherichia coli O157:H7-specific nucleic acid molecule
PT and a polypeptide and its use, a polypeptide, a vector and a host cell.

XX
PS Claim 3; SEQ ID NO 1146; 2067pp; Japanese.

XX
CC The invention relates to a novel enterohaemorrhagic Escherichia coli
CC O157:H7-specific nucleic acid molecule. A polynucleotide of the invention
CC has anti-bacterial activity. The polypeptide can be used in detection
CC and/or treatment of O157:H7 infection. The nucleotide sequence of the
CC genome of Enterohaemorrhagic E. coli O157:H7 was determined. The present
CC sequence represents an E. coli O157:H7-specific polypeptide of the

CC invention.
XX
SQ Sequence 433 AA;

Query Match 73.9%; Score 34; DB 7; Length 433;
Best Local Similarity 75.0%; Pred. No. 3e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EVRLRYFD 8
| |||||
Db 47 EARLRFPD 54

RESULT 31

ID ABU20820 standard; protein; 661 AA.

XX
AC ABU20820;

XX
DT 19-JUN-2003 (first entry)

XX
DE Protein encoded by Prokaryotic essential gene #6347.

XX
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX
OS Bacteroides fragilis.

XX
PN W0200277183-A2.

XX
PD 03-OCT-2002.

XX
PF 21-MAR-2002; 2002WO-US009107.

XX
PR 21-MAR-2001; 2001US-00815242.

XX
PR 06-SEP-2001; 2001US-00948593.

XX
PR 25-OCT-2001; 2001US-0342923P.

XX
PR 08-FEB-2002; 2002US-00072851.

XX
PR 06-MAR-2002; 2002US-0362699P.

XX
PA (EUITR-) EUITRA PHARM INC.

XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KU, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX
DR WPI; 2003-0293926/02.

XX
N-PSDB; ACPA24690.

XX
PS Claim 25; SEQ ID NO 48744; 1766pp; English.

XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of

CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs; or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 661 AA;

XX Query Match 73.9%; Score 34; DB 6; Length 661;

XX Best Local Similarity 55.6%; Pred. No. 4.6e+02; Mismatches 2; Indels 0; Gaps 0;

XX Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EVRLRYFDV 9

Db 322 ETNRYFDI 330

RESULT 32

ADXT1265 ADX1265 standard; protein; 705 AA.

XX ADXT1265;

DT 21-APR-2005 (first entry)

DE Plant full length insert polypeptide seqid 40631.

XX plant protectant; plant growth regulant; gene therapy; plant;
KM recombinant DNA construct; physical array; plant breeding marker;
KM cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KM extreme osmotic condition; pathogen tolerance; pest tolerance;
KM growth rate; cell cycle pathway; disease resistance;
KM galactomannan production; lignin production; plant growth regulator;
KM yield; plant growth; plant development; seed oil; protein yield;
KM protein content.

XX Unidentified.

XX US200403488-A1.

XX 19-FEB-2004.

XX 28-APR-2003; 2003US-00425114.

XX 06-MAY-1999; 99US-00304517.

XX 05-NOV-2001; 2001US-00985678.

XX (LIUJ/) LIU J.

XX (ZHOU/) ZHOU Y.

XX (KOVA/) KOVALIC D K.

XX (SCRE/) SCREEN S E.

XX (TABAK/) TABASKA J E.

XX (CAOY/) CAO Y.

XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;

XX WPI; 2004-180133/17.

XX New recombinant DNA construct, useful for improving plant tolerance to

XX cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or

XX pests, for conferring increased resistance to plant disease, or for

XX improving yield.

XX Claim 1; SEQ ID NO 40631; 15pp; English.

XX The invention describes a recombinant DNA construct comprising a

XX polynucleotide consisting of a sequence encoding an amino acid sequence

CC available in electronic form from the US patent office at
CC ftp.segdata.uspo.gov/sequence.html?docid:200403488. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This is the amino acid sequence of a plant full length insert
CC polypeptide that can be used in the recombinant DNA construct of the
CC invention.

SQ Sequence 705 AA;

Qy Query Match 73.9%; Score 34; DB 8; Length 705;

Db Best Local Similarity 75.0%; Pred. No. 4.9e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VRLRYFDV 9

Db 40 VKLQYFDV 47

RESULT 33

AAR72798 AAR72798 standard; protein; 780 AA.

XX AAR72798;

DT 04-MAR-1996 (first entry)

DE Phospholipase D.

KM phospholipase D; measurement; reagent; phospholipid level.

XX Zea mays.

XX WO9509234-A1.

XX 06-APR-1995.

XX 30-SEP-1994; 94WO-JP001627.

XX 30-SEP-1993; 93JP-00267884.

XX (NISB) JAPAN TOBACCO INC.

XX Ueki J, Morioka S;

XX WPI; 1995-147433/19.

XX N-PSDB; AAQ86784.

XX Claimed DNA coding plant derived phospholipase D - controls expression of

XX plant derived PUD gene.

XX Claim 5; Page 23-29; 41pp; Japanese.

XX AAR72798 is a plant derived phospholipase D (PUD). The PUD is useful for

XX measuring phospholipid levels and for producing derivs. by e.g. base

XX exchange reactions. DNA controlling the expression of the plant derived

XX PUD is also claimed and shown in AAQ86785

XX Sequence 780 AA;

Qy Query Match 73.9%; Score 34; DB 2; Length 780;

Db Best Local Similarity 75.0%; Pred. No. 5.5e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 VRLRYFDV 9
|:|:|:|
Db 147 VKLQYFDV 154

RESULT 34
ID ADX77858
ADK77858 standard; protein; 780 AA.

AC ADX77858;
DT 21-APR-2005 (first entry)
XX
XX Plant full length insert polypeptide seqid 47224.
DE
XX plant protectant; plant growth regulant; gene therapy; plant;
XX recombinant DNA construct; physical array; plant breeding marker;
XX cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
XX extreme osmotic condition; pathogen tolerance; pest tolerance;
XX growth rate; cell cycle pathway; disease resistance;
XX galactomannan production; lignin production; plant growth regulator;
XX yield; plant growth; plant development; seed oil; protein yield;
XX protein content.
XX unidentified.
XX OS
XX US2004034888-A1.
XX
XX 19-FEB-2004.
PD
XX 28-APR-2003; 2003US-00425114.
PF
XX 06-MAY-1999; 99US-00304517.
PR 05-NOV-2001; 2001US-00985678.
XX
XX (LIU//) LIU J.
PA (ZHOU//) ZHOU Y.
PA (KOVA//) KOVALLIC D K.
PA (SCRE//) SCREWN S E.
PA (TABAK//) TABAKA J E.
PA (CAOY//) CAO Y.
XX
XX Liu J, Zhou Y, Kovallic DK, Screen SE, Tabaska JE, Cao Y;
PI WPI; 2004-180133/17.
XX
DR New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX
XX Claim 1; SEQ ID NO 47224; 15pp; English.
PS
XX The invention describes a recombinant DNA construct comprising a
XX polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?docID:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This is the amino acid sequence of a plant full length insert
CC polypeptide that can be used in the recombinant DNA construct of the
XX invention.
SQ Sequence 780 AA;

Query Match 73.9%; Score 34; DB 8; Length 780;
Best Local Similarity 75.0%; Pred. No. 5.5e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 VRLRYFDV 9
|:|:|:|
Db 115 VKLQYFDV 122

RESULT 35
ID ADA20755
ADA20755 standard; protein; 809 AA.

AC ADA20755;
DT 20-NOV-2003 (first entry)
XX
XX Soybean phospholipase D alpha #2.
DE
XX Enzyme; plant; respiratory burst oxidase; Rboh; tRNA-mnm-s-U-MT;
XX chromomethylase; cytosine 5-methyltransferase; phospholipase D;
XX transcription factor 11F; asparaginyl tRNA transferase;
XX glutamyl tRNA transferase; EDS1; adaptin AP50; adaptin alpha;
XX adaptin betaas; stress resistance; quality grain improvement; starch;
XX herbicide.
XX
XX Glycine max.
OS
XX US2003003471-A1.
PN
XX 02-JAN-2003.
PD
XX 19-FEB-2002; 2002US-00078770.
PF
XX 12-JUL-1999; 99US-0143400P.
PR 12-JUL-1999; 99US-0143409P.
XX 12-JUL-1999; 99US-0143410P.
PR 13-SEP-1999; 99US-0153534P.
XX 01-OCT-1999; 99US-0157401P.
PR 15-OCT-1999; 99US-0159878P.
XX 22-OCT-1999; 99US-0161223P.
PR 11-JUL-2000; 2000US-00614188.
XX
XX (FAMO//) FAMODU O O.
PA (MIAO//) MIAO G.
PA (SIMM//) SIMMONS C R.
PA (WENG//) WENG Z.
PA (CAHO//) CAHOON R E.
PA (SAKA//) SAKAI H.
PA (OUNZ//) OUN Z.
PA (THOR//) THORPE C J.
PA (FADE//) FADER G M.
PA (LIBB//) LI B.
XX
XX Famodu OO, Miao G, Simmons CR, Weng Z, Cahoon RE, Sakai H;
PI Qun Z, Thorpe CJ, Fader GM, Li B;
XX WPI; 2003-311885/30.
DR N-PSDB; ADA20754.
XX
XX New phospholipase D polypeptides and polynucleotides, useful for
PT genetically and physically mapping the genes that they are part of, and
PT subsequently in plant breeding for developing lines with the desired
PT phenotypes.
XX
XX Claim 1; Page 121-123; 189pp; English.
PS
XX The invention relates to an isolated polynucleotide encoding a
XX phospholipase D comprising a nucleotide sequence (encoding a polypeptide
CC of at least 80 amino acids having at least 92% identity based on the
CC Clustal method of alignment when compared to the proteins appearing as ID
CC 120-134 (even numbers) or their complements. Also included are


```

DE      Phospholipase D.
XX
XX      Phospholipase D; phospholipid; food; medicine; rice plant; monocotyledon.
XX
XX      Oryza sativa.
XX
XX      WO9731106-A1.
XX
XX      28-AUG-1997.
XX
XX      20-FEB-1997; 97WO-JP000466.
XX
XX      21-FEB-1996; 96JP-00058320.
XX
XX      (NISR ) JAPAN TOBACCO INC.
XX
XX      Ueki J, Morioka S;
XX
XX      WPI; 1997-43159/40.
XX      N-PSDB; MAT85509.
XX
XX      Changing the composition of phospholipid(s) produced by host cells -
XX      PT produces phospholipid(s) of better usability than natural
XX      PT phospholipid(s), applicable in food, medicine etc.
XX
XX      Example 1; Page 12-17; 22pp; Japanese.
XX
XX      A novel method has been developed for changing the composition of
XX      CC phospholipids produced by host cells. The method comprises transforming
XX      CC host cells with a recombinant DNA having a sequence antisense to the
XX      CC phospholipase D gene which generates mRNA which prevents the expression
XX      CC of phospholipase D gene by hybridizing with the phospholipase D mRNA from
XX      CC the host cell, and expressing the antisense gene in the host cells. The
XX      CC present sequence represents phospholipase D, which was isolated from
XX      CC rice. Changing the composition of phospholipids produced by host cells,
XX      CC produces phospholipids of better usability than natural phospholipids,
XX      CC applicable in food, medicine
XX
XX      Sequence 812 AA:
SQ
Query Match      73.9%; Score 34; DB 2; Length 812;
Best Local Similarity 75.0%; Pred. NO. 5.7e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY      2 VRLRYFDV 9
Db      147 VKLOYFDV 154

RESULT 39
ADY22319
ID      ADY22319 standard; protein; 813 AA.
XX
XX      ADY22319;
XX
XX      21-APR-2005 (first entry)
XX
XX      Plant full length insert polypeptide seqid 70103.
XX
XX      plant protectant; plant growth regulant; gene therapy; plant;
XX      KW recombinant DNA construct; physical array; plant breeding marker;
XX      KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
XX      KW extreme osmotic condition; pathogen tolerance; pest tolerance;
XX      KW growth rate; cell cycle pathway; disease resistance;
XX      KW galactomannan production; lignin production; plant growth regulator;
XX      KW yield; plant growth; plant development; seed oil; protein yield;
XX
XX      Unidentified.
XX
XX      US2004034888-A1.
XX
XX      19-FEB-2004.

```

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XX
XX      28-APR-2003; 2003US-00425114.
XX
XX      06-MAY-1999; 99US-00304517.
XX      PR 05-NOV-2001; 2001US-00985678.
XX
XX      (LIU/) LIU J.
XX      PA (ZHOU/) ZHOU Y.
XX      PA (KOVA/) KOVALIC D K.
XX      PA (SCRE/) SCREEN S E.
XX      PA (TABAS) TABASKA J E.
XX      PA (CAOY/) CAO Y.
XX
XX      Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX
XX      WPI; 2004-180133/17.
XX
XX      New recombinant DNA construct, useful for improving plant tolerance to
XX      PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
XX      PT pests, for conferring increased resistance to plant disease, or for
XX      PT improving yield.
XX
XX      Claim 1; SEQ ID NO 70103; 15pp; English.
XX
XX      The invention describes a recombinant DNA construct comprising a
XX      CC polynucleotide consisting of a sequence encoding an amino acid sequence
XX      CC available in electronic form from the US patent office at
XX      CC ftp.segdata.uspto.gov/sequence.html?docID:2004034888. The polynucleotide
XX      CC of the invention are also useful in physical arrays of molecules and as
XX      CC plant breeding markers. The recombinant DNA construct is useful for
XX      CC improving plant tolerance to cold, heat, drought, herbicides, extreme
XX      CC osmotic conditions, pathogens or pests, for manipulating growth rate in
XX      CC plant cells by modification of the cell cycle pathway, for conferring
XX      CC increased resistance to plant disease, for producing galactomannan,
XX      CC lignin or plant growth regulators, for increasing the rate of homologous
XX      CC recombination in plants, for improving yield by modification of
XX      CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
XX      CC or by providing improved plant growth and development under at least one
XX      CC stress condition or for modifying seed oil or protein yield and/or
XX      CC content. This is the amino acid sequence of a plant full length insert
XX      CC polypeptide that can be used in the recombinant DNA construct of the
XX      CC invention.
XX
XX      Sequence 813 AA:
SQ
Query Match      73.9%; Score 34; DB 8; Length 813;
Best Local Similarity 75.0%; Pred. NO. 5.7e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY      2 VRLRYFDV 9
Db      148 VKLOYFDV 155

RESULT 40
ADX77899
ID      ADX77899 standard; protein; 817 AA.
XX
XX      ADX77899;
XX
XX      21-APR-2005 (first entry)
XX
XX      Plant full length insert polypeptide seqid 47265.
XX
XX      plant protectant; plant growth regulant; gene therapy; plant;
XX      KW recombinant DNA construct; physical array; plant breeding marker;
XX      KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
XX      KW extreme osmotic condition; pathogen tolerance; pest tolerance;
XX      KW growth rate; cell cycle pathway; disease resistance;
XX      KW galactomannan production; lignin production; plant growth regulator;
XX      KW yield; plant growth; plant development; seed oil; protein yield;
XX      KW protein content.

```

OS Unidentified.
 XX US2004034888-A1.
 XX
 XX 19-FEB-2004.
 XX
 XX 28-APR-2003; 2003US-00425114.
 XX
 XX 06-MAY-1999; 99US-00304517.
 XX 05-NOV-2001; 2001US-00985678.
 XX
 XX (LIU/) LIU J.
 XX (ZHOU/) ZHOU Y.
 XX (KOVA/) KOVALIC D K.
 XX (SCRE/) SCREEN S E.
 XX (TABA/) TABASKA J E.
 XX (CAO/) CAO Y.
 XX
 XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
 XX WPI; 2004-180133/17.
 XX
 XX New recombinant DNA construct, useful for improving plant tolerance to
 XX cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
 XX pests, for conferring increased resistance to plant disease, or for
 XX improving yield.
 XX
 XX Claim 1; SEQ ID NO 47265; 15pp; English.
 XX
 XX The invention describes a recombinant DNA construct comprising a
 XX polynucleotide consisting of a sequence encoding an amino acid sequence
 XX available in electronic form from the US patent office at
 XX ftp.segdata.uspto.gov/sequence.html?docid:2004034888. The polynucleotide
 XX of the invention are also useful in physical arrays of molecules and as
 XX plant breeding markers. The recombinant DNA construct is useful for
 XX improving plant tolerance to cold, heat, drought, herbicides, extreme
 XX osmotic conditions, pathogens or pests, for manipulating growth rate in
 XX plant cells by modification of the cell cycle pathway, for conferring
 XX increased resistance to plant disease, for producing galactomannan,
 XX lignin or plant growth regulators, for increasing the rate of homologous
 XX recombination in plants, for improving yield by modification of
 XX photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 XX or by providing improved plant growth and development under at least one
 XX stress condition or for modifying seed oil or protein yield and/or
 XX content. This is the amino acid sequence of a plant full length insert
 XX polypeptide that can be used in the recombinant DNA construct of the
 XX invention.
 XX
 XX Sequence 817 AA;
 XX
 XX
 XX
 QY 2 VRLRYFDV 9
 Db 152 VKLQYFDV 159
 Query Match 73.9%; Score 34; DB 8; Length 817;
 Best Local Similarity 75.0%; Pred. No. 5.8e+02;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

RESULT 41
 ADY22413
 ID ADY22413 standard; protein; 820 AA.
 XX
 XX ADY22413;
 XX
 XX 21-APR-2005 (first entry)
 XX
 XX Plant full length insert polypeptide seqid 70197.
 XX
 XX Plant protecan; plant growth regulant; gene therapy; plant;
 XX Recombinant DNA construct; physical array; plant breeding marker;
 XX cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
 XX extreme osmotic condition; pathogen tolerance; pest tolerance;

KW growth rate; cell cycle pathway; disease resistance;
 KW galactomannan production; lignin production; plant growth regulator;
 KW yield; plant growth; plant development; seed oil; protein yield;
 KW protein content.
 XX
 XX Unidentified.
 XX
 XX US2004034888-A1.
 XX
 XX 19-FEB-2004.
 XX
 XX 28-APR-2003; 2003US-00425114.
 XX
 XX 06-MAY-1999; 99US-00304517.
 XX 05-NOV-2001; 2001US-00985678.
 XX
 XX (LIU/) LIU J.
 XX (ZHOU/) ZHOU Y.
 XX (KOVA/) KOVALIC D K.
 XX (SCRE/) SCREEN S E.
 XX (TABA/) TABASKA J E.
 XX (CAO/) CAO Y.
 XX
 XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
 XX WPI; 2004-180133/17.
 XX
 XX New recombinant DNA construct, useful for improving plant tolerance to
 XX cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
 XX pests, for conferring increased resistance to plant disease, or for
 XX improving yield.
 XX
 XX Claim 1; SEQ ID NO 70197; 15pp; English.
 XX
 XX The invention describes a recombinant DNA construct comprising a
 XX polynucleotide consisting of a sequence encoding an amino acid sequence
 XX available in electronic form from the US patent office at
 XX ftp.segdata.uspto.gov/sequence.html?docid:2004034888. The polynucleotide
 XX of the invention are also useful in physical arrays of molecules and as
 XX plant breeding markers. The recombinant DNA construct is useful for
 XX improving plant tolerance to cold, heat, drought, herbicides, extreme
 XX osmotic conditions, pathogens or pests, for manipulating growth rate in
 XX plant cells by modification of the cell cycle pathway, for conferring
 XX increased resistance to plant disease, for producing galactomannan,
 XX lignin or plant growth regulators, for increasing the rate of homologous
 XX recombination in plants, for improving yield by modification of
 XX photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 XX or by providing improved plant growth and development under at least one
 XX stress condition or for modifying seed oil or protein yield and/or
 XX content. This is the amino acid sequence of a plant full length insert
 XX polypeptide that can be used in the recombinant DNA construct of the
 XX invention.
 XX
 XX Sequence 820 AA;
 XX
 XX
 XX
 QY 2 VRLRYFDV 9
 Db 155 VKLQYFDV 162
 Query Match 73.9%; Score 34; DB 8; Length 820;
 Best Local Similarity 75.0%; Pred. No. 5.8e+02;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

RESULT 42
 ADX91040
 ID ADX91040 standard; protein; 820 AA.
 XX
 XX ADX91040;
 XX
 XX 21-APR-2005 (first entry)
 XX
 XX Plant full length insert polypeptide seqid 53704.

```

XX plant protectant; plant growth regulator; gene therapy; plant;
KM recombinant DNA construct; physical array; plant breeding marker;
KM cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KM extreme osmotic condition; pathogen tolerance; pest tolerance;
KM growth rate; cell cycle pathway; disease resistance;
KM galactomannan production; lignin production; plant growth regulator;
KM yield; plant growth; plant development; seed oil; protein yield;
KM protein content.
XX
XX Unidentified.
OS
XX US2004034888-A1.
XX
XX 19-FEB-2004.
XX
XX 28-APR-2003; 2003US-00425114.
XX
XX 06-MAY-1999; 99US-00304517.
XX
XX 05-NOV-2001; 2001US-00985678.
XX
XX (LITUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABAS/) TABASKA J E.
PA (CAOY/) CAO Y.
XX
XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX
XX WPI; 2004-180133/17.
XX
XX New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX
XX Claim 1; SEQ ID NO 53704; 15pp; English.
XX
XX The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This is the amino acid sequence of a plant full length insert
CC polypeptide that can be used in the recombinant DNA construct of the
CC invention.
XX
XX Sequence 820 AA:
SQ
Query Match 73.9%; Score 34; DB 8; Length 820;
Best Local Similarity 75.0%; Pred. No. 5.8e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 2 VRLRYFDV 9
Db 155 VKLQYFDV 162

```

```

AC ADX95175;
XX
XX 21-APR-2005 (first entry)
XX
XX plant full length insert polypeptide seqid 57839.
XX
XX plant protectant; plant growth regulator; gene therapy; plant;
KM recombinant DNA construct; physical array; plant breeding marker;
KM cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KM extreme osmotic condition; pathogen tolerance; pest tolerance;
KM growth rate; cell cycle pathway; disease resistance;
KM galactomannan production; lignin production; plant growth regulator;
KM yield; plant growth; plant development; seed oil; protein yield;
KM protein content.
XX
XX Unidentified.
OS
XX US2004034888-A1.
XX
XX 19-FEB-2004.
XX
XX 28-APR-2003; 2003US-00425114.
XX
XX 06-MAY-1999; 99US-00304517.
XX
XX 05-NOV-2001; 2001US-00985678.
XX
XX (LITUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABAS/) TABASKA J E.
PA (CAOY/) CAO Y.
XX
XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX
XX WPI; 2004-180133/17.
XX
XX New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX
XX Claim 1; SEQ ID NO 57839; 15pp; English.
XX
XX The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This is the amino acid sequence of a plant full length insert
CC polypeptide that can be used in the recombinant DNA construct of the
CC invention.
XX
XX Sequence 821 AA:
SQ
Query Match 73.9%; Score 34; DB 8; Length 821;
Best Local Similarity 75.0%; Pred. No. 5.8e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 2 VRLRYFDV 9
Db 156 VKLQYFDV 163

```

RESULT 43
 ADX95175
 ID ADX95175 standard; protein; 821 AA.
 XX

XX	RESULT 44
XX	ADXT77856
ID	ADXT77856 standard; protein; 849 AA.
XX	
AC	ADXT77856;
XX	
DT	21-APR-2005 (first entry)
XX	
DE	Plant full length insert polypeptide seqid 47222.
XX	
XX	plant protectant; plant growth regulant; gene therapy; plant;
KW	recombinant DNA construct; physical array; plant breeding marker;
KW	cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW	extreme osmotic condition; pathogen tolerance; pest tolerance;
KW	growth rate; cell cycle pathway; disease resistance;
KW	galactomannan production; lignin production; plant growth regulator;
KW	yield; plant growth; plant development; seed oil; protein yield;
KW	protein content.
XX	
OS	unidentified.
XX	
XX	US2004034888-A1.
PD	
XX	19-FEB-2004.
XX	
PF	28-APR-2003; 2003US-00425114.
XX	
PR	06-MAY-1999; 99US-00304517.
XX	
PR	05-NOV-2001; 2001US-00985678.
XX	
PA	(LIUYU/) LIU J.
PA	(ZHOU/) ZHOU Y.
PA	(KOVA/) KOVALIC D K.
PA	(SCRE/) SCREEN S E.
PA	(TABAS/) TABASKA J E.
PA	(CAOY/) CAO Y.
XX	
PI	Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
DR	
XX	WPI; 2004-180133/17.
PT	
PT	New recombinant DNA construct, useful for improving plant tolerance to
PT	cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT	pests, for conferring increased resistance to plant disease, or for
PT	improving yield.
XX	
PS	Claim 1; SEQ ID NO 47222; 15pp; English.
XX	
CC	The invention describes a recombinant DNA construct comprising a
CC	polynucleotide consisting of a sequence encoding an amino acid sequence
CC	available in electronic form from the US patent office at
CC	ftp.segdata.uspto.gov/sequence.html;DocID:2004034888. The polynucleotide
CC	of the invention are also useful in physical arrays of molecules and as
CC	plant breeding markers. The recombinant DNA construct is useful for
CC	improving plant tolerance to cold, heat, drought, herbicides, extreme
CC	osmotic conditions, pathogens or pests, for manipulating growth rate in
CC	plant cells by modification of the cell cycle pathway, for conferring
CC	increased resistance to plant disease, for producing galactomannan,
CC	lignin or plant growth regulators, for increasing the rate of homologous
CC	recombination in plants, for improving yield by modification of
CC	photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC	or by providing improved plant growth and development under at least one
CC	stress condition or for modifying seed oil or protein yield and/or
CC	content. This is the amino acid sequence of a plant full length insert
CC	polypeptide that can be used in the recombinant DNA construct of the
CC	invention.
XX	
XX	Sequence 849 AA;
XX	

QY 2 VRLRYFDV 9
|:|:|
Db 184 VKLQYFDV 191

```

RESULT 45
ADH86225
ID ADH86225 standard; protein, 151 AA.
XX
XX
XX ADH86225;
AC
XX
XX
DT 22-APR-2004 (first entry)
XX
XX Enterococcus faecalis polypeptide #705.
DE
XX Enterococcus faecalis infection; transcription regulatory element;
KW antibacterial.
XX
XX Enterococcus faecalis.
OS
XX
XX US6617156-B1.
XX
XX 09-SEP-2003.
PD
XX
XX 13-AUG-1998; 98US-00134000.
PF
XX
XX 15-AUG-1997; 97US-0055778P.
PR
XX
XX (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
XX
XX Doucette-Stamm LA, Bush D;
PI
XX
XX WPI; 2003-895394/82.
DR
XX N-PSDB, ADH82820.
XX
XX
XX New nucleic acid comprising a sequence encoding an Enterococcus faecalis
XX polypeptide, useful for preparing a composition for diagnosing or
XX treating E. faecalis infection.
XX
XX
XX Disclosure; SEQ ID NO 4110; 193pp; English.
XX
XX
XX The invention relates to Enterococcus faecalis polynucleotides and
XX polypeptides. The invention also relates to a recombinant expression
XX vector comprising a polynucleotide operably linked to a transcription
XX regulatory element, a cell comprising a recombinant vector, a method for
XX producing an E. faecalis polypeptide, an isolated nucleic acid comprising
XX a sequence not given in the specification, a recombinant vector
XX comprising the nucleic acid and a cell comprising the recombinant vector.
XX The polynucleotides can be used to detect the presence of E. faecalis in
XX a sample. The sequences are useful for preparing a composition for
XX diagnosing or treating Enterococcus faecalis infection. This sequence
XX represents an E. faecalis polypeptide of the invention.
XX
XX
SQ Sequence 151 AA;
Query Match 71.7%; Score 33; DB 7; Length 151;
Best Local Similarity 75.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 1 EVRLRYPD 8
||:||||
||:||||
Db 121 EVTVRYPD 128
RESULT 46
ABB63459
ID ABB63459 standard; protein, 202 AA.

```

Query Match	73.9%;	Score 34;	DB 8;	Length 849;
Best Local Similarity	75.0%;	Pred. No. 6+02;		
Matches	6;	Conservative	2;	Mismatches 0;
				Indels 0;
				Gaps 0

RESULT	46
ABB63459	
ID	ABB63459 standard; protein; 202 AA
XX	
AC	ABB63459;
XX	
DT	26-MAR-2002 (first entry)

XX Drosophila melanogaster polypeptide SEQ ID NO 17169.
DE
XX Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
XX 27-SEP-2001.
PD
XX 23-MAR-2001; 2001WO-US009231.
PF
XX 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
XX WPI; 2001-656860/75.
DR N-PSDB; ABL07562.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX
XX Disclosure; SEQ ID NO 17169; 21pp + Sequence listing; English.
PS
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides) therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB16176-ABL30511), expressed DNA
CC sequences (AB101840-AB16175) and the encoded proteins (AB57737-
CC AB872072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 202 AA;
Query Match 71.7%; Score 33; DB 4; Length 202;
Best Local Similarity 100.0%; Pred. No. 2.1e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 RLRYFD 8
Db 158 RLRYFD 163
RESULT 47
AEB44584
ID AEB44584 standard; protein; 304 AA.
XX
AC AEB44584;
XX
DT 08-SEP-2005 (first entry)
XX
DE Sleep disorder related protein shaker SEQ ID NO 50.
XX
KW hypnotic; gene expression; diagnosis; sleep disorder; hypnotic;
KW neurological disease.
XX
XX Drosophila melanogaster.
OS
PN WO2005061736-A2.
XX
XX 07-JUL-2005.
PD
XX 15-DEC-2004; 2004WO-US041948.
PF
XX

PR 15-DEC-2003; 2003US-0529536P.
PR 20-APR-2004; 2004US-0563858P.
XX
PA (WISC) WISCONSIN ALUMNI RES FOUND.
XX
XX Tononi G, Cirelli C;
XX
XX WPI; 2005-512536/52.
DR N-PSDB; AEB44581.
XX
XX Screening for sleep altering composition for treating sleep disorders, by
PT contacting a Drosophila cell with a candidate compound and measuring the
PT effect of the compound on expression level or activity of a gene product.
XX
XX Disclosure; SEQ ID NO 50; 268pp; English.
PS
XX The invention describes a method of screening for a sleep altering
CC composition comprising contacting a Drosophila cell with a candidate
CC compound and measuring the effect of the compound on expression level or
CC activity of a gene product, where a change in the expression level or
CC activity of the gene product indicates that the candidate compound is a
CC sleep altering composition. Also described are: reducing the need for
CC sleep in a subject; promoting recovery from sleep loss in a subject;
CC inhibiting sleep in a subject; increasing sleep in a subject; and
CC identifying the basis of a sleep disorder in a subject. The method is
CC useful for screening for sleep altering composition. It is useful for
CC identifying compositions for treating sleep disorders and sleep
CC deprivation. Sleep altering compositions are useful for reducing the need
CC for sleep in a subject, promoting recovery from sleep loss in a subject,
CC inhibiting sleep in a subject, increasing sleep in a subject, and
CC identifying the basis of a sleep disorder in a subject. This is the amino
CC acid sequence of a protein displaying altered expression in a sleep
XX disorder.
XX
SQ Sequence 304 AA;
Query Match 71.7%; Score 33; DB 9; Length 304;
Best Local Similarity 100.0%; Pred. No. 3.2e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 RLRYFD 8
Db 84 RLRYFD 89
RESULT 48
ABO80046
ID ABO80046 standard; protein; 311 AA.
XX
AC ABO80046;
XX
XX 29-JUL-2004 (first entry)
DT
XX
DE Pseudomonas aeruginosa polypeptide #12221.
XX
XX Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
XX
XX Pseudomonas aeruginosa.
OS
PN US6551795-B1.
XX
XX 22-APR-2003.
PD
XX 18-FEB-1999; 99US-00252391.
PF
XX 18-FEB-1998; 98US-0074788P.
PR 27-JUL-1998; 98US-0094190P.
XX
XX (GENO-) GENOME THERAPEUTICS CORP.
PA
XX Rubenfield MJ, Nolling J, Deloughery C, Bush D;
PI
XX WPI; 2003-615309/58.
DR

DR N-PSDB; ABD13617.
XX Novel isolated nucleic acid encoding *Pseudomonas aeruginosa* polypeptide,
PT useful as molecular targets for diagnostics, prophylaxis and treatment of
XX pathological conditions resulting from bacterial infection.
PS Disclosure; SEQ ID NO 28792; 455bp; English.
XX The invention relates to *Pseudomonas aeruginosa* polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics,
CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polypeptide,
CC for the ability to bind a *P. aeruginosa* nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-*P. aeruginosa* drugs, as templates for recombinant
CC production of *P. aeruginosa*-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of *P. aeruginosa*-caused
CC infection, and in detection of *P. aeruginosa* sequences or other sequences
CC of *Pseudomonas* species using biochip technology. Sequences ABO67826-
CC ABO84396 represent *P. aeruginosa* polypeptides of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
SQ Sequence 311 AA;
Query Match 71.7%; Score 33; DB 7; Length 311;
Best Local Similarity 66.7%; Pred. No. 3.3e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
OY 1 EVRLRYFPDV 9
Db 120 EVERLRFFEV 128
RESULT 49
ID ABB65205 standard; protein; 345 AA.
XX ABB65205;
AC 26-MAR-2002 (first entry)
XX
DT 26-MAR-2002 (first entry)
XX
DE *Drosophila melanogaster* polypeptide SEQ ID NO 22407.
XX
KM *Drosophila*; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX
OS *Drosophila melanogaster*.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US009231.
XX
PR 23-MAR-2000; 2000US-0191637P.
XX
PT 11-JUL-2000; 2000US-00614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
XX
DR N-PSDB; ABL09308.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from *Drosophila* and for elucidating cell signalling and cell-cell
XX interactions.
PS Disclosure; SEQ ID NO 22407; 21pp + Sequence Listing; English.
XX

CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from *Drosophila*. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB116176-AB130511), expressed DNA
CC sequences (AB101840-AB116175) and the encoded proteins (ABBS7737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
SQ Sequence 345 AA;
Query Match 71.7%; Score 33; DB 4; Length 345;
Best Local Similarity 85.7%; Pred. No. 3.7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 EVRLRYF 7
Db 290 QVRLRYF 296
RESULT 50
ID ADT58054 standard; protein; 359 AA.
XX ADT58054;
XX
AC ADT58054;
XX
DT 13-JAN-2005 (first entry)
XX
DE Plant polypeptide, SEQ ID 8131.
XX
XX Plant; transgenic; cold tolerance; growth rate; drought tolerance;
KW disease resistance; galactomannan production; plant growth regulator;
KW heat tolerance; herbicide tolerance; lignin production;
KW extreme osmotic condition tolerance; pathogens resistance;
KW pest resistance; yield improvement; seed oil yield; seed protein yield.
XX
OS Viridiplantae.
XX
PN US2004216190-A1.
XX
PD 28-OCT-2004.
XX
PF 18-DEC-2003; 2003US-00739930.
XX
PR 28-APR-2003; 2003US-00424599.
XX
PR 28-APR-2003; 2003US-00425115.
XX
PA (KOVA/) KOVALIC D K.
XX
PI Kovalic DK;
XX
DR WPI; 2004-757369/74.
XX
XX New recombinant DNA constructs useful in the field of biochemistry and
PT genetics, and in particular for producing transgenic plants with improved
PT biological characteristics.
XX
PS Claim 2; SEQ ID NO 8131; 14pp; English.
XX
XX The invention relates a recombinant DNA construct comprising a
CC polynucleotide having any of 5544 nucleotide sequences (cDNAs SEQ ID NO:
CC 1-5544) and encoding a polypeptide with any of 5544 amino acid sequences
CC (SEQ ID NO: 5545-11088). The cDNAs and proteins are from corn, soybean,
CC Arabidopsis, wheat and rape but the specification does not indicate which
CC sequences is derived from which organism. Also included is a method of
CC producing a plant having an improved property, comprising transforming a
CC plant with a recombinant DNA construct comprising a promoter region
CC functional in a plant cell operably joined to a polynucleotide encoding a
CC polypeptide associated with the property, and growing the transformed
CC plant. The property is selected from improving plant cold tolerance, for
CC manipulating growth rate in plant cells by modification of the cell cycle

CC pathway, for improving plant drought tolerance, for providing increased
 CC resistance to plant disease, for galactomannan production, for production
 CC of plant growth regulators, for improving plant heat tolerance, for
 CC improving plant tolerance to herbicides, for increasing the rate of
 CC homologous recombination in plants, for lignin production, for improving
 CC plant tolerance to extreme osmotic conditions, for improving plant
 CC tolerance to pathogens or pests, for yield improvement by modification of
 CC photosynthesis, for modifying seed oil yield and/or content, for
 CC modifying seed protein yield and/or content, for yield improvement by
 CC modification of carbohydrate, nitrogen or phosphorus use and/or uptake
 CC and for yield improvement by providing improved plant growth and
 CC development under at least one stress condition. The polynucleotide may
 CC also encode a plant transcription factor. The methods and compositions of
 CC the present invention are useful in the field of biochemistry and
 CC genetics, in particular for producing transgenic plants with improved
 CC biological characteristics such as increased yield, improved nitrogen
 CC flow, increasing plant tolerance to cold or heat, improving plant
 CC tolerance to extreme osmotic and drought conditions, and improving plant
 CC tolerance to plant pests or pathogens. They can also be used in physical
 CC arrays of molecules, plant breeding markers, computer-based storage and
 CC analysis systems. The present sequence is one of the 554 plant protein
 CC sequences of the invention. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?docID=20040216190.
 XX

SO Sequence 359 AA:

Query Match 71.7%; Score 33; DB 8; Length 359;
 Best Local Similarity 66.7%; Pred. No. 3.9e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EVRLRYPDV 9
 :|||:|||
 Db 313 DVRLHFDPV 321

Search completed: May 4, 2006, 12:57:21
 Job time : 122 secs

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OM protein - protein search, using sw model

Run on: May 4, 2006, 13:00:03 ; Search time 12.8571 Seconds
(without alignments)
67.352 Million cell updates/sec

Title: US-10-700-632-3
Perfect score: 46
Sequence: 1 EVRLRFPDV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37	80.4	470	2 AC1861	hypothetical prote
2	37	80.4	809	2 T11695	phospholipase D (B
3	35	76.1	228	2 A64712	hypothetical prote
4	35	76.1	332	2 T41149	probable trascript
5	35	76.1	338	2 T15074	hypothetical prote
6	34	73.9	81	2 A49103	sequence-specific
7	34	73.9	181	2 S00555	matng type protei
8	34	73.9	433	2 D91111	probable adherence
9	34	73.9	433	2 H85956	probable cytoloxin
10	34	73.9	619	2 T34451	hypothetical prote
11	34	73.9	812	2 T03402	probable phosphol
12	34	73.9	812	2 T03659	phospholipase D (B
13	33	71.7	132	2 G87405	ribosomal protein
14	33	71.7	304	2 S02284	potassasium channel
15	33	71.7	321	2 S54403	I-phosphatidylinos
16	33	71.7	359	2 A27159	potassasium channel
17	33	71.7	388	2 T16563	hypothetical prote
18	33	71.7	413	2 T43170	probable triacylg1
19	33	71.7	421	1 A43294	isocitrate dehydro
20	33	71.7	452	1 S33859	isocitrate dehydro
21	33	71.7	514	2 C49507	potassasium channel
22	33	71.7	563	2 A72300	beta-glucuronidase
23	33	71.7	592	2 H84018	Mg-protoporphyrin
24	33	71.7	598	2 S66669	potassasium channel
25	33	71.7	603	2 A49507	potassasium channel
26	33	71.7	642	2 S00480	potassasium channel
27	33	71.7	656	2 JH0193	potassasium channel
28	33	71.7	1220	2 T32916	hypothetical prote
29	33	71.7	2206	2 JC5280	voltage-dependent

30	32	69.6	250	2 A82919	integrase-recombin
31	32	69.6	279	2 A80285	probable regulator
32	32	69.6	308	2 G70696	hypothetical prote
33	32	69.6	452	2 S57499	isocitrate dehydro
34	32	69.6	896	2 S76064	hypothetical prote
35	32	69.6	896	2 S5990	phycobillosome anch
36	32	69.6	1007	2 H72734	hypothetical prote
37	32	69.6	81	2 H90862	hypothetical prote
38	31	67.4	81	2 A85756	hypothetical prote
39	31	67.4	81	2 B64878	ymJA protein - Bac
40	31	67.4	189	2 G84230	hypothetical prote
41	31	67.4	202	2 A52665	hypothetical prote
42	31	67.4	202	2 F97447	hypothetical prote
43	31	67.4	291	2 H96971	N-terminal Chey re
44	31	67.4	297	2 AF0671	conserved hypothet
45	31	67.4	297	2 C64899	yddE protein - Bac
46	31	67.4	297	2 C90887	hypothetical prote
47	31	67.4	297	2 F85730	hypothetical prote
48	31	67.4	326	2 B44882	embryogenesis prot
49	31	67.4	327	2 A44882	embryogenesis prot
50	31	67.4	330	2 C64627	ADPGlyceromanno-he
51	31	67.4	346	2 A45885	MHC class I histoc
52	31	67.4	366	2 T26449	hypothetical prote
53	31	67.4	373	2 I69008	MHC class I RT1.B
54	31	67.4	377	2 A45851	MHC class I histoc
55	31	67.4	420	1 S53324	glycogen synthase
56	31	67.4	420	1 TVRTKB	tau-protein kinase
57	31	67.4	420	2 I51692	glycogen synthase
58	31	67.4	420	2 I51425	intracellular kina
59	31	67.4	444	2 E90192	DNA repair protein
60	31	67.4	476	2 F75133	hypothetical prote
61	31	67.4	476	2 S21144	potassasium channel
62	31	67.4	478	2 T12683	embryogenesis prot
63	31	67.4	483	1 TVRTKA	protein kinase (BC
64	31	67.4	489	2 I51532	potassasium channel
65	31	67.4	495	2 I57680	potassasium channel
66	31	67.4	495	2 A40090	potassasium channel
67	31	67.4	495	2 B39113	potassasium channel
68	31	67.4	496	2 T15691	hypothetical prote
69	31	67.4	499	2 T47928	hypothetical prote
70	31	67.4	499	2 JH0313	potassasium channel
71	31	67.4	499	2 I77466	potassasium channel
72	31	67.4	499	2 I84204	potassasium channel
73	31	67.4	499	2 A33814	potassasium channel
74	31	67.4	515	1 DEHUG6	glucose-6-phosphat
75	31	67.4	523	1 DEHUG6	glucose-6-phosphat
76	31	67.4	523	2 A38101	potassasium channel
77	31	67.4	524	2 A47740	glucose-6-phosphat
78	31	67.4	525	2 A43531	potassasium channel
79	31	67.4	528	2 I84205	potassasium channel
80	31	67.4	701	2 JG8062	L-glutamate oxidas
81	31	67.4	729	2 JG7501	oligopeptide trans
82	31	67.4	749	2 C84508	probable cap-bindi
83	31	67.4	764	2 S49849	aconitate hydratase
84	31	67.4	898	2 T04693	hypothetical prote
85	31	67.4	1380	2 T52844	hypothetical prote
86	30	65.2	41	2 D72271	hypothetical prote
87	30	65.2	69	2 D69302	conserved hypothet
88	30	65.2	172	2 T32134	hypothetical prote
89	30	65.2	172	2 C71038	hypothetical prote
90	30	65.2	219	2 AD1449	hypothetical prote
91	30	65.2	224	2 T32606	hypothetical prote
92	30	65.2	224	2 G95212	Mg/Ca/SaP family P
93	30	65.2	236	2 G98076	Mg(12+) transport A
94	30	65.2	244	2 A11414	meRR-family transc
95	30	65.2	244	2 A11790	meRR-family transc
96	30	65.2	262	2 C95193	cell division prot
97	30	65.2	265	1 NMVURV	nonstructural prot
98	30	65.2	266	2 H98059	hypothetical prote
99	30	65.2	280	2 C69343	diaminopimelate ep
100	30	65.2	281	2 A52090	hypothetical prote
101	30	65.2	291	2 AC1029	hypothetical prote
102	30	65.2	302	1 R3SP55	ribosomal protein

103	30	65.2	325	2	S60335	TGF-beta receptor
104	30	65.2	326	2	C86872	UDP-glucose 4-epime
105	30	65.2	327	2	A70392	UDP-glucose 4-epim
106	30	65.2	327	2	A81384	UDP-glucose 4-epim
107	30	65.2	328	2	AG1759	UDP-glucose 4-epim
108	30	65.2	329	2	C97264	UDP-glucose 4-ep
109	30	65.2	339	2	T30907	conserved transp
110	30	65.2	341	2	C69149	conserved hypot
111	30	65.2	343	2	AP2641	UDP-galactose 4-ep
112	30	65.2	343	2	H97423	UDP-galactose 4-ep
113	30	65.2	348	2	B84448	hypothetical prote
114	30	65.2	353	2	T33678	hypothetical prote
115	30	65.2	375	2	B75072	tyrosyl-tRNA synth
116	30	65.2	375	2	F71093	tyrosine-tRNA lig
117	30	65.2	402	2	H64599	poly(A) polymerase
118	30	65.2	402	2	E71912	polynucleotide ade
119	30	65.2	415	1	B64089	diaminopimelate de
120	30	65.2	420	1	D82709	colicin V secretio
121	30	65.2	438	2	B84363	peptide chain rele
122	30	65.2	447	2	D69358	alkylidihydroxyacet
123	30	65.2	481	1	A45288	protein kinase (EC
124	30	65.2	481	1	UC2438	protein kinase (EC
125	30	65.2	481	1	H69275	signal-transducing
126	30	65.2	507	2	D64575	hypothetical prote
127	30	65.2	530	1	A56841	glucose-6-phosphat
128	30	65.2	548	2	T49948	hypothetical prote
129	30	65.2	557	2	S73434	aspartate-tRNA lig
130	30	65.2	587	2	A10180	conserved hypot
131	30	65.2	603	2	T26877	hypothetical prote
132	30	65.2	612	2	S35066	protein-tyrosine k
133	30	65.2	645	2	C82849	cell division prot
134	30	65.2	715	2	T26307	hypothetical prote
135	30	65.2	796	2	JC7966	xylian 1,4-beta-xy
136	30	65.2	808	2	T04092	phospholipase D (E
137	30	65.2	808	2	T10171	phospholipase D (E
138	30	65.2	832	2	A31246	neurogenic protein
139	30	65.2	833	2	S19087	gene Delta protein
140	30	65.2	858	2	A44919	GCR3 protein - yea
141	30	65.2	880	2	S00670	neurogenic repetit
142	30	65.2	1068	2	S64015	pleiotropic drug r
143	30	65.2	1088	2	E86312	FLNA.9 protein -
144	30	65.2	1214	2	T47659	spliceosomal-1like
145	30	65.2	1354	2	T13363	phosphoribosylform
146	30	65.2	1375	2	JT0345	dextranucrase (EC
147	29	63.0	58	2	S31683	Ig heavy chain V r
148	29	63.0	89	2	H75053	molybdopterin conv
149	29	63.0	139	2	G75127	hypothetical prote
150	29	63.0	139	2	E71003	hypothetical prote
151	29	63.0	162	1	G64478	hypothetical prote
152	29	63.0	175	2	S61599	probable membrane
153	29	63.0	210	2	T39799	hypothetical prote
154	29	63.0	213	2	D71669	adenylate kinase (
155	29	63.0	215	2	E86540	CT253 hypothetical
156	29	63.0	215	2	F72081	conserved hypot
157	29	63.0	215	2	A81693	conserved hypot
158	29	63.0	215	2	G71537	hypothetical prote
159	29	63.0	218	2	B71183	hypothetical prote
160	29	63.0	219	2	E75143	phosphoglycolate p
161	29	63.0	219	2	F83826	hypothetical prote
162	29	63.0	228	2	B89889	conserved hypot
163	29	63.0	235	2	S76974	hypothetical prote
164	29	63.0	235	2	S73468	hypothetical prote
165	29	63.0	246	2	A90165	conserved hypot
166	29	63.0	259	1	ONGAOL	ovulation hormone
167	29	63.0	268	2	C72312	conserved hypot
168	29	63.0	282	1	D95190	phosphoesterase-re
169	29	63.0	282	1	F98056	phosphoesterase-re
170	29	63.0	293	2	E89796	N-acetylneuraminat
171	29	63.0	301	2	H70644	hypothetical prote
172	29	63.0	304	2	A38100	S-cysteallin - S10
173	29	63.0	310	1	G70330	ADPglycerolmano-he
174	29	63.0	312	2	D70687	hypothetical prote
175	29	63.0	317	2	A81320	ADPglycerolmano-he
176	29	63.0	319	2	H90055	hypothetical prote
177	29	63.0	326	2	C72483	probable formate d
178	29	63.0	327	2	T32310	hypothetical prote
179	29	63.0	327	2	D82080	conserved hypot
180	29	63.0	329	2	D71887	ADPglycerolmano-he
181	29	63.0	332	1	A44509	UDP-glucose 4-epi
182	29	63.0	332	2	C83228	ADP-L-glycero-D-ma
183	29	63.0	338	2	S73902	UDP-glucose 4-epim
184	29	63.0	348	2	AD3026	D-threo-aldose 1-d
185	29	63.0	348	2	A70311	hypothetical prote
186	29	63.0	355	2	C64644	integrase/recombin
187	29	63.0	357	2	E98258	probable oxidoredu
188	29	63.0	357	2	F63537	4-hydroxyphenylpyr
189	29	63.0	357	2	S21209	4-hydroxyphenylpyr
190	29	63.0	360	2	I54554	MHC class I RT1.Aw
191	29	63.0	363	2	T34631	probable integral
192	29	63.0	369	2	C82211	4-hydroxyphenylpyr
193	29	63.0	370	2	I54531	MHC class I protei
194	29	63.0	371	2	B81256	hypothetical prote
195	29	63.0	401	2	T36078	probable two-compo
196	29	63.0	405	1	B64556	diaminopimelate de
197	29	63.0	405	2	F71950	probable icdt prot
198	29	63.0	409	2	B70846	hypothetical prote
199	29	63.0	409	2	T45797	hypothetical prote
200	29	63.0	423	2	T18784	hypothetical prote
201	29	63.0	427	2	T48159	hypothetical prote
202	29	63.0	450	2	H81338	probable sugar tra
203	29	63.0	452	2	T20223	hypothetical prote
204	29	63.0	453	2	A10833	signal recognition
205	29	63.0	453	2	B65039	signal recognition
206	29	63.0	453	2	B85907	signal recognition
207	29	63.0	453	2	A91063	signal recognition
208	29	63.0	457	2	F83178	signal recognition
209	29	63.0	461	2	D95083	ABC transporter. A
210	29	63.0	461	2	H97950	hypothetical prote
211	29	63.0	465	2	T14997	hypothetical prote
212	29	63.0	486	2	T26483	hypothetical prote
213	29	63.0	489	2	A81166	type II site-speci
214	29	63.0	514	2	T25534	hypothetical prote
215	29	63.0	514	2	JC7915	glutamate decarbox
216	29	63.0	515	1	A66686	glucose-6-phosphat
217	29	63.0	515	1	S01233	signal recognition
218	29	63.0	521	2	H87111	probable fth prote
219	29	63.0	525	2	D70747	hypothetical prote
220	29	63.0	525	2	T20662	hypothetical prote
221	29	63.0	533	2	B86207	hypothetical prote
222	29	63.0	534	2	B84590	hypothetical prote
223	29	63.0	534	2	A89953	alkaline phosphata
224	29	63.0	579	2	H97194	uncharacterized AB
225	29	63.0	619	2	G75321	ABC transporter, A
226	29	63.0	624	1	BHTLB	hemocyanin chain e
227	29	63.0	628	1	A40802	protein-tyrosine k
228	29	63.0	628	1	A66707	protein-tyrosine k
229	29	63.0	628	1	A66707	protein-tyrosine k
230	29	63.0	635	1	A53596	protein-tyrosine k
231	29	63.0	637	2	S42251	probable nucleosid
232	29	63.0	695	2	S51433	MDJ1 protein - yea
233	29	63.0	699	2	B72479	probable transito
234	29	63.0	729	2	I52481	PEPT 2 - human
235	29	63.0	788	2	B75209	dark protein - Syn
236	29	63.0	823	2	G83905	hypothetical prote
237	29	63.0	830	2	S25198	vacuolar membrane
238	29	63.0	868	2	S65186	NiR80 protein - ye
239	29	63.0	869	2	A71400	probable disease r
240	29	63.0	928	2	B84483	hypothetical prote
241	29	63.0	969	2	C86394	protein T74P13.14
242	29	63.0	993	2	C55226	CyM protein - Ent
243	29	63.0	1001	2	T20373	hypothetical prote
244	29	63.0	1100	2	T30967	transcription acti
245	29	63.0	1112	2	D66753	similar to disease
246	29	63.0	1152	2	T31911	hypothetical prote
247	29	63.0	1159	1	A44280	inner layer protei
248	29	63.0	1197	2	S26947	DNA-directed DNA p

249	29	63.0	1209	2	T13153	322	28	60.9	237	2	G82768	vinulence protein
250	29	63.0	1321	2	T23476	323	28	60.9	241	2	F64865	muselin hydrolase E
251	29	63.0	1321	2	S27337	324	28	60.9	241	2	H90839	muselin transglycos
252	29	63.0	1449	2	T10857	325	28	60.9	241	2	H85697	muselin transglycos
253	29	63.0	1449	2	T10855	326	28	60.9	245	2	T51081	hypothetical prote
254	29	63.0	1592	2	S48933	327	28	60.9	251	2	T22839	hypothetical prote
255	29	63.0	1652	2	T16799	328	28	60.9	254	2	A13084	conserved hypotnet
256	29	63.0	2103	1	JQ1621	329	28	60.9	254	2	H98201	hypothetical prote
257	29	63.0	2178	2	S29237	330	28	60.9	255	2	A81099	1-acyl-sn-glycerol
258	29	63.0	2222	2	A37490	331	28	60.9	255	2	A81842	1-acyl-glycerol-3-p
259	29	63.0	2223	2	A47447	332	28	60.9	255	2	S70545	1-acyl-glycerol-3-p
260	29	63.0	2237	2	T45115	333	28	60.9	256	2	S54406	zinc metalloprotei
261	29	63.0	2251	2	B54972	334	28	60.9	256	2	F70812	hypothetical Ipqr prot
262	29	63.0	2259	2	S29236	335	28	60.9	257	2	S70544	1-acylglycerol-3-p
263	29	63.0	2270	2	A54972	336	28	60.9	258	2	AB2770	hydrolyase limpothe
264	29	63.0	2272	2	C54972	337	28	60.9	261	2	C97550	hydrolyase (Aa27164
265	29	63.0	2326	2	B47447	338	28	60.9	267	2	D83313	probable permease
266	29	63.0	2339	2	A42566	339	28	60.9	275	2	E71269	probable riboflavi
267	29	63.0	2731	1	VPIHJH	340	28	60.9	278	2	G81139	hypothetical prote
268	29	63.0	2733	2	S15760	341	28	60.9	281	2	A81880	probable lipoprote
269	29	63.0	4488	1	RRIHM2	342	28	60.9	289	2	AD2519	hypothetical prote
270	29	63.0	5126	2	S40450	343	28	60.9	301	2	C82615	haloalkane dehalog
271	28	60.9	17	2	PT0234	344	28	60.9	302	2	AE3127	transcription regu
272	28	60.9	25	2	I67552	345	28	60.9	302	2	D98160	oxidative stress t
273	28	60.9	31	2	S53160	346	28	60.9	306	1	A71183	probable UDP-gluc
274	28	60.9	52	2	T32835	347	28	60.9	307	2	D75143	UDP-glucose 4-epim
275	28	60.9	63	2	B84092	348	28	60.9	310	2	S40253	deacetoxycephalo
276	28	60.9	86	2	A25150	349	28	60.9	311	2	AF2810	transcription regu
277	28	60.9	88	2	B25155	350	28	60.9	313	2	T13685	hypothetical prote
278	28	60.9	112	2	H69447	351	28	60.9	314	2	S30900	deacetoxycephalo
279	28	60.9	118	2	C65078	352	28	60.9	315	2	AD3209	hypothetical prote
280	28	60.9	118	2	F70516	353	28	60.9	316	2	AF2244	nucleotide sugar e
281	28	60.9	120	1	MEMS15	354	28	60.9	318	2	A39204	deacetoxycephalo
282	28	60.9	121	2	B56272	355	28	60.9	319	2	B71332	conserved hypotnet
283	28	60.9	138	2	D83639	356	28	60.9	319	2	A97589	transcription regu
284	28	60.9	145	1	CSYC42	357	28	60.9	321	1	C64522	chemotaxis protein
285	28	60.9	145	2	C26674	358	28	60.9	321	2	G71984	probable chemotaxi
286	28	60.9	147	2	B27893	359	28	60.9	323	2	T25029	hypothetical prote
287	28	60.9	147	2	H69742	360	28	60.9	325	2	B70782	hypothetical prote
288	28	60.9	148	2	S58591	361	28	60.9	327	2	H83659	serine/threonine-p
289	28	60.9	149	1	R5R222	362	28	60.9	328	2	A84167	UDP-glucose 4-epim
290	28	60.9	150	2	S54442	363	28	60.9	332	2	A29711	deacetoxycephalo
291	28	60.9	150	2	T12747	364	28	60.9	332	2	A12394	UDP-glucose 4-epim
292	28	60.9	153	2	C86304	365	28	60.9	332	2	T10209	hypothetical prote
293	28	60.9	154	2	AC0979	366	28	60.9	333	2	G71165	probable dehydroge
294	28	60.9	155	1	S47797	367	28	60.9	335	2	AF2162	UDP-glucose 4-epim
295	28	60.9	155	2	D85899	368	28	60.9	339	2	D72509	hypothetical prote
296	28	60.9	155	2	A91055	369	28	60.9	339	2	C83606	hypothetical prote
297	28	60.9	159	2	H87499	370	28	60.9	339	2	B97261	hypothetical prote
298	28	60.9	164	2	F65031	371	28	60.9	340	2	S74768	UDPglucose 4-epime
299	28	60.9	165	2	AH1014	372	28	60.9	343	2	T24700	hypothetical prote
300	28	60.9	173	2	AB1684	373	28	60.9	344	2	H64554	UDP-glucose 4-epim
301	28	60.9	173	2	G97729	374	28	60.9	344	2	G71858	UDP-glucose 4-epim
302	28	60.9	179	2	D90280	375	28	60.9	345	2	T44521	polysaccharide bio
303	28	60.9	184	2	D72307	376	28	60.9	345	2	T44510	Vi polysaccharide
304	28	60.9	186	2	H95232	377	28	60.9	346	2	JQ1388	Me1a protein - She
305	28	60.9	186	2	B98097	378	28	60.9	346	2	T24567	hypothetical prote
306	28	60.9	192	2	AT3413	379	28	60.9	347	1	VICWV1	major capsid prote
307	28	60.9	194	2	AB1312	380	28	60.9	348	2	AG1041	Vi polysaccharide
308	28	60.9	196	2	F83312	381	28	60.9	348	2	T39490	UDPglucose 4-epime
309	28	60.9	202	2	C72240	382	28	60.9	348	2	C36892	Vi polysaccharide
310	28	60.9	203	2	AC3611	383	28	60.9	350	2	T41829	capsid protein VP3
311	28	60.9	206	2	S38626	384	28	60.9	350	2	C26984	probable regulator
312	28	60.9	208	2	SQ3615	385	28	60.9	358	2	AC1062	protein kinase lim
313	28	60.9	208	2	T28974	386	28	60.9	361	2	G70959	hypothetical prote
314	28	60.9	212	2	A57823	387	28	60.9	364	2	T46604	MHC PD14 transplan
315	28	60.9	214	2	F83208	388	28	60.9	366	2	A60369	MHC class I histoc
316	28	60.9	215	2	D75161	389	28	60.9	366	2	I46603	MHC PD14 transpla
317	28	60.9	217	1	H71208	390	28	60.9	370	2	B83128	probable hydrolase
318	28	60.9	228	2	G70902	391	28	60.9	372	2	H70595	probable entC prot
319	28	60.9	231	2	G86918	392	28	60.9	375	2	H83290	conserved hypotnet
320	28	60.9	231	2	T49830	393	28	60.9	375	2	C82642	hypothetical prote
321	28	60.9	232	2	B70653	394	28	60.9	382	2	D84856	hypothetical prote

395	28	60.9	391	2	P64366	flavoprotein - Met
396	28	60.9	395	2	C90328	transposase ISCl31
397	28	60.9	395	2	T22692	hypothetical prote
398	28	60.9	396	2	H81328	probable two-compo
399	28	60.9	397	2	T38701	hypothetical prote
400	28	60.9	401	2	S65044	phosphoglycerate k
401	28	60.9	402	2	F82495	spindolin-related
402	28	60.9	403	2	E90073	hypothetical prote
403	28	60.9	410	2	P96683	hypothetical prote
404	28	60.9	412	2	S28423	isocitrate dehydro
405	28	60.9	414	2	G82705	conserved hypothet
406	28	60.9	415	2	S65065	isocitrate dehydro
407	28	60.9	416	2	A96585	NADP specific isoc
408	28	60.9	418	2	H83128	probable porin PA4
409	28	60.9	419	2	G95221	sugar ABC transpor
410	28	60.9	419	2	P96085	hypothetical prote
411	28	60.9	420	2	AB0098	diaminopimelate de
412	28	60.9	432	2	F70411	adenylosuccinate s
413	28	60.9	433	2	T09619	isocitrate dehydro
414	28	60.9	437	2	H70301	nucleotide sugar d
415	28	60.9	437	2	S74591	sensory transducti
416	28	60.9	440	2	T35925	diaminopimelate de
417	28	60.9	444	2	JC7084	alpha-1,3-mannosyl
418	28	60.9	446	2	E85691	probable tail comp
419	28	60.9	457	2	T05651	hypothetical prote
420	28	60.9	460	2	F70975	probable glutamate
421	28	60.9	462	2	C81701	hypothetical prote
422	28	60.9	478	2	A40747	kinetochore compon
423	28	60.9	483	2	D86486	protein F28J9.5 (i
424	28	60.9	500	2	AF0357	conserved hypothet
425	28	60.9	502	2	A23547	keratin, type II c
426	28	60.9	508	2	F97830	methionine-tRNA 1i
427	28	60.9	508	2	AC2342	hypothetical prote
428	28	60.9	510	2	D6782	hypothetical prote
429	28	60.9	527	2	T16909	hypothetical prote
430	28	60.9	527	2	T04659	hypothetical prote
431	28	60.9	528	2	B88989	protein F02C9.2 (i
432	28	60.9	562	2	T32581	hypothetical prote
433	28	60.9	564	2	S73615	threonine-tRNA 1i9
434	28	60.9	579	2	T15135	hypothetical prote
435	28	60.9	586	2	S64363	hypothetical prote
436	28	60.9	587	2	T01829	hypothetical prote
437	28	60.9	596	2	JN0895	succinate dehydrog
438	28	60.9	597	2	G70403	lysine-tRNA ligase
439	28	60.9	598	2	D71391	MAH2 dehydrogenas
440	28	60.9	602	2	JH0166	potassiun voltage-
441	28	60.9	609	1	A42358	vibriolysin (EC 3.
442	28	60.9	609	1	JT0903	vibriolysin (EC 3.
443	28	60.9	609	1	JC5756	vibriolysin (EC 3.
444	28	60.9	611	1	A47015	vibriolysin (EC 3.
445	28	60.9	618	2	B64564	transketolase B -
446	28	60.9	618	2	H71946	1-deoxyxylulose-5-
447	28	60.9	620	2	AF0554	1-deoxyxylulose-5-
448	28	60.9	620	2	D64771	dxs protein - Esch
449	28	60.9	620	2	F85538	1-deoxy-D-xylulose
450	28	60.9	620	2	B90688	1-deoxy-D-xylulose
451	28	60.9	627	2	G83139	1-deoxyxylulose-5-
452	28	60.9	635	2	A36868	copa homolog - Xan
453	28	60.9	637	2	D81034	1-deoxyxylulose-5-
454	28	60.9	637	2	T41546	probable 1-deoxyxy
455	28	60.9	657	2	T41546	hypothetical prote
456	28	60.9	670	2	G82672	ATP sulfurylase, 1
457	28	60.9	670	2	A82582	deoxyxylulose-5-ph
458	28	60.9	685	2	F96032	hypothetical prote
459	28	60.9	686	2	T15795	hypothetical prote
460	28	60.9	698	2	AH1013	probable lipoprote
461	28	60.9	698	2	H86095	hypothetical prote
462	28	60.9	698	2	D65210	YjH protein precu
463	28	60.9	698	2	D91255	hypothetical prote
464	28	60.9	699	2	A70300	translation elonga
465	28	60.9	708	2	A38326	glycogen(starch) s
466	28	60.9	729	2	JQ1898	probable RNA-direc
467	28	60.9				
468	28	60.9	731	2	A99106	hypothetical prote
469	28	60.9	737	2	F81049	GTP pyrophosphokin
470	28	60.9	741	2	T05250	probable disease r
471	28	60.9	749	2	C87618	exonuclease ABC,
472	28	60.9	769	2	D81828	GTP pyrophosphokin
473	28	60.9	775	2	G64616	penta-phosphate gu
474	28	60.9	776	2	C71898	guanosine-3',5'-bi
475	28	60.9	781	2	A85035	hypothetical prote
476	28	60.9	819	2	C86201	protein Fl2K1.7 (
477	28	60.9	824	2	T23923	hypothetical prote
478	28	60.9	835	2	T05259	probable disease r
479	28	60.9	849	2	C90834	tail length tape m
480	28	60.9	853	1	TUBPHL	minor tail protein
481	28	60.9	865	2	C71897	preprotein translo
482	28	60.9	899	1	P3XRPH	core protein Vp3 -
483	28	60.9	900	2	B87957	protein Y1066D.7
484	28	60.9	907	2	T04820	aconitate hydratase
485	28	60.9	908	2	T22376	hypothetical prote
486	28	60.9	941	2	B96553	hypothetical prote
487	28	60.9	944	2	S69679	hypothetical prote
488	28	60.9	948	2	T26417	hypothetical prote
489	28	60.9	954	2	T22369	hypothetical prote
490	28	60.9	971	1	JQ1634	outer capsid prote
491	28	60.9	982	1	S58881	mutS protein homol
492	28	60.9	991	2	T52400	receptor-like prot
493	28	60.9	1019	2	AB2136	polyketide synthas
494	28	60.9	1020	2	T42229	probable EI-E2 ATP
495	28	60.9	1052	2	F97268	superfamily II DNA
496	28	60.9	1078	2	D87647	hypothetical prote
497	28	60.9	1099	2	C72363	carbamoyl-phosphat
498	28	60.9	1179	2	AG1101	transcription-repa
499	28	60.9	1179	2	AG1463	transcription-repa
500	28	60.9	1186	2	T51793	hypothetical prote
501	28	60.9	1195	2	B96615	hypothetical prote
502	28	60.9	1196	2	H85061	hypothetical prote
503	28	60.9	1210	2	CS9431	centaurin, delta 2
504	28	60.9	1210	2	AC2506	hypothetical prote
505	28	60.9	1211	2	D64702	DNA polymerase III
506	28	60.9	1365	2	A41483	glucosyltransferas
507	28	60.9	1403	2	S64142	hypothetical prote
508	28	60.9	1447	2	T22643	hypothetical prote
509	28	60.9	1459	2	T24088	hypothetical prote
510	28	60.9	1462	2	T50338	probable guanine-n
511	28	60.9	1475	2	B31335	grtB protein precu
512	28	60.9	1481	2	S78373	DNA-directed RNA p
513	28	60.9	1592	2	A38175	glucosyltransferas
514	28	60.9	1613	2	F89528	protein vit-2 (imp
515	28	60.9	1616	2	T16600	vitellogenin vit-1
516	28	60.9	1639	2	T50119	probable sensory t
517	28	60.9	1999	2	AB2018	hypothetical prote
518	28	60.9	2143	2	G96595	hypothetical prote
519	28	60.9	2149	2	C96685	ribulose biphosph
520	28	60.9	2212	2	A41058	calcium channel pr
521	28	60.9	2273	2	T14677	calcium channel BI
522	28	60.9	2424	2	T14680	peptide synthetase
523	28	60.9	2617	2	AE2136	gene X protein - h
524	27	58.7	31	2	S53258	hypothetical prote
525	27	58.7	60	2	D97841	hypothetical prote
526	27	58.7	67	2	T18080	hypothetical prote
527	27	58.7	73	2	A98919	hypothetical prote
528	27	58.7	73	2	F85767	hypothetical prote
529	27	58.7	81	2	S75710	molybdopterin bios
530	27	58.7	120	2	A70382	hypothetical prote
531	27	58.7	128	2	AC2678	hypothetical prote
532	27	58.7	131	2	S08328	Ig heavy chain V r
533	27	58.7	134	2	B24574	T-cell receptor ga
534	27	58.7	136	1	RWHUGV	T-cell receptor ga
535	27	58.7	140	2	G72555	hypothetical prote
536	27	58.7	141	2	C86521	hypothetical prote
537	27	58.7	141	2	G72100	hypothetical prote
538	27	58.7	145	2	S06307	T-cell receptor ga
539	27	58.7	146	2	A11652	Bacillus phage phi
540	27	58.7	150	2	JC5398	leukorrhene C4 syn

541	27	58.7	150	2	138595	leukotriene-C4 syn
542	27	58.7	150	2	S68961	leukotriene C4 syn
543	27	58.7	154	2	S23044	T-cell receptor ga
544	27	58.7	154	2	H75562	hypothetical prote
545	27	58.7	155	2	AH2473	hypothetical prote
546	27	58.7	156	2	T12893	hypothetical prote
547	27	58.7	160	2	AD1874	hypothetical prote
548	27	58.7	163	2	B96818	hypothetical prote
549	27	58.7	168	2	T35737	probable integral
550	27	58.7	169	2	A42716	antirestriction pr
551	27	58.7	170	2	F82908	conserved hypotet
552	27	58.7	178	2	F90204	conserved hypotet
553	27	58.7	185	2	F70479	flavodoxin - Aquif
554	27	58.7	185	2	T31636	hypothetical prote
555	27	58.7	189	2	G95126	conserved hypotet
556	27	58.7	189	2	C97997	conserved hypotet
557	27	58.7	204	2	T10766	patatin-like latex
558	27	58.7	205	2	G01942	mitotic feedback c
559	27	58.7	206	2	T11626	NADH2 dehydrogen
560	27	58.7	207	2	T11935	conserved hypotet
561	27	58.7	209	2	G72321	protein P37F2.1 li
562	27	58.7	210	2	D87724	hypothetical prote
563	27	58.7	210	2	T33051	ABC transporter pe
564	27	58.7	227	2	C75029	glycosyl transfera
565	27	58.7	238	2	A69463	hypothetical prote
566	27	58.7	241	2	F86691	probable periplasm
567	27	58.7	242	2	S74744	probable Spou-fam
568	27	58.7	245	2	D87307	calcium-binding pr
569	27	58.7	257	2	AE2807	hypothetical prote
570	27	58.7	257	2	C97586	hypothetical prote
571	27	58.7	257	2	AB0353	hypothetical prote
572	27	58.7	262	1	K1CHI	probable iron-sulf
573	27	58.7	264	2	D85507	cell division-like
574	27	58.7	266	2	D90656	hypothetical prote
575	27	58.7	266	2	F81687	hypothetical prote
576	27	58.7	269	2	T16115	conserved hypotet
577	27	58.7	271	2	G01790	hypothetical prote
578	27	58.7	274	2	D81013	probable thiol-spe
579	27	58.7	274	2	B81955	DNA ligase NMB2048
580	27	58.7	280	2	A12704	probable secreted
581	27	58.7	283	2	B87546	conserved hypotet
582	27	58.7	284	2	F89907	acetoin dehydrogen
583	27	58.7	285	2	S51247	hypothetical prote
584	27	58.7	285	2	A97487	thioredoxin homolo
585	27	58.7	287	2	T45963	probable iron-sulf
586	27	58.7	287	2	F96738	hypothetical prote
587	27	58.7	289	2	T40596	hypothetical prote
588	27	58.7	290	2	F85760	probable DNA repa
589	27	58.7	290	2	A99859	hypothetical prote
590	27	58.7	291	2	A10653	hypothetical prote
591	27	58.7	291	2	H64874	probable pseudouri
592	27	58.7	293	2	S57376	hypothetical prote
593	27	58.7	298	2	D69537	hypothetical prote
594	27	58.7	301	2	H84192	deoxyhypusine synt
595	27	58.7	303	2	B83367	hypothetical prote
596	27	58.7	304	2	S04663	probable glycosyl
597	27	58.7	305	2	T31740	T-cell receptor ga
598	27	58.7	308	2	H86857	hypothetical prote
599	27	58.7	311	2	T32118	highly conserved h
600	27	58.7	315	2	E71729	hypothetical prote
601	27	58.7	316	2	G70110	protease DO (hr
602	27	58.7	317	2	A83621	L-lactate dehydrog
603	27	58.7	318	2	A83621	hydrogen peroxide-
604	27	58.7	322	2	A83621	probable RNA pseud
605	27	58.7	323	2	S01895	pyruvate dehydrog
606	27	58.7	323	2	JQ1552	T-cell receptor ga
607	27	58.7	323	2	G87358	C1 protein - Panic
608	27	58.7	325	2	T04677	dienealactone hydro
609	27	58.7	325	2	D82662	hypothetical prote
610	27	58.7	327	2	AB1211	hypothetical prote
611	27	58.7	328	2	F81317	glycosyltransferas
612	27	58.7	328	2	A84901	UDPglucose 4-epime
613	27	58.7	328	2	H84900	hypothetical prote
614	27	58.7	328	2	S60256	TGF-beta receptor
615	27	58.7	328	2	H71954	probable lipid A b
616	27	58.7	329	2	JC5168	UDPglucose 4-epime
617	27	58.7	329	2	H64115	phenylalanine-tRNA
618	27	58.7	338	1	NMBEKL	cell fusion protei
619	27	58.7	338	1	NMBEKL	cell fusion protei
620	27	58.7	340	2	AG2922	oxidoreductase Atu
621	27	58.7	340	2	H97696	probable oxidoredu
622	27	58.7	340	2	C69466	probable glycerald
623	27	58.7	342	2	T23500	hypothetical prote
624	27	58.7	344	1	BXAG58	vitB11 protein - A
625	27	58.7	344	2	AG3249	component of type
626	27	58.7	345	2	A95230	conserved hypotet
627	27	58.7	345	2	D98094	conserved hypotet
628	27	58.7	345	2	C81300	probable helix-cur
629	27	58.7	346	2	T41913	G protein-coupled
630	27	58.7	346	2	T74568	hypothetical prote
631	27	58.7	346	2	T31987	hypothetical prote
632	27	58.7	347	2	T31921	hypothetical prote
633	27	58.7	351	2	AE2979	aldo/keto reductas
634	27	58.7	351	2	H98303	hypothetical prote
635	27	58.7	352	2	B83133	probable alcohol d
636	27	58.7	352	2	G90228	conserved hypotet
637	27	58.7	353	2	F95403	probable oxidoredu
638	27	58.7	354	2	C95381	probable oxidoredu
639	27	58.7	356	2	S13221	GTP-binding regula
640	27	58.7	359	2	A35714	fetuin precursor -
641	27	58.7	359	2	T13289	probable integrase
642	27	58.7	360	2	T33124	hypothetical prote
643	27	58.7	364	2	S22394	fetuin precursor -
644	27	58.7	370	2	I40085	gucs protein - Bac
645	27	58.7	372	2	S46344	env polyprotein -
646	27	58.7	374	2	T06276	benzochiadiazole-i
647	27	58.7	374	2	E64489	hypothetical prote
648	27	58.7	375	2	T00467	probable UDPglucos
649	27	58.7	375	2	S46345	env polyprotein -
650	27	58.7	379	2	E72284	oxidoreductase, al
651	27	58.7	379	2	T10588	UDPglucose 4-epime
652	27	58.7	379	2	AE3225	ABC transporter, m
653	27	58.7	380	2	S66728	hypothetical prote
654	27	58.7	380	2	AE1377	two-component sens
655	27	58.7	380	2	AP1746	two-component sens
656	27	58.7	386	2	G84386	oligopeptide trans
657	27	58.7	390	2	AD3213	oxidoreductase Atu
658	27	58.7	391	2	T00675	hypothetical prote
659	27	58.7	394	2	A75303	UDP-glucose 4-epim
660	27	58.7	396	2	T19294	hypothetical prote
661	27	58.7	397	2	B72294	adenylosuccinate s
662	27	58.7	398	2	A72338	conserved hypotet
663	27	58.7	399	2	H72288	isocitrate dehydro
664	27	58.7	401	2	F69834	multidrug-efflux t
665	27	58.7	402	2	F81450	diminopimelate de
666	27	58.7	406	2	UC4600	isocitrate dehydro
667	27	58.7	409	2	A75136	flavoprotein (fpra
668	27	58.7	412	2	S51419	isocitrate dehydro
669	27	58.7	413	2	C70361	conserved hypotet
670	27	58.7	414	2	JU0292	streptokinase - St
671	27	58.7	416	2	AC0198	lipoprotein releas
672	27	58.7	416	2	C96725	hypothetical prote
673	27	58.7	417	2	A64918	membrane-associate
674	27	58.7	419	2	B86431	T518.7 protein - A
675	27	58.7	420	2	S62921	isocitrate dehydro
676	27	58.7	420	2	T08691	hypothetical prote
677	27	58.7	425	2	B81236	nitrogen assimilac
678	27	58.7	425	2	D82009	probable two-compo
679	27	58.7	425	2	G91104	probable oxidoredu
680	27	58.7	428	1	DCBYIS	isocitrate dehydro
681	27	58.7	431	2	AB9761	hypothetical prote
682	27	58.7	434	2	D75212	asparagine-tRNA li
683	27	58.7	434	2	B71248	asparagine-tRNA li
684	27	58.7	439	2	B81291	hypothetical prote
685	27	58.7	440	2	S04168	streptokinase A pr
686	27	58.7	440	2	AP0615	killing factor K1c

687	27	58.7	440	2	S43911	760	27	58.7	660	2	S24125	potassium channel
688	27	58.7	440	2	E90754	761	27	58.7	662	2	T46005	receptor-like prot
689	27	58.7	440	2	C85618	762	27	58.7	670	2	G64921	probable membrane
690	27	58.7	440	2	AE0171	763	27	58.7	670	2	F85771	hypothetical prote
691	27	58.7	440	2	T44138	764	27	58.7	678	2	B99923	hypothetical prote
692	27	58.7	445	2	T46225	765	27	58.7	670	2	A71287	probable cytoplasm
693	27	58.7	450	2	A97740	766	27	58.7	679	2	AE0694	probable membrane
694	27	58.7	450	2	A71678	767	27	58.7	680	2	S46308	initiator-binding
695	27	58.7	455	2	F64617	768	27	58.7	685	2	S46309	initiator-binding
696	27	58.7	468	2	T35928	769	27	58.7	687	2	T26332	hypothetical prote
697	27	58.7	477	2	A10616	770	27	58.7	687	2	E69733	PBX prophage ORF
698	27	58.7	477	2	D90112	771	27	58.7	687	2	S64954	hypothetical prote
699	27	58.7	479	2	T39953	772	27	58.7	689	2	T26331	hypothetical prote
700	27	58.7	479	2	E97337	773	27	58.7	691	2	T33637	hypothetical prote
701	27	58.7	480	2	F81220	774	27	58.7	692	2	C91653	probable thiol-dis
702	27	58.7	480	2	S11780	775	27	58.7	703	2	B61146	F22L12 protein -
703	27	58.7	483	1	SYBSET	776	27	58.7	707	2	AE6210	protein F22G5.8 li
704	27	58.7	487	2	JT0407	777	27	58.7	715	2	T04881	hypothetical prote
705	27	58.7	489	2	S05474	778	27	58.7	728	2	T27884	hypothetical prote
706	27	58.7	490	2	U80658	779	27	58.7	729	2	A89946	GFP pyrophosphokin
707	27	58.7	491	2	F83383	780	27	58.7	745	2	C98618	protein ZK520.4 li
708	27	58.7	497	2	B97729	781	27	58.7	754	2	E87185	phosphoribosylform
709	27	58.7	497	2	T40586	782	27	58.7	754	2	D70536	probable puri prot
710	27	58.7	499	2	A48672	783	27	58.7	772	2	T49573	hypothetical prote
711	27	58.7	499	2	T27630	784	27	58.7	774	2	T27630	probable ATP-bind
712	27	58.7	500	2	C91251	785	27	58.7	786	2	T02729	serine/threonine-s
713	27	58.7	502	2	E90442	786	27	58.7	787	2	S54535	hypothetical prote
714	27	58.7	512	2	S59828	787	27	58.7	788	2	H96545	hypothetical prote
715	27	58.7	517	2	F86921	788	27	58.7	790	2	T49542	hypothetical prote
716	27	58.7	518	2	C70887	789	27	58.7	791	2	T41655	major facilitator
717	27	58.7	520	2	J50291	790	27	58.7	809	2	A46747	Na+/H+-exchanging
718	27	58.7	524	2	A23518	791	27	58.7	810	2	D96566	hypothetical prote
719	27	58.7	524	2	F66784	792	27	58.7	813	2	A46748	Na+/H+-exchanging
720	27	58.7	526	2	E71423	793	27	58.7	829	2	B87305	TonB-dependent rec
721	27	58.7	527	2	H81701	794	27	58.7	851	2	AE2469	hypothetical prote
722	27	58.7	529	2	F71547	795	27	58.7	872	2	T37789	Scd1 protein - tis
723	27	58.7	534	2	T30019	796	27	58.7	874	2	AC2287	hypothetical prote
724	27	58.7	536	2	A83038	797	27	58.7	877	2	C46356	env polypeptide
725	27	58.7	537	2	D71296	798	27	58.7	879	2	F81453	DNA-directed DNA p
726	27	58.7	538	2	T27433	799	27	58.7	880	2	F75103	conserved hypothet
727	27	58.7	538	2	H86329	800	27	58.7	884	2	A11928	glucose transport
728	27	58.7	542	2	B83192	801	27	58.7	888	2	S78288	preprotein translo
729	27	58.7	545	2	T51438	802	27	58.7	888	2	A38539	p101 protein precu
730	27	58.7	546	2	G90318	803	27	58.7	891	2	T36423	probable large, mu
731	27	58.7	550	2	I64203	804	27	58.7	892	2	B82831	translational initia
732	27	58.7	552	2	T23171	805	27	58.7	896	2	S57723	ltp protein - huma
733	27	58.7	552	2	E72283	806	27	58.7	899	1	A43969	core protein VP3 -
734	27	58.7	554	2	A70904	807	27	58.7	901	1	F3XR17	core protein VP3 -
735	27	58.7	554	2	A69392	808	27	58.7	901	2	S07419	exoribonuclease RN
736	27	58.7	561	2	A99248	809	27	58.7	925	2	C83030	hypothetical prote
737	27	58.7	564	2	AP2351	810	27	58.7	925	2	AC3130	preprotein translo
738	27	58.7	565	1	A64134	811	27	58.7	930	2	AC2412	hypothetical prote
739	27	58.7	567	2	S25521	812	27	58.7	930	2	B88157	hypothetical prote
740	27	58.7	568	2	G83558	813	27	58.7	948	2	UC2190	preprotein translo
741	27	58.7	568	2	T49962	814	27	58.7	948	2	S75991	hypothetical prote
742	27	58.7	570	2	A75201	815	27	58.7	977	2	C96745	hypothetical prote
743	27	58.7	572	2	JC7833	816	27	58.7	977	2	AC1963	DNA polymerase I l
744	27	58.7	573	2	D86464	817	27	58.7	978	2	H81311	transcription-repa
745	27	58.7	575	2	C90143	818	27	58.7	983	2	F86160	F1003.18 protein -
746	27	58.7	579	2	T16237	819	27	58.7	984	2	D70461	preprotein translo
747	27	58.7	581	2	C96538	820	27	58.7	987	2	T50850	receptor protein k
748	27	58.7	582	2	G81288	821	27	58.7	996	2	D86872	beta-galactosidase
749	27	58.7	589	2	S06694	822	27	58.7	996	2	T25512	hypothetical prote
750	27	58.7	601	2	A55921	823	27	58.7	1006	2	JC5526	kinase-defective E
751	27	58.7	608	2	H86783	824	27	58.7	1010	2	C81524	glycyl-tRNA synthe
752	27	58.7	612	2	JH0799	825	27	58.7	1014	2	H86608	glycyl-tRNA synthe
753	27	58.7	612	2	S42629	826	27	58.7	1015	1	A72016	transposase - Esch
754	27	58.7	643	2	H81361	827	27	58.7	1015	2	TOECT	transposase - Esch
755	27	58.7	652	2	C95177	828	27	58.7	1021	2	T08601	hypothetical prote
756	27	58.7	652	2	S47979	829	27	58.7	1032	2	H64100	acetylflavine resist
757	27	58.7	652	2	E98044	830	27	58.7	1039	2	T22117	hypothetical prote
758	27	58.7	653	2	A39922	831	27	58.7	1070	2	T30848	Duffy receptor - p
759	27	58.7	654	2	S11049	832	27	58.7	1075	2	T00341	hypothetical prote

833	27	58.7	1121	2	T13796	906	26	56.5	179	2	B83087	conserved hypotet
834	27	58.7	1121	2	T13750	907	26	56.5	180	2	S76762	hypothetical prote
835	27	58.7	1136	2	T40355	908	26	56.5	181	2	S76188	MHC cell surface g
836	27	58.7	1182	2	C70619	909	26	56.5	181	2	A28782	cytochrome-c oxida
837	27	58.7	1189	2	T52346	910	26	56.5	182	2	S53822	fucoxanthin chloro
838	27	58.7	1203	2	G89734	911	26	56.5	185	2	S36290	T-cell receptor ga
839	27	58.7	1203	2	A33165	912	26	56.5	187	2	T30679	probable DNA-direc
840	27	58.7	1265	2	T06916	913	26	56.5	187	2	AF3542	formylmethionine d
841	27	58.7	1327	2	T21268	914	26	56.5	188	2	H90106	60S ribosomal prot
842	27	58.7	1361	2	S50943	915	26	56.5	188	2	A72745	hypothetical prote
843	27	58.7	1391	2	S50608	916	26	56.5	188	2	H62349	transferase, hexap
844	27	58.7	1404	1	A48196	917	26	56.5	189	2	A45239	septum formation m
845	27	58.7	1426	1	T30567	918	26	56.5	189	2	S49598	hypothetical prote
846	27	58.7	1476	2	AC2220	919	26	56.5	192	1	ASLJ01	vif protein - huma
847	27	58.7	1501	2	S57198	920	26	56.5	192	2	S43007	viral infectivity
848	27	58.7	1526	2	JN0598	921	26	56.5	192	2	S43006	viral infectivity
849	27	58.7	1526	2	A44406	922	26	56.5	192	2	S42961	viral infectivity
850	27	58.7	1528	2	J50703	923	26	56.5	192	2	S42978	viral infectivity
851	27	58.7	1530	2	A40493	924	26	56.5	192	2	S42966	viral infectivity
852	27	58.7	1735	1	S22812	925	26	56.5	192	2	S42980	viral infectivity
853	27	58.7	1838	2	T18448	926	26	56.5	192	2	S42944	viral infectivity
854	27	58.7	2698	2	B96671	927	26	56.5	192	2	S42988	viral infectivity
855	27	58.7	3396	2	T22613	928	26	56.5	192	2	S42976	viral infectivity
856	27	58.7	5147	1	J0FPTM	929	26	56.5	192	2	S42999	viral infectivity
857	27	57.6	433	2	T43924	930	26	56.5	192	2	S42962	viral infectivity
858	26.5	57.6	775	2	S65769	931	26	56.5	192	2	S42949	viral infectivity
859	26	56.5	24	2	T42390	932	26	56.5	192	2	S42952	viral infectivity
860	26	56.5	25	2	PH1717	933	26	56.5	192	2	S42977	viral infectivity
861	26	56.5	51	2	S00576	934	26	56.5	192	2	A53914	light-repressed pr
862	26	56.5	67	2	D55210	935	26	56.5	195	2	G66683	prophage p11 prote
863	26	56.5	75	2	A54355	936	26	56.5	197	2	T09257	late embryonic abu
864	26	56.5	79	2	A10052	937	26	56.5	197	2	FA4257	hypothetical prote
865	26	56.5	88	2	E71358	938	26	56.5	202	2	S74437	hypothetical prote
866	26	56.5	91	2	FA4188	939	26	56.5	202	2	T16717	hypothetical prote
867	26	56.5	92	2	S24230	940	26	56.5	203	2	S36291	T-cell receptor ga
868	26	56.5	103	2	G82716	941	26	56.5	203	2	S23043	hypothetical prote
869	26	56.5	103	2	B64334	942	26	56.5	203	2	C38179	hypothetical prote
870	26	56.5	106	2	E97001	943	26	56.5	203	2	G84390	hypothetical prote
871	26	56.5	106	2	C66690	944	26	56.5	203	2	S47487	fucoxanthin chloro
872	26	56.5	106	2	AC0636	945	26	56.5	204	2	C98218	UDP-glucose 4-epim
873	26	56.5	107	2	T15335	946	26	56.5	204	2	B90112	60S ribosomal prot
874	26	56.5	109	2	S33836	947	26	56.5	206	2	I37529	H1A-Cw7 - human (f
875	26	56.5	115	2	C47274	948	26	56.5	211	2	S53824	fucoxanthin chloro
876	26	56.5	122	2	AG1597	949	26	56.5	212	2	H71188	hypothetical prote
877	26	56.5	122	2	FA4035	950	26	56.5	213	2	T21899	hypothetical prote
878	26	56.5	128	2	S78148	951	26	56.5	213	2	B83386	hypothetical prote
879	26	56.5	129	2	S28237	952	26	56.5	214	2	D82839	hemolysin III prot
880	26	56.5	130	2	H82057	953	26	56.5	214	2	T27259	hypothetical prote
881	26	56.5	130	2	A64094	954	26	56.5	215	2	E75623	probable ABC trans
882	26	56.5	132	2	G82713	955	26	56.5	216	2	S60048	chlorophyll a/c-bi
883	26	56.5	132	2	AE3348	956	26	56.5	216	2	S53821	fucoxanthin chloro
884	26	56.5	135	2	H64344	957	26	56.5	217	2	S53820	fucoxanthin chloro
885	26	56.5	139	1	S03579	958	26	56.5	217	2	S53819	fucoxanthin chloro
886	26	56.5	139	1	FA4415	959	26	56.5	223	1	A41031	glutathione transf
887	26	56.5	140	2	S41785	960	26	56.5	226	2	BE4441	hypothetical prote
888	26	56.5	142	2	C75271	961	26	56.5	229	2	S47859	Glc8 protein - Yea
889	26	56.5	147	2	C90094	962	26	56.5	230	2	G83683	two-component resp
890	26	56.5	147	2	B36529	963	26	56.5	231	2	D69980	purine nucleoside
891	26	56.5	148	2	T37532	964	26	56.5	232	2	D90254	conserved hypotet
892	26	56.5	148	2	H71644	965	26	56.5	235	2	F71249	hypothetical prote
893	26	56.5	150	2	T49563	966	26	56.5	236	2	B69335	succinate dehydrog
894	26	56.5	153	2	S58092	967	26	56.5	237	2	G72129	hypothetical prote
895	26	56.5	157	2	A66906	968	26	56.5	237	2	H86491	hypothetical prote
896	26	56.5	161	2	S72986	969	26	56.5	237	2	BE4643	hypothetical prote
897	26	56.5	163	2	D64025	970	26	56.5	238	2	D84729	probable disease r
898	26	56.5	165	2	C69065	971	26	56.5	239	2	A97358	glucose-inhibited
899	26	56.5	168	2	T15663	972	26	56.5	240	2	H81420	probable iron-bind
900	26	56.5	168	2	E97860	973	26	56.5	240	2	G83401	hypothetical prote
901	26	56.5	168	2	S18655	974	26	56.5	243	2	C64505	coenzyme PQQ synth
902	26	56.5	168	2	S72898	975	26	56.5	244	2	A82855	oxotidine 5'-phosp
903	26	56.5	171	2	AD0017	976	26	56.5	244	2	S25988	hypothetical prote
904	26	56.5	175	2	B71732	977	26	56.5	244	2	S30860	hypothetical prote
905	26	56.5	177	2	C96774	978	26	56.5	247	2	E90493	hypothetical prote

979 26 56.5 248 2 T24225 hypothetical prote
980 26 56.5 249 2 C72243 flagellar basal-bo
981 26 56.5 249 2 E90048 hypothetical prote
982 26 56.5 251 2 E90428 hypothetical prote
983 26 56.5 252 2 G70543 hypothetical prote
984 26 56.5 254 2 E87793 protein C27A12.5 (i
985 26 56.5 257 2 A71522 probable arginine
986 26 56.5 259 2 G81678 amino acid ABC tra
987 26 56.5 261 2 A83281 periplasmic histid
988 26 56.5 263 2 A64506 hypothetical prote
989 26 56.5 263 2 T39487 hypothetical prote
990 26 56.5 263 2 T29199 hypothetical prote
991 26 56.5 265 2 A83207 probable short-cha
992 26 56.5 265 2 G95058 integrase/recombin
993 26 56.5 265 2 G97927 terminal protein -
994 26 56.5 266 1 ER88NP hypothetical prote
995 26 56.5 266 2 E90354 hypothetical prote
996 26 56.5 267 2 B81541 arginine-binding p
997 26 56.5 269 2 AE3455 probable hydrolase
998 26 56.5 272 2 T36181 hypothetical prote
999 26 56.5 272 2 T27062 hypothetical prote
1000 26 56.5 273 2 A82475

ALIGNMENTS

RESULT 1
AC1861
hypothetical protein alr0436 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AC1861
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Itiguchi, N.; Nakazaki, N.; Shimp, S.; Sugimoto, M.; Takazawa, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena PCC 7120
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AC1861
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-470 <KUR>
A:Cross-References: UNIPROT:O8VZM1; UNIPARC:UPI000000CDP50; GB:BA000019; PIND:BA872394.1;
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr0436

Query Match 80.4%; Score 37; DB 2; Length 470;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 VRLRYFD 8
DB 407 VRLRYFD 413

RESULT 2
T11695
phospholipase D (BC 3.1.4.4) - cowpea
C:Species: Vigna unguiculata (cowpea)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T11695
R:El Maarouf, H.; Pham Thi, A.T.; Garell, M.; d'Arcy-Lameta, A.; Zully-Fodil, Y.
submitted to the EMBL Data Library, March 1997
A:Reference number: Z17317
A:Accession: T11695
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-809 <ELM>
A:Cross-References: UNIPROT:O04865; UNIPARC:UPI0000013147E; EMBL:U92656; NID:G1928978; PI
A:Experimental source: strain EPA9C-1; leaf; clone D10a
C:Superfamily: phospholipase D, plant type

C:Keywords: phosphoric diester hydrolase

Query Match 80.4%; Score 37; DB 2; Length 809;
Best Local Similarity 87.5%; Pred. No. 15;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 VRLRYFD 9
DB 143 VRLRYFD 150

RESULT 3
A64712
hypothetical protein HP1537 - Helicobacter pylori (strain 26695)
C:Species: Helicobacter pylori
C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C:Accession: A64712
R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khaliq, H.G.; Glodek, A.; McKenney, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watney, L.; Nature 388, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A:Reference number: A64520; MUID:97394467; PMID:9252185
A:Accession: A64712
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-228 <TOM>
A:Cross-References: UNIPROT:O26063; UNIPARC:UPI000000C0945; GB:AE000651; GB:AE000511; NID
C:Superfamily: Helicobacter pylori hypothetical protein HP1537

Query Match 76.1%; Score 35; DB 2; Length 228;
Best Local Similarity 66.7%; Pred. No. 10;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 EVRLRYFDV 9
DB 170 EVRLRYFDI 178

RESULT 4
T41149
probable transcription factor, ccr4-associated factor homolog - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T41149
R:Hilbert, H.; Duestenhoef, A.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, October 1998
A:Reference number: Z21973
A:Accession: T41149
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-332 <HIL>
A:Cross-References: UNIPROT:O74856; UNIPARC:UPI000006AA0E; EMBL:AL031907; PIND:CAA21420.
A:Experimental source: strain 972h-; cosmid c18
C:Genetics:
A:Gene: SPDB:SPCC18.06c
A:Map position: 3

Query Match 76.1%; Score 35; DB 2; Length 332;
Best Local Similarity 75.0%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 EVRLRYFD 8
DB 250 EVRLRYFD 257

RESULT 5
T15074
hypothetical protein T08B6.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C:Accession: T15074
R:Rolling, T.; Hawkins, J.; Woldmann, P.; Keppler, D.; Wilson, R.
submitted to the EMBL Data Library, December 1997
A:Description: The sequence of C. elegans cosmid T08B6.
A:Reference number: 218287
A:Accession: T15074
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-338 <ROH>
A:Cross-references: UNIPROT:O44528; UNIPARC:UPI000007FABC; EMBL:AF038623; NID:g2736335;
A:Experimental source: strain Bristol N2; clone T08B6
C:Genetics:
A:Gene: CESP:T08B6.3
A:Map position: 4
A:Introns: 63/3; 95/1; 121/2; 165/2; 211/3; 255/3; 315/1

Query Match 76.1%; Score 35; DB 2; Length 338;
Best Local Similarity 87.5%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 EVRLRYFD 8
122 EGRRLRYFD 129

RESULT 6
A:Accession: A49103
C:Species: Schizosaccharomyces pombe
C:Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 31-Dec-2004
R:Docljes, D.; van de Wetering, M.; Knippels, L.; Clevers, H.
J. Biol. Chem. 268, 24813-24817, 1993
A:Title: The Schizosaccharomyces pombe mating-type gene mat-Mc encodes a sequence-specific
A:Reference number: A49103; MUID:94043341; PMID:8227043
A:Accession: A49103
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-81 <DOO>
A:Cross-references: UNIPARC:UPI000017A241
A:Note: sequence extracted from NCBI backbone (NCBIR:139668)
F:1-76/Domain: HMG box homology <HMG1>

Query Match 73.9%; Score 34; DB 2; Length 81;
Best Local Similarity 85.7%; Pred. No. 5.7;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVRLRYFD 7
48 EVRLRYFD 54

Db 48 EVRLRYFD 54

RESULT 7
S00555
mating type protein Mc - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1998 #text_change 05-Oct-2004
R:Kelly, M.; Burke, J.; Smith, M.; Klar, A.; Beach, D.
EMBO J. 7, 1537-1547, 1988
A:Title: Four mating-type genes control sexual differentiation in the fission yeast.
A:Reference number: S00555; MUID:88312604; PMID:2900761
A:Accession: S00555
A:Molecule type: DNA
A:Residues: 1-181 <KEL>
A:Cross-references: UNIPROT:P10840; UNIPARC:UPI000012F801; EMBL:X07642; NID:g4979; PIDN:
R:Yang, Z.; Aves, S.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, January 1999
A:Reference number: Z1893
A:Accession: T39955
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-181 <XIA>

A:Cross-references: UNIPARC:UPI000012F801; EMBL:AL035065; PIDN:CAA22625.1; GSPDB:GN00067
A:Experimental source: strain 972h-; cosmid C23G7
C:Comment: This protein is necessary for meiosis and sporulation, and determines the h-m
C:Comment: A silent copy of this gene is located at the mat3 locus. Activation requires
C:Genetics:
A:Gene: mat1-Mc
A:Map position: 2
C:Keywords: DNA binding; meiosis; nucleus; sporulation; transcription regulation
F:101-175/Domain: HMG box homology <HMG1>

Query Match 73.9%; Score 34; DB 2; Length 181;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVRLRYFD 7
147 EVRLRYFD 153

Db 147 EVRLRYFD 153

RESULT 8
D91111
probable adherence factor [imported] - Escherichia coli (strain O157:H7, substrain R1MD
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: D91111
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shibata, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: D91111
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-433 <HAY>
A:Cross-references: UNIPROT:O8L1L9; UNIPARC:UPI00001654E8; GB:BA000007; PIDN:BA837283.1,
A:Experimental source: strain O157:H7, substrain R1MD 0509952
C:Genetics:
A:Gene: ECs3860

Query Match 73.9%; Score 34; DB 2; Length 433;
Best Local Similarity 75.0%; Pred. No. 33;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EVRLRYFD 8
47 EVRLRYFD 54

Db 47 EVRLRYFD 54

RESULT 9
H85956
probable cytotoxin Z4332 [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: H85956
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Diallanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85460; MUID:21074935; PMID:11206551
A:Accession: H85956
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-433 <STO>
A:Cross-references: UNIPROT:Q8XEH7; UNIPARC:UPI00000D023C; GB:AE005174; NID:g12517540; P
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: Z4332

Query Match 73.9%; Score 34; DB 2; Length 433;
Best Local Similarity 75.0%; Pred. No. 33;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EVRLRYFD 8

Db | ||| ||
47 EARLRFDD 54

RESULT 10

T34451
hypochemical protein T19H12.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T34451
R:Davidson, S.

A:Submitted to: The EMBL Data Library, April 1997
A:Description: The sequence of C. elegans cosmid T19H12.

A:Reference number: 221528

A:Accession: T34451

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-619 <DAV>

A:Cross-references: UNIPROT:Q01610; UNIPARC:UPI000007C887; EMBL:U97009; PIDN:AAC69031.1;

A:Experimental source: strain Bristol N2; clone T19H12

C:Genetics:

A:Gene: CESP:T19H12.6

A:Map position: 5

A:introns: 17/1; 94/2; 198/1; 287/2; 465/1; 547/2; 606/2

Query Match 73.9%; Score 34; DB 2; Length 619;
Best Local Similarity 85.7%; Pred. No. 47;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 EVLRYPDV 9
|:|:|:|:|
Db 563 KLRYPDV 569

RESULT 11

T03402
probable phospholipase D (EC 3.1.4.4) - rice

C:Species: Oryza sativa (rice)

C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004

C:Accession: T03402

R:Ueki, J.; Morioka, S.; Komari, T.; Kumashiro, T.

Plant Cell Physiol. 36, 903-914, 1995

A:Title: Purification and characterization of phospholipase D (PLD) from rice (Oryza sat

A:Reference number: Z14933; MUID:96012933; PMID:7551587

A:Accession: T03402

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-812 <UEK>

A:Cross-references: UNIPROT:Q43007; UNIPARC:UPI000013147A; EMBL:AB001920; NID:g1902902;

A:Experimental source: cv. Koshihikari, leaf

C:Genetics:

A:introns: 35/3; 668/1

C:Superfamily: phospholipase D, plant type

C:Keywords: phosphoric diester hydrolase

Query Match 73.9%; Score 34; DB 2; Length 812;
Best Local Similarity 75.0%; Pred. No. 63;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLRYPDV 9
|:|:|:|:|
Db 147 VKLQYFDV 154

RESULT 12

T03659
phospholipase D (EC 3.1.4.4) - maize

C:Species: Zea mays (maize)

C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004

C:Accession: T03659

R:Ueki, J.; Morioka, S.; Komari, T.; Kumashiro, T.

Plant Cell Physiol. 36, 903-914, 1995

A:Title: Purification and characterization of phospholipase D (PLD) from rice (Oryza sat

A:Reference number: Z14933; MUID:96012933; PMID:7551587

A:Accession: T03659

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-812 <UEK>

A:Cross-references: UNIPROT:Q43270; UNIPARC:UPI0000131477; EMBL:D73410; NID:g1020408; PI

A:Experimental source: cultivar Mo17

C:Superfamily: phospholipase D, plant type

C:Keywords: phosphoric diester hydrolase

Query Match 73.9%; Score 34; DB 2; Length 812;
Best Local Similarity 75.0%; Pred. No. 63;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLRYPDV 9
|:|:|:|:|
Db 147 VKLQYFDV 154

RESULT 13

G87405
ribosomal protein S8 [imported] - Caulobacter crescentus

C:Species: Caulobacter crescentus

C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004

C:Accession: G87405

R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Bisen, J.; Heidelberg, J.

B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Burklin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon

n, U.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.

Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A:Title: Complete Genome Sequence of Caulobacter crescentus.

A:Reference number: A87249; MUID:21173698; PMID:11259647

A:Accession: G87405

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-132 <STO>

A:Cross-references: UNIPROT:Q9A8T9; UNIPARC:UPI000013514F; GB:AE005673; NID:g13422593; P

C:Genetics:

A:Superfamily: Escherichia coli ribosomal protein S8

Query Match 71.7%; Score 33; DB 2; Length 132;
Best Local Similarity 62.5%; Pred. No. 15;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EVLRYPDV 8
|:|:|:|:|
Db 62 EELKYPDV 69

RESULT 14

S02284
potassium channel protein A (clone Sh-delta) - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004

C:Accession: S02284

R:Baumann, A.; Krah-Jentgens, I.; Mueller, R.; Mueller-Holtkamp, F.; Seidel, R.; Keckem

EMBO J. 6, 3419-3429, 1987

A:Title: Molecular organization of the maternal effect region of the Shaker complex of D

A:Reference number: S02284

A:Accession: S02284

A:Molecule type: DNA

A:Residues: 1-304 <BAU>

A:Cross-references: UNIPROT:P08510; UNIPARC:UPI0000072E0; EMBL:X06184; NID:g8608; PID:g

C:Genetics:

A:Gene: Shaker

A:Cross-references: FlyBase:FBgn0003380

A:Map position: X 16F

A:introns: 16/2; 114/1; 146/2; 211/3; 252/2

C:Superfamily: potassium channel protein drk1

C:Keywords: alternative splicing; transmembrane protein

Query Match 71.7%; Score 33; DB 2; Length 304;
Best Local Similarity 100.0%; Pred. No. 37;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 RLRYFD 8
Db 84 RLRYFD 89

RESULT 15
S54403
1-phosphatidylinositol phosphodiesterase (EC 3.1.4.10) - *Listeria ivanovii*
C:Species: *Listeria ivanovii*
C>Date: 19-Jul-1996 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
C:Accession: S54403; S34726
R:Ramplid, R.; Gross, R.; Sokolovic, Z.; Goebel, W.; Kreft, J.
Mol. Microbiol. 13, 141-151, 1994
A>Title: The virulence regulator protein of *Listeria ivanovii* is highly homologous to P
A:Reference number: S54403; MUID:95075291; PMID:7984088
A:Accession: S54403
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-321 <LIM>
A:Cross-references: UNIPROT:O59488; UNIPARC:UPI00000B32DB; EMBL:X72685; NID:g396074; PID
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1993
C:Superfamily: 1-phosphatidylinositol phosphodiesterase
C:Keywords: phosphoric diester hydrolase

Query Match 1 71.7%; Score 33; DB 2; Length 321;
Best Local Similarity 55.6%; Pred. No. 39;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EVRLRYFDV 9
Db 97 EARIRYIDI 105

RESULT 16
A27159
potassium channel protein A - fruit fly (*Drosophila melanogaster*) (fragment)
C:Species: *Drosophila melanogaster*
C>Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 17-Nov-2000
C:Accession: A27159
R:Kamb, A.; Iversen, L.E.; Tanouye, M.A.
Cell 50, 405-413, 1987
A>Title: Molecular characterization of Shaker, a *Drosophila* gene that encodes a potassium
A:Reference number: A27159; MUID:87273502; PMID:2440582
A:Accession: A27159
A:Molecule type: mRNA
A:Residues: 1-359 <KAM>
A:Cross-references: UNIPARC:UPI000016BB3F; GB:M17155; NID:g903723; PIDN:AAA70217.1; PID:
C:Genetics:
A:Gene: Sh
A:Cross-references: FlyBase:FBgn0003380
C:Superfamily: potassium channel protein drk1

Query Match 71.7%; Score 33; DB 2; Length 359;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RLRYFD 8
Db 161 RLRYFD 166

RESULT 17
T16563
hypothetical protein K05B2.4 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 31-Dec-2004
C:Accession: T16563
R:Chis8908, S.
Submitted to the EMBL Data Library, June 1995
A>Description: The sequence of C. elegans csmid K05B2.
A:Reference number: Z18536

A:Accession: T16563
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-388 <CHI>
A:Cross-references: UNIPROT:Q9GYN3; UNIPARC:UPI00000755BB; EMBL:U29379; NID:g868192; PID
A:Experimental source: strain Bristol M2
C:Genetics:
A:Gene: CESP:K05B2.4
A:Introns: 36/2; 107/2; 163/3; 198/3; 235/3; 285/3; 341/1

Query Match 71.7%; Score 33; DB 2; Length 388;
Best Local Similarity 75.0%; Pred. No. 47;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EVRLRYFD 8
Db 191 EVRLRYFD 198

RESULT 18
T43170
probable triacylglycerol lipase (EC 3.1.1.3) - fission yeast (*Schizosaccharomyces pombe*)
C:Species: *Schizosaccharomyces pombe*
C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C:Accession: T43170
R:Yoshioka, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H.
DNA Res. 4, 363-369, 1997
A>Title: Identification of open reading frames in *Schizosaccharomyces pombe* cDNAs.
A:Reference number: Z17323; MUID:98162722; PMID:9501991
A:Accession: T43170
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-413 <YOS>
A:Cross-references: UNIPROT:P78898; UNIPARC:UPI000016911F; EMBL:D89249; NID:g1749705; PI
A:Experimental source: strain PR745
C:Superfamily: triacylglycerol lipase, lingual
C:Keywords: carboxylic ester hydrolase

Query Match 71.7%; Score 33; DB 2; Length 413;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RLRYFD 8
Db 387 RLRYFD 392

RESULT 19
A43294
isocitrate dehydrogenase (NADP) (EC 1.1.1.42), mitochondrial - pig
C:Species: *Sus scrofa domestica* (domestic pig)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 31-Dec-2004
C:Accession: A43294; A27371; A27372; A39333
R:Haselbeck, R.U.; Colman, R.F.; McAllister-Henn, L.
Biochemistry 31, 6219-6223, 1992
A>Title: Isolation and sequence of a cDNA encoding porcine mitochondrial NADP-specific i
A:Reference number: A43294; MUID:92329444; PMID:1627563
A:Accession: A43294
A:Molecule type: mRNA
A:Residues: 1-421 <HMS>
A:Cross-references: UNIPROT:P33198; UNIPARC:UPI000012D1C5; GB:M86719; NID:g294222; PIDN:
A>Note: sequence extracted from NCBI backbone (NCBI:108410, NCBI:P108411)
R:Enrlich, R.S.; Colman, R.F.
J. Biol. Chem. 262, 12614-12619, 1987
A>Title: Characterization of an active site peptide modified by the substrate analogue 3
A:Accession: A27371
A:Molecule type: protein
A:Residues: 383-386, 'X', 388-395 <EHR>
A:Cross-references: UNIPARC:UPI0000171F5B
R:Bailey, J.M.; Colman, R.F.
J. Biol. Chem. 262, 12620-12626, 1987
A>Title: Isolation of the glutamyl peptide labeled by the nucleotide analogue 2-(4-bromo

e dehydrogenase.
A:Reference number: A27372; MUID:87308293; PMID:2687570
A:Accession: A27372
A:Molecule type: protein
A:Residues: 383-386, 'E', 388-395 <BAI>
A:Cross-references: UNIPARC:UPI000012DB7
A>Note: later work from this lab showed this fragment is not a glutamyl peptide, but a c
nzyme site
R:Smith, G.E.; Colman, R.
J. Biol. Chem. 266, 14918-14925, 1991
A>Title: Cysteine1 peptides of pig heart NADP-dependent isocitrate dehydrogenase that ar
A:Reference number: A39333; MUID:91332002; PMID:1869531
A:Accession: A39333
A:Status: preliminary
A:Molecule type: protein
A:Residues: 82-91,119-124,372-382;201-211;269-278;383-395 <SMV>
A:Cross-references: UNIPARC:UPI0000171F5C; UNIPARC:UPI0000171F5D; UNIPARC:UPI0000171F5E;
C:Superfamily: isocitrate dehydrogenase (NADP)
C:Keywords: homodimer; mitochondrion; NADP; oxidoreductase; tricarboxylic acid cycle

Query Match 71.7%; Score 33; DB 1; Length 421;
Best Local Similarity 55.6%; Pred. No. 51;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVRLRYFDV 9
:|:|:|:|:
Db 45 DVQLKTFDL 53

RESULT 20
S33859
isocitrate dehydrogenase (NADP) (EC 1.1.1.42) precursor, mitochondrial - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 31-Dec-2004
C:Accession: S33859; S31390
R:Hubb, T.L.; Ryu, J.H.; Hubb, J.W.; Sung, H.C.; Oh, I.U.; Song, B.J.; Veech, R.L.
Biochem. J. 292, 705-710, 1993
A>Title: Cloning of a cDNA encoding bovine mitochondrial NADP(+) -specific isocitrate deh
A:Reference number: S33859; MUID:93305052; PMID:8318002
A:Accession: S33859
A:Molecule type: mRNA
A:Residues: 1-452 <HUB>
A:Cross-references: UNIPROT:Q04467; UNIPARC:UPI000012DLC2; EMBL:X69432; NID:9429; PIDN:C
C:Superfamily: isocitrate dehydrogenase (NADP)
C:Keywords: homodimer; mitochondrion; NADP; oxidoreductase

Query Match 71.7%; Score 33; DB 1; Length 452;
Best Local Similarity 55.6%; Pred. No. 55;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVRLRYFDV 9
:|:|:|:|:
Db 76 DVQLKTFDL 84

RESULT 21
C49507
potassium channel Kv1.5, form 3 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 17-Nov-2000
C:Accession: C49507
R:Altali, B.; Lesage, F.; Zilliani, P.; Guillemane, E.; Honore, E.; Waldmann, R.; Hugnot,
J. Biol. Chem. 268, 24283-24289, 1993
A>Title: Multiple mRNA isoforms encoding the mouse cardiac Kv1.5 delayed rectifier K(+)
A:Reference number: A49507; MUID:94043264; PMID:8226976
A:Accession: C49507
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-514 <ATT>
A:Cross-references: UNIPARC:UPI00001779F5; GB:L22218
C:Superfamily: potassium channel protein drki
C:Keywords: alternative splicing

Query Match 71.7%; Score 33; DB 2; Length 514;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RLRYFD 8
|||
Db 143 RLRYFD 148

RESULT 22
A72300
beta-glucuronidase - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: A72300
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Grim, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.W.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C.M.
Nature 399, 323-329, 1999
A>Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A:Reference number: A72200; MUID:99287316; PMID:10360571
A:Accession: A72300
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-563 <ARN>
A:Cross-references: UNIPROT:Q9XOF2; UNIPARC:UPI00000D393B; GB:AE001766; GB:AE000512; NID
C:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM1062
C:Superfamily: beta-glucuronidase

Query Match 71.7%; Score 33; DB 2; Length 563;
Best Local Similarity 55.6%; Pred. No. 70;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EVRLRYFDV 9
:|:|:|:|:
Db 426 DVALKYFDI 434

RESULT 23
H84018
Mg-protoporphyrin IX monomethyl ester oxidative cyclase BH2952 [imported] - Bacillus hal
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: H84018
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A>Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: H84018
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-592 <STO>
A:Cross-references: UNIPROT:Q9K9Q1; UNIPARC:UPI00000C406C; GB:AP001517; GB:BA000004; NID
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH2952

Query Match 71.7%; Score 33; DB 2; Length 592;
Best Local Similarity 66.7%; Pred. No. 73;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EVRLRYFDV 9
||:|:|:|:
Db 198 EVGRYFDL 206

RESULT 24
S66669
potassium channel (Kv1.5) - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004

C;Accession: S66669
R;Saaki, Y.; Ishii, K.; Nunoki, K.; Yamagishi, T.; Taira, N.
FEBS Lett. 372, 20-24, 1995
A;Title: The voltage-dependent K(+) channel (Kv1.5) cloned from rabbit heart and facilit
A;Reference number: S66669; MUID:96032538; PMID:7556635
A;Accession: S66669
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-598 <SAS>
A;Cross-references: UNIPROT:P50638; UNIPARC:UPI00001279AB; EMBL:D45025; NID:g1060972; PI
C;Superfamily: potassium channel protein drkl

Query Match 71.7%; Score 33; DB 2; Length 598;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RLRYPD 8
Db 136 RLRYPD 141

RESULT 25
A49507
potassium channel Kv1.5 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: A49507; B49507
R;Altali, B.; Lesage, F.; Ziliant, P.; Guillemane, E.; Honore, E.; Waldmann, R.; Hugnot,
J. Biol. Chem. 268, 24283-24289, 1993
A;Title: Multiple mRNA isoforms encoding the mouse cardiac Kv1.5 delayed rectifier K(+)
A;Reference number: A49507; MUID:94043264; PMID:8226976
A;Accession: A49507
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-602 <ATT>
A;Cross-references: UNIPROT:O61762; UNIPARC:UPI0000028BE9; GB:L22218; NID:g435603; PIDN:
A;Accession: B49507
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 201-602 <AT2>
A;Cross-references: UNIPARC:UPI000002A65A; GB:L22218
C;Superfamily: potassium channel protein drkl
C;Keywords: alternative splicing

Query Match 71.7%; Score 33; DB 2; Length 602;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RLRYPD 8
Db 143 RLRYPD 148

RESULT 26
S00400
potassium channel protein A (clone Sh-beta) - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 17-Nov-2000
C;Accession: S00400; S01111
R;Pongs, O.; KecsKemethy, N.; Mueller, R.; Krahn-Jentgens, I.; Baumann, A.; Kiltz, H.H.;
EMBO J. 7, 1087-1096, 1988
A;Title: Shaker encodes a family of putative potassium channel proteins in the nervous s
A;Reference number: S00479; MUID:88296413; PMID:2456921
A;Accession: S00480
A;Molecule type: DNA
A;Residues: 1-643 <PON>
A;Cross-references: UNIPARC:UPI000007DC42; EMBL:X07132; NID:98602; PIDN:CAA30144.1; PID:
A;Note: the clone is designated as Sh-beta
R;Schwarz, T.L.; Tempel, B.L.; Papazian, D.M.; Jan, Y.N.; Jan, L.Y.
Nature 331, 137-142, 1988
A;Title: Multiple potassium-channel components are produced by alternative splicing at t
A;Reference number: S00508; MUID:88122563; PMID:2448635
A;Accession: S01111

A;Molecule type: mRNA
A;Residues: 1-643 <SCH>
A;Cross-references: UNIPARC:UPI000007DC42
A;Note: the clone is designated as Sh1
R;Schwarz, T.L.; Tempel, B.L.; Papazian, D.M.; Jan, Y.N.; Jan, L.Y.
Nature 332, 740, 1988
A;Reference number: S01113
A;Contents: annotation; erratum
C;Genetics:
A;Gene: Shaker
A;Cross-references: FlyBase:FBgn0003380
C;Superfamily: potassium channel protein drkl
C;Keywords: alternative splicing; transmembrane protein

Query Match 71.7%; Score 33; DB 2; Length 643;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RLRYPD 8
Db 117 RLRYPD 122

RESULT 27
JH0193
potassium channel shaker form epsilon - fruit fly (Drosophila melanogaster)
N;Alternate names: potassium channel protein A
C;Species: Drosophila melanogaster
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: JH0193; S00508; S01110; S00479; S00482; S02822; S01674
R;Kamb, A.; Tseng-Crank, J.; Tanouye, M.A.
Neuron 1, 421-430, 1988
A;Title: Multiple products of the Drosophila Shaker gene may contribute to potassium cha
A;Reference number: JH0193; MUID:90166523; PMID:3272175
A;Accession: JH0193
A;Molecule type: mRNA
A;Residues: 1-656 <KAM>
A;Cross-references: UNIPROT:P08510; UNIPARC:UPI00001779EC
A;Note: the sequence Tyr-Phe-Ile-Thr, residues 323-326, is present in the putative G pro
R;Schwarz, T.L.; Tempel, B.L.; Papazian, D.M.; Jan, Y.N.; Jan, L.Y.
Nature 331, 137-142, 1988
A;Title: Multiple potassium-channel components are produced by alternative splicing at t
A;Reference number: S00508; MUID:88122563; PMID:2448635
A;Accession: S00508
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-512,514-564,'Q',565-583,'HV',586-656 <SCH>
A;Cross-references: UNIPARC:UPI00001279B3; GB:X06742; NID:g288441; PIDN:CAA29917.1; PID:
A;Accession: S01110
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 'MGM',57,'VNG',61-452,'F',454-462,'VV',465-488,'A',490,'R',492-505,'S',507-
'QL',577-579,'LQ',582-584,'QS',587,'SPHG',592-593,'MT',596-599,'LG',602-604,'LRS',643-647,
R;Pongs, O.; KecsKemethy, N.; Mueller, R.; Krahn-Jentgens, I.; Baumann, A.; Kiltz, H.H.;
EMBO J. 7, 1087-1096, 1988
A;Title: Shaker encodes a family of putative potassium channel proteins in the nervous s
A;Reference number: S00479; MUID:88296413; PMID:2456921
A;Accession: S00479
A;Molecule type: DNA
A;Residues: 1-452,'F',454-462,'V',464-488,'A',490,'R',492-505,'S',507-510,'A',512,514-51
'582-584,'QS',587,'SPHG',592-593,'MT',596-599,'LG',602-604,'LRS',640,'QL',643-647,
A;Cross-references: UNIPARC:UPI00001779EE; EMBL:X07131
A;Accession: S00482
A;Molecule type: DNA
A;Residues: 1-348,'V' <PO2>
A;Cross-references: UNIPARC:UPI000002A660; EMBL:X07134; NID:98606; PIDN:CAA30146.1; PID:
R;Pongs, O.
submitted to the EMBL data library, March 1988
A;Reference number: S02822
A;Accession: S02822
A;Molecule type: mRNA
A;Residues: 1-452,'F',454-462,'VV',465-488,'A',490,'R',492-505,'S',507-510,'A',512,514-5

, 582-584, 'QS', 587, 'SPHG', 592-593, 'MT', 596-599, 'LG', 602-604, 'LRS', 'TNS', 640, 'QU', 643-647
A:Cross-references: UNIPARC:UPI000016BB40; EMBL:X07131; NID:g8600; PID:g8601
R:Tempele, B.L.; Papazian, D.M.; Schwarz, T.L.; Jan, Y.N.; Jan, L.Y.
A:Title: Sequence of a probable potassium channel component encoded at Shaker locus of D
A:Reference number: S01674; MUID:87292096; PMID:2441471
A:Accession: S01674
A:Molecule type: mRNA
A:Residues: 1-452, 'F', 454-462, 'VV', 465-488, 'A', 490, 'R', 492-505, 'S', 507-510, 'A', 512, 514-5
, 582-584, 'QS', 587, 'SPHG', 592-593, 'MT', 596-599, 'LG', 602-604, 'LRS', 'TNS', 640, 'QU', 643-647
A:Cross-references: UNIPARC:UPI000016BB40; EMBL:M17211; NID:g157063; PIDN:AAA28417.1; PI
A:Note: 360-Met and 464-Ile were also found
C:Comment: This protein is a component of a fast, transient, voltage-dependent, or A-type
C:Genetics:
A:Gene: Shaker
A:Cross-references: FlyBase:FBgn0003380
A:Introns: 61/2; 102/3; 159/1; 191/2; 256/3; 297/2; 348/3; 406/1; 449/2; 514/1
C:Superfamily: potassium channel protein drkl
C:Keywords: alternative splicing; glycoprotein; phosphoprotein; potassium channel; trans
F:228-246/Domain: transmembrane #status predicted <TM1>
F:279-300/Domain: transmembrane #status predicted <TM2>
F:311-332/Domain: transmembrane #status predicted <TM3>
F:358-382/Domain: S4-like region #status predicted <S4L>
F:396-417/Domain: transmembrane #status predicted <TM4>
F:433-453/Domain: transmembrane #status predicted <TM5>
F:457-478/Domain: transmembrane #status predicted <TM6>
F:102, 229, 263/Binding site: carboxylate (Asn) (covalent) #status predicted
F:521/Binding site: phosphate (Ser) (covalent) #status predicted
Query Match 71.7%; Score 33; DB 2; Length 656;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 EVRLRYFD 8
Db 129 RLRYFD 134
RESULT 28
T32916
hypotheetical protein K02F2.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T32916
R:Maggi, L.; Goela, D.
submitted to the EMBL Data Library, January 1998
A:Description: The sequence of C. elegans cosmid K02F2.
A:Reference number: 221246
A:Accession: T32916
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1220 <MAG>
A:Cross-references: UNIPROT:Q44985; UNIPARC:UPI000007C3F1; EMBL:AF043699; PIDN:AA897566.
A:Experimental source: strain Bristol N2; clone K02F2
C:Genetics:
A:Gene: CESP:K02F2.3
A:Map position: 1
A:Introns: 29/3; 52/3; 105/3; 191/3; 276/3; 357/2; 411/3; 468/1; 518/3; 570/3; 663/3; 70
Query Match 71.7%; Score 33; DB 2; Length 1220;
Best Local Similarity 62.5%; Pred. No. 1.6e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVRLRYFD 8
Db 325 EMKLYFD 332
RESULT 29
JCS280
voltage-dependent calcium channel alpha 1 chain - Bleeker's squid
C:Species: Loligo bleekeri (Bleeker's squid)
C>Date: 16-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004

C:Accession: JCS280
R:Kimura, T.; Shiono, O.; Hirota, K.; Saito, T.; Matsumoto, G.; Sato, C.
Biochem. Biophys. Res. Commun. 230, 147-154, 1997
A:Title: Molecular cloning and characterization of a putative neural calcium channel alpi
A:Reference number: JCS280; MUID:97148591; PMID:9020033
A:Contents: optic lobe
A:Accession: JCS280
A:Molecule type: mRNA
A:Residues: 1-2206 <KIM>
A:Cross-references: UNIPROT:P91744; UNIPARC:UPI0000178AFA; DBJ:D86600; NID:g1817549; PI
C:Comment: This protein plays roles in the regulation of a variety of cellular functions,
ion and secretion.
C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain
Query Match 71.7%; Score 33; DB 2; Length 2206;
Best Local Similarity 75.0%; Pred. No. 2.9e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 VRLRYFDV 9
Db 902 VMLRYFDL 909
RESULT 30
A82919
integrase-recombinase protein U0222 [imported] - Ureaplasma urealyticum
C:Species: Ureaplasma urealyticum
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C:Accession: A82919
R:Glass, J.I.; Letkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Casseil, G.H.
submitted to GenBank, February 2000
A:Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min
A:Reference number: A82870
A:Accession: A82919
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-250 <GLA>
A:Cross-references: UNIPARC:UPI00000C1BD7; GB:AE02121; GB:AF222894; NID:g6899184; PIDN:
A:Experimental source: serovar 3; biovar 1
C:Genetics:
A:Gene: xetC, U0222
A:Genetic code: SGC3
Query Match 69.6%; Score 32; DB 2; Length 250;
Best Local Similarity 44.4%; Pred. No. 48;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 1 EVRLRYFDV 9
Db 82 QLEMKYFDV 90
RESULT 31
AB0265
Probable regulatory protein YPO2337 [imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C:Accession: AB0265
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tittball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davies, P.; Dougan, G.;
Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett,
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AB0265
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-279 <KUR>
A:Cross-references: UNIPROT:Q8Z547; UNIPARC:UPI00000DC928; GB:AL590842; PIDN:CAC91142.1;
C:Genetics:
A:Gene: YPO2337
Query Match 69.6%; Score 32; DB 2; Length 279;

Best Local Similarity 75.0%; Pred. No. 54;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 EVRLRYFD 8
DB 15 EFNLRYFD 22

RESULT 32

G70696
hypothetical protein RV3787c - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: G70696
R:Coile, S.T.; Broesch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Felwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: G70696
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-308 <COU>
A:Cross-references: UNIPROT:P72053; UNIPARC:UPI00000D120F; GB:Z80343; GB:AL123456; NID:G
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: RV3787c
C:Superfamily: Mycobacterium tuberculosis hypothetical protein RV0731c

Query Match 69.6%; Score 32; DB 2; Length 308;
Best Local Similarity 85.7%; Pred. No. 60;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 VRLRYFD 8
DB 85 VRLRYFD 91

RESULT 33

S57499
isocitrate dehydrogenase (NADP) (EC 1.1.1.42) precursor, mitochondrial - human

C:Species: Homo sapiens (man)
C:Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 31-Dec-2004
C:Accession: S57499

R:Hub, T.L.; Oh, I.U.; Kim, Y.O.; Huh, J.W.; Song, B.J.

A:Submitted to the EMBL Data Library, November 1992

A:Description: Characterization of a cDNA clone for human mitochondrial NADP+-specific I

A:Reference number: S57499

A:Accession: S57499

A:Molecule type: mRNA

A:Residues: 1-452 <HDH>

A:Cross-references: UNIPROT:P48735; UNIPARC:UPI000014B892; EMBL:X69433; NID:9872120; PID

C:Genetics:
A:Gene: GDB:IDH2

A:Cross-references: GDB:119326; OMIM:147650

A:Map position: 15q21-15qter

C:Superfamily: isocitrate dehydrogenase (NADP)

C:Keywords: homodimer; mitochondrion; NADP; oxidoreductase

Query Match 69.6%; Score 32; DB 2; Length 452;
Best Local Similarity 44.4%; Pred. No. 89;
Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVRLRYFDV 9
DB 76 DIQLRYFDL 84

RESULT 34

S76064
hypothetical protein - Synechocystis sp. (strain PCC 6803)

C:Species: Synechocystis sp.

A:Variety: PCC 6803

C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

C:Accession: S76064

R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asanizu, E.; Nakamura, Y.; Miyajima, N.; O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda

DNA Res. 3, 109-136, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis

S.

A:Reference number: S74322; MUID:97061201; PMID:8905231

A:Accession: S76064

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-896 <KAN>

A:Cross-references: UNIPROT:O55544; UNIPARC:UPI00000D35A8; EMBL:D63999; GB:AB001339; NID

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 69.6%; Score 32; DB 2; Length 896;
Best Local Similarity 55.6%; Pred. No. 1.8e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EVRLRYFDV 9
DB 218 EIVLQYFDI 226

RESULT 35
S59990
phycobilisome anchor protein apcE - Synechocystis sp. (strain PCC 6714)

N:Alternate names: core-membrane linker protein

C:Species: Synechocystis sp.

A:Variety: PCC 6714

C:Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004

C:Accession: S59990

R:DiMagno, L.; Haselkorn, R.

Plant Mol. Biol. 21, 835-845, 1993

A:Title: Isolation and characterization of the gene encoding allophycocyanin subunits a

A:Reference number: S33623; MUID:93222481; PMID:8467079

A:Accession: S59990

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-896 <DIM>

A:Cross-references: UNIPROT:Q02907; UNIPARC:UPI0000125C35; EMBL:L02309; NID:9154474; PID

A:Experimental source: PCC 6714

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1992

C:Genetics:
A:Gene: apcE

Query Match 69.6%; Score 32; DB 2; Length 896;
Best Local Similarity 55.6%; Pred. No. 1.8e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EVRLRYFDV 9
DB 218 EIVLQYFDI 226

RESULT 36
H72734
hypothetical protein APE0416 - Aeropyrum pernix (strain K1)

C:Species: Aeropyrum pernix

C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004

C:Accession: H72734

R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Halkawa, Y.; Jin-no, K.; Takah

awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K

DNA Res. 6, 83-101, 1999

A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr

A:Reference number: A72450; MUID:99310339; PMID:10382966

A:Accession: H72734

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1007 <KAW>

A:Cross-references: UNIPROT:Q9YF24; UNIPARC:UPI000005DB29; DDBJ:AP000059; NID:95103911;

A:Experimental source: strain K1

C:Genetics:

A:Gene: APG0416

C:Superfamily: conserved hypothetical protein PH0905

Query Match 69.6%; Score 32; DB 2; Length 1007;

Best Local Similarity 77.8%; Pred. No. 2; 1e+02;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 EVRLRYFDV 9
: : : : :
DB 636 EGRRLRYFV 644

RESULT 37

h90862 hypothetical protein Ecs1872 [imported] - Escherichia coli (strain O157:H7, substrain R1)

C:Species: Escherichia coli

C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004

C:Accession: H90862

R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.

gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc

A:Reference number: A99629; MUID:21156231; PMID:11258796

A:Accession: H90862

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-81 <STO>

A:Cross-references: UNIPROT:Q8X7F7, UNIPROT:Q8FH57, UNIPARC:UPI00000D0A6D; GB:BA000007;

A:Experimental source: strain O157:H7, substrain R1MD 0509952

C:Genetics:

A:Gene: Ecs1872

Query Match 67.4%; Score 31; DB 2; Length 81;

Best Local Similarity 44.4%; Pred. No. 24;

Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 EVRLRYFDV 9
: : : : :
DB 4 DIPKTFDI 12

RESULT 38

A85756 hypothetical protein ymjA [imported] - Escherichia coli (strain O157:H7, substrain EDL93

C:Species: Escherichia coli

C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004

C:Accession: A85756

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glaeser, J.D.; Rose, D.J.; Mayhew

iller, L.; Grobeck, E.J.; Davis, N.W.; Llm, A.; Dimalanta, E.; Potamousis, K.; Apodaca,

Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: A85756

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-81 <STO>

A:Cross-references: UNIPROT:Q8X7F7, UNIPROT:Q8FH57, UNIPARC:UPI00000D0A6D; GB:AE005174;

A:Experimental source: strain O157:H7, substrain EDL933

C:Genetics:

A:Gene: ymjA

Query Match 67.4%; Score 31; DB 2; Length 81;

Best Local Similarity 44.4%; Pred. No. 24;

Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 EVRLRYFDV 9
: : : : :
DB 4 DIPKTFDI 12

RESULT 39

B64878 ymjA protein - Escherichia coli (strain K-12)

C:Species: Escherichia coli

C>Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004

C:Accession: B64878

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co

-A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A:Title: The complete genome sequence of Escherichia coli K-12.

A:Reference number: A64720; MUID:97426617; PMID:9278503

A:Accession: B64878

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-81 <BLAT>

A:Cross-references: UNIPROT:P76036; UNIPARC:UPI000013B9E2; GB:AE000227; GB:U00096; NID:97

A:Experimental source: strain K-12, substrain MG1655

C:Genetics:

A:Gene: ymjA

Query Match 67.4%; Score 31; DB 2; Length 81;

Best Local Similarity 44.4%; Pred. No. 24;

Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 EVRLRYFDV 9
: : : : :
DB 4 DIPKTFDI 12

RESULT 40

G84230 hypothetical protein Vng0733h [imported] - Halobacterium sp. NRC-1

C:Species: Halobacterium sp. NRC-1

C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C:Accession: G84230

R:Ng, W.V.; Kennedy, S.P.; Mahiras, G.G.; Bergquist, B.; Pan, M.; Shukla, H.D.; Lasky, S

; Leithausner, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablor

Jung, K.H.; Alam, M.; Freitas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; Li

A:Title: Genome sequence of Halobacterium species NRC-1.

A:Reference number: A84160; MUID:20504483; PMID:11016950

A:Accession: G84230

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-189 <STO>

A:Cross-references: UNIPROT:Q9HRE7, UNIPARC:UPI00000636F7; GB:AE004437; NID:g10580311; P1

C:Genetics:

A:Gene: VNG0733H

Query Match 67.4%; Score 31; DB 2; Length 189;

Best Local Similarity 83.3%; Pred. No. 58;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 4 LRYFDV 9
: : : : :
DB 49 LRYFDI 54

RESULT 41

AG2665 hypothetical protein Atu0725 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)

C:Species: Agrobacterium tumefaciens

C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004

C:Accession: AG2665

R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monke, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L

erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kuttyavin, T.; Levy, R.; Li, M.; McClellan

; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, F

ster, E.W.

A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A:Reference number: AB2577; MUID:21608550; PMID:11743193

A:Accession: AG2665

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-202 <KUR>
A:Cross-references: UNIPROT:08UHF7; UNIPARC:UPI00000D1B81; GB:AE008668; PIDN:AAL41741.1;
A:Experimental source: strain C58 (Dupont)
A:Genetics:
A:Gene: AtU0725
A:Map position: circular chromosome

Query Match 67.4%; Score 31; DB 2; Length 202;
Best Local Similarity 83.3%; Pred. No. 63;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 RLRYFD 8
|:|:|
Db 6 RLRYFD 11

RESULT 42
F97447
hypothetical protein AGR_C_1317 [imported] - Agrobacterium tumefaciens (strain C58, Cere
C:Species: Agrobacterium tumefaciens
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C:Accession: F97447
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughy, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A57359; MUID:21608551; PMID:11743194
A:Accession: F97447
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-202 <KUR>
A:Cross-references: UNIPROT:08UHF7; UNIPARC:UPI00000D1B81; GB:AE007869; PIDN:AAK86535.1;
A:Genetics:
A:Gene: AGR_C_1317
A:Map position: circular chromosome

Query Match 67.4%; Score 31; DB 2; Length 202;
Best Local Similarity 83.3%; Pred. No. 63;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 RLRYFD 8
|:|:|
Db 6 RLRYFD 11

RESULT 43
H96971
N-terminal CheY reciever domain fused to C-terminal uncharacterized CheX-like domain [im
C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C:Accession: H96971
R:Noelling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J.; Daily, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl
A:Reference number: A86900; MUID:21359325; PMID:21359325
A:Accession: H96971
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-291 <KUR>
A:Cross-references: UNIPROT:097LH6; UNIPARC:UPI00000C9EFL; GB:AE001437; PIDN:AAK78563.1;
A:Experimental source: Clostridium acetobutylicum ATCC874
A:Genetics:
A:Gene: CAC0585

Query Match 67.4%; Score 31; DB 2; Length 291;
Best Local Similarity 55.6%; Pred. No. 91;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EVRLRYFDV 9
|:|:|:|:|

Db 128 ELKDRYFDI 136

RESULT 44
AF0671
conserved hypothetical protein STY1484 [imported] - Salmonella enterica subsp. enterica
C:Species: Salmonella enterica subsp. enterica serovar Typh
A:Note: this species has also been called Salmonella typh
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AF0671
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AF0671
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-297 <PAR>
A:Cross-references: UNIPARC:UPI0000059EC1; GB:AL513382; PIDN:CAD01743.1; PID:gl6502593;
A:Genetics:
A:Gene: STY1484

Query Match 67.4%; Score 31; DB 2; Length 297;
Best Local Similarity 71.4%; Pred. No. 93;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVRLRYF 7
|:|:|
Db 57 DVRLRYF 63

RESULT 45
C64899
ydda protein - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C:Accession: C64899; S11432
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: C64899
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-297 <BLAT>
A:Cross-references: UNIPROT:P37757; UNIPARC:UPI000013A939; GB:AE00243; GB:U00096; MID:G
A:Experimental source: strain K-12, substrain MG1655
R:Blasco, F.; Iobbi, C.; Ratouchniak, J.; Bonnetoy, V.; Chipaux, M.
Mol. Gen. Genet. 222, 104-111, 1990
A:Title: Nitrate reductases of Escherichia coli: sequence of the second nitrate reductas
A:Reference number: S11427; MUID:91042410; PMID:2233673
A:Accession: S11432
A:Molecule type: DNA
A:Residues: 1-34 <BLA>
A:Cross-references: UNIPARC:UPI000017971C; EMBL:X17110
A:Genetics:
A:Gene: ydda

Query Match 67.4%; Score 31; DB 2; Length 297;
Best Local Similarity 71.4%; Pred. No. 93;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVRLRYF 7
|:|:|
Db 57 DVRLRYF 63

RESULT 46
C90887

hypothetical protein ECs2067 [imported] - Escherichia coli (strain O157:H7, substrain R1
 C:Species: Escherichia coli
 C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
 C:Accession: C90887
 R:Hayashi, T.; Makino, K.; Okunishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
 Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
 DNA Res. 8, 11-22, 2001
 A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
 A:Reference number: A59629; MUID:21156231; PMID:11258796
 A:Accession: C90887
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-297 <HAY>
 A:Cross-references: UNIPROT:P58292; UNIPARC:UPI000013A938; GB:BA000007; PIDN:BA035490.1;
 A:Experimental source: strain O157:H7, substrain R1MD 050952
 C:Genetics:
 A:Gene: ECs2067

Query Match 67.4%; Score 31; DB 2; Length 297;
 Best Local Similarity 71.4%; Pred. No. 93;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVRLRYF 7
 :|||
 Db 57 DVRLRYF 63

RESULT 47

hypothetical protein yddE [imported] - Escherichia coli (strain O157:H7, substrain EDL93
 C:Species: Escherichia coli
 C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
 C:Accession: F85730
 R:Perma, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
 Miller, L.; Grobeck, E.J.; Davis, N.W.; Lam, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
 Nature 409, 529-533, 2001
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A:Reference number: A85480; MUID:21074935; PMID:11206551
 A:Accession: F85730
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-297 <STO>
 A:Cross-references: UNIPROT:P58292; UNIPARC:UPI000013A938; GB:AE005174; NID:G12515224; H
 A:Experimental source: strain O157:H7, substrain EDL933
 C:Genetics:
 A:Gene: yddE

Query Match 67.4%; Score 31; DB 2; Length 297;
 Best Local Similarity 71.4%; Pred. No. 93;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVRLRYF 7
 :|||
 Db 57 DVRLRYF 63

RESULT 48

embryogenesis protein H beta 58 homolog - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 31-Mar-1993 #sequence_revision 16-Apr-1999 #text_change 09-Jul-2004
 C:Accession: B44882
 R:Lee, J.J.; Radice, G.; Perkins, C.P.; Costantini, F.
 Development 115, 277-288, 1992
 A:Title: Identification and characterization of a novel, evolutionarily conserved gene d
 A:Reference number: A44882; MUID:92347186; PMID:1638986
 A:Accession: B44882
 A:Status: nucleic acid sequence not shown; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-326 <LEB>
 A:Cross-references: UNIPROT:P40336; UNIPARC:UPI000017C004
 A:Note: this sequence comes from Fig. 9; the sequences are incorrectly identified in the
 C:Comment: The sequence corresponding to Entrez entry AAB22719, PID:G252484, is from mou

Query Match 67.4%; Score 31; DB 2; Length 326;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VRLRYF 7
 :|||
 Db 125 VRLRYF 130

RESULT 49

embryogenesis protein H beta 58 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 C:Accession: A44882
 R:Lee, J.J.; Radice, G.; Perkins, C.P.; Costantini, F.
 Development 115, 277-288, 1992
 A:Title: Identification and characterization of a novel, evolutionarily conserved gene d
 A:Reference number: A44882; MUID:92347186; PMID:1638986
 A:Accession: A44882
 A:Molecule type: mRNA
 A:Residues: 1-327 <LEB>
 A:Cross-references: UNIPROT:P40336; UNIPARC:UPI00000271B5; GB:S41204; NID:G252482; PIDN:
 A:Experimental source: embryo
 A:Note: sequence extracted from NCBI backbone (NCBIN:109839, NCBI:P109840)
 A:Note: sequence extracted from NCBI backbone (NCBI:P109890); the sequences are incorrec
 C:Comment: The sequence corresponding to PID:G252484 is from mouse, not chicken as indic

Query Match 67.4%; Score 31; DB 2; Length 327;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VRLRYF 7
 :|||
 Db 126 VRLRYF 131

RESULT 50

ADPglyceromanno-heptose 6-epimerase (EC 5.1.3.20) HP0859 [similarity] - Helicobacter pylori
 C:Species: Helicobacter pylori
 C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
 C:Accession: C64627
 R:Tomb, J.F.; White, O.; Kellaway, A.R.; Clayton, R.A.; Sutton, R.G.; Fleischmann, R.D.
 Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney,
 son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.W.; Fujii, C.; Bowman, C.; Watthey, L.
 Nature 388, 539-547, 1997
 A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
 A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
 A:Reference number: A64520; MUID:97394467; PMID:9252185
 A:Accession: C64627
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-330 <TOM>
 A:Cross-references: UNIPROT:O25530; UNIPARC:UPI000003D303; GB:AE000596; GB:AE000511; NID
 C:Superfamily: ADPglyceromanno-heptose 6-epimerase; UDPglucose 4-epimerase homology
 C:Keywords: isomerase

Query Match 67.4%; Score 31; DB 2; Length 330;
 Best Local Similarity 66.7%; Pred. No. 1e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EVRLRYF 9
 :|||
 Db 181 QVRLRYF 189

Search completed: May 4, 2006, 13:08:29
 Job time : 39.8571 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 4, 2006, 12:46:39 ; Search time 84.2857 Seconds

(without alignments)
75.336 Million cell updates/sec

Title: US-10-700-632-3

Perfect score: 46

Sequence: 1 EVRLRYFDV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 1000 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	82.6	596	2 Q8BXJ0	mus muscu
2	38	82.6	1122	2 Q6ZQLO	mouse
3	38	82.6	1171	2 Q4T237	terradon n
4	38	82.6	1217	1 Sp3B3	HUMAN
5	38	82.6	1217	2 Q6NT18	HUMAN
6	38	82.6	1217	2 Q5R815	PONPY
7	38	82.6	1217	2 Q921M3	MOUSE
8	37	80.4	470	2 Q8YZM1	ANASP
9	37	80.4	598	2 Q4SAX2	TING
10	37	80.4	809	1 P1DA1	VIGIN
11	37	80.4	949	2 Q5LDN2	BACFN
12	37	80.4	949	2 Q64UQ7	BACFR
13	36	78.3	331	2 Q5JYD5	PYRKO
14	36	78.3	440	2 Q5LJY0	DROME
15	36	78.3	441	2 Q7P1M4	DROME
16	36	78.3	722	2 Q9U0H5	PIAF7
17	36	78.3	1206	1 R5E1	SCHPO
18	36	78.3	1217	2 Q802W7	BRARE
19	35	76.1	79	1 DARC	CHRYO
20	35	76.1	228	2 Q26063	HELPL
21	35	76.1	242	2 Q77SA9	9NUCL
22	35	76.1	332	2 Q74856	SCHPO
23	35	76.1	338	2 Q44528	CABEL
24	35	76.1	446	2 Q5E419	VIBF1
25	35	76.1	496	2 Q8SWF5	ENCUC
26	35	76.1	910	2 Q9AMB3	ORYSA
27	35	76.1	1010	2 Q4P102	USTMA
28	35	76.1	1217	2 Q70722	ANOGA
29	35	76.1	1227	2 Q5B186	DROME
30	35	76.1	1227	2 Q9W0W7	DROME
31	34	73.9	149	2 Q6FST1	CANGA

32	34	73.9	149	2 Q412K0	GIBBE
33	34	73.9	149	2 Q4WCUI	ASPFU
34	34	73.9	150	2 Q51MH3	MAGGR
35	34	73.9	151	2 Q7SDM1	NEURC
36	34	73.9	154	2 Q74257	ASHGO
37	34	73.9	168	2 Q4P877	USTMA
38	34	73.9	181	1 MATMC	SCHPO
39	34	73.9	181	1 MATMC	SCHPO
40	34	73.9	272	2 Q7ME27	VIBVY
41	34	73.9	273	2 Q72BA3	DESH
42	34	73.9	313	2 Q4Z1T8	PESEY
43	34	73.9	349	2 Q41AV3	GIBBE
44	34	73.9	356	2 Q87UJ7	PESEM
45	34	73.9	412	2 P96988	RHOMR
46	34	73.9	414	2 Q88EC2	PEEPK
47	34	73.9	418	1 RFL	HAIMA
48	34	73.9	433	2 Q7AAU7	ECOS7
49	34	73.9	433	2 Q8XEH7	ECOS7
50	34	73.9	516	2 Q71199	CHICK
51	34	73.9	605	2 Q61NM3	XENLA
52	34	73.9	619	2 Q01610	CABEL
53	34	73.9	620	2 Q5DGB1	SCHTA
54	34	73.9	678	2 Q9AMB8	LYCES
55	34	73.9	743	2 Q5LDW6	BACFN
56	34	73.9	743	2 Q64V08	BACFR
57	34	73.9	806	2 Q9AMB9	LYCES
58	34	73.9	807	2 Q9FR61	LYCES
59	34	73.9	807	2 Q9FXF8	CRAPL
60	34	73.9	808	2 Q70EW5	CYNCA
61	34	73.9	812	1 P1DA1	MA12B
62	34	73.9	812	1 P1DA1	ORYSA
63	34	73.9	813	2 Q8VME5	PAP90
64	34	73.9	817	2 Q8MB12	PAP90
65	34	73.9	867	2 Q81B47	PIAF7
66	34	73.9	920	2 Q50U74	ENTH1
67	34	73.9	997	2 Q7W1N6	RHOMR
68	34	73.9	1124	2 Q7NLY7	GLOVY
69	34	73.9	1234	2 Q6XYX3	ORYSA
70	34	73.9	1316	2 Q7MR17	WOLNLA
71	34	73.9	1308	2 Q5DKN7	GENTR
72	34	73.9	1323	2 Q5K5U8	ECOLI
73	34	73.9	1323	2 Q8L119	ECOLI
74	34	73.9	1323	2 Q8VNR6	ECOLI
75	34	73.9	1323	2 Q8VQR2	ECOLI
76	34	73.9	1323	2 Q9RM48	ECOLI
77	34	73.9	1323	2 Q9RPH1	ECOLI
78	34	73.9	3223	2 Q5MBA6	ECOLI
79	33	71.7	81	2 Q6D6U9	ERWGT
80	33	71.7	90	2 Q73J24	TREDE
81	33	71.7	98	2 Q8ZV27	PYRAR
82	33	71.7	132	1 R58	CAUCR
83	33	71.7	132	1 R58	RH10
84	33	71.7	132	1 R58	RHOP
85	33	71.7	132	1 Q51W66	PROWI
86	33	71.7	154	2 Q41H6	GIBBE
87	33	71.7	157	2 Q51H6	GIBBE
88	33	71.7	159	2 Q870Y0	VIBPA
89	33	71.7	171	2 Q7NSA5	CHRYO
90	33	71.7	183	2 Q51AF7	ENTH1
91	33	71.7	183	2 Q5NT35	ENTH1
92	33	71.7	189	2 Q74J19	LACJO
93	33	71.7	226	2 Q6AIR8	DESPS
94	33	71.7	231	2 Q745J1	MYCPA
95	33	71.7	299	2 Q8TMA3	METAC
96	33	71.7	318	2 Q5TUJ4	ANODA
97	33	71.7	321	2 Q59488	LISIV
98	33	71.7	328	2 Q8END1	OCEIH
99	33	71.7	331	2 Q8MSZ1	DROME
100	33	71.7	331	2 Q81P96	DROME
101	33	71.7	345	2 Q9VKB3	DROME
102	33	71.7	345	2 Q9U6H7	DROME
103	33	71.7	349	2 Q7KUW5	DROME
104	33	71.7	351	2 Q4Q084	LEIMA

Q412K0	Gibberella
Q4WCUI	Aspergillus
Q51MH3	Magnaporthe
Q7SDM1	Neurospora
Q74257	Aschysa goss
Q4P877	Ustilago ma
Q6WXR6	Schizosacch
P10840	Schizosacch
Q7ME27	Vibrio vuln
Q72BA3	Desulfovibr
Q4Z1T8	Pseudomonas
Q41AV3	Gibberella
Q87UJ7	Pseudomonas
P96988	Rhodocetmus
Q88EC2	Pseudomonas
Q5UXJ3	Halococcus
Q7AAU7	Escherichia
Q8XEH7	Escherichia
Q71199	Gallus gall
Q61NM3	Xenopus lae
Q01610	Caenorhabdi
Q5DGB1	Schistosoma
Q9AMB8	Lycopersico
Q5LDW6	Bacteroides
Q64V08	Bacteroides
Q9AMB9	Lycopersico
Q9FR61	Lycopersico
Q9FXF8	Craterosfig
Q70EW5	Cynara card
Q43270	Zea mays (m
Q43007	Oryza sativ
Q8W69	Papaver som
Q8W1B2	Papaver som
Q81B47	Plasmodium
Q50U74	Entamoeba h
Q7W1N6	Rhodocetmus
Q7NLY7	Gloeobacter
Q6XYX3	Oryza sativ
Q7MR17	Wolfinella s
Q5DKN7	Citrobacter
Q5K5U8	Escherichia
Q8L119	Escherichia
Q8VNR6	Escherichia
Q8VQR2	Escherichia
Q9RM48	Escherichia
Q9RPH1	Escherichia
Q5MBA6	Escherichia
Q6D6U9	Erywinia car
Q73J24	Trepionema d
Q8ZV27	Bradrythob
Q9ABT9	Caulobacter
Q9AN43	Rhizobium l
Q6N4U7	Rhodospirillum
Q51W66	Proteobacteria
Q41H6	Gibberella
Q51H6	Gibberella
Q870Y0	Vibrio para
Q7NSA5	Chromobacter
Q51AF7	Enterobacter
Q5NT35	Enterobacter
Q74J19	Lactobacillus
Q6AIR8	Deinococcus
Q745J1	Mycobacteri
Q8TMA3	Methanobacter
Q5TUJ4	Anoda
Q59488	Listeria iv
Q8END1	Oceanobacill
Q8MSZ1	Drosophila
Q81P96	Drosophila
Q9VKB3	Drosophila
Q9U6H7	Drosophila
Q7KUW5	Drosophila
Q4Q084	Leishmania

105	33	71.7	380	2	050UV5_ENTHI	050uv5 entamoeba h	178	32	69.6	241	2	09P3F2_NEUCR	09P3f2 neurospora
106	33	71.7	415	2	09GYN3_CABEL	09gyn3 caenorhabdi	179	32	69.6	250	1	XERC_UREPA	09pgs0 ueaplasma
107	33	71.7	419	2	013584_HUMAN	013584 homo sapien	180	32	69.6	251	1	089RC7_BRAIA	089rc7 bradyrhizob
108	33	71.7	421	1	IDHP_PIG	P33198 sus scrofa	181	32	69.6	279	2	066A76_YERBS	066a76 yerbes
109	33	71.7	439	2	04UCR7_THEPA	04ucr7 theileria a	182	32	69.6	279	2	082B47_YERBS	082b47 yerbes
110	33	71.7	449	2	04N0H5_THEPA	04n0h5 theileria p	183	32	69.6	281	2	053WG5_THET8	053wg5 thesina pe
111	33	71.7	452	1	IDHP_BOVIN	004467 bos taurus	184	32	69.6	289	2	05UF05_9PROT	05uf05 uncultured
112	33	71.7	452	2	09EOK1_MOUSE	09eok1 mus musculu	185	32	69.6	295	2	08F14_XYLFt	08f14 xyella fas
113	33	71.7	452	2	08C2R9_MOUSE	08c2r9 m mus muscu	186	32	69.6	296	2	075AL7_ASHGO	075al7 ashya goes
114	33	71.7	452	2	06DGF1_RAT	06dgf1 rattus norv	187	32	69.6	305	2	08TMB9_METAC	08tmb9 methanobarc
115	33	71.7	452	2	05ZL82_CHICK	05z182 gallus gall	188	32	69.6	308	2	07TVN7_MYCBO	07tvn7 mycobacteri
116	33	71.7	465	2	07OF14_ANOGA	07of14 anopheles g	189	32	69.6	308	2	P72053_MYCTU	P72053 mycobacteri
117	33	71.7	471	2	07OLH1_ANOGA	07qlh1 anopheles g	190	32	69.6	313	2	091AR4_ALCEU	091ar4 alcalligenes
118	33	71.7	493	2	07ODZ0_ANOGA	07odzo anopheles g	191	32	69.6	318	2	0890Y9_CLOTE	0890y9 clostridium
119	33	71.7	513	2	055TMB_CRYNE	055tmb anopheles g	192	32	69.6	320	2	07W6Z2_BORPA	07w6z2 bordetella
120	33	71.7	513	2	05KIQ7_CRYNE	05k1q7 cryptococcu	193	32	69.6	325	2	08MVN9_PASCI	08mvn9 bolteria vi
121	33	71.7	523	1	IDHP_MOUSE	P54071 mus musculu	194	32	69.6	328	2	04MSN7_BACCE	04msn7 bacillus ce
122	33	71.7	563	2	09XOF2_THEMEA	09xof2 thermotoga	195	32	69.6	343	2	06UDG0_MANSM	06udg0 manheimia
123	33	71.7	592	2	09K8Q1_BACHD	09k8q1 bacillus ha	196	32	69.6	347	2	084EN6_9BURK	084en6 cupriavidus
124	33	71.7	593	2	028248_CANFA	028248 canis famli	197	32	69.6	356	2	04J9P4_SULAC	04j9p4 sulfolobus
125	33	71.7	598	1	KCNAS_FABIT	P50638 cryptoclaugs	198	32	69.6	366	2	04JYK3_STRPN	04jyk3 streptococc
126	33	71.7	598	2	05G6G4_BOVIN	05g6g4 bos taurus	199	32	69.6	367	2	083J00_ENTPA	083j00 enterococcu
127	33	71.7	600	2	05USC2_PIG	05usc2 sus scrofa	200	32	69.6	398	2	061VN7_9GAMM	061vn7 uncultured
128	33	71.7	601	2	0866G0_CANFA	0866g0 canis famli	201	32	69.6	398	2	06Q959_9GAMM	06q959 uncultured
129	33	71.7	601	1	KCNAS_MUSBP	P79197 mustela put	202	32	69.6	398	2	09F7P9_PEB01	09f7p9 gamma-prote
130	33	71.7	602	2	KCNAS_MOUSE	061762 mus musculu	203	32	69.6	399	2	071G33_LILLO	071g33 lillium long
131	33	71.7	602	2	09Z1R6_MOUSE	09z1r6 mus musculu	204	32	69.6	415	2	04RES7_TETNG	04res7 tetradon n
132	33	71.7	613	2	04VAVJ_HUMAN	04vavj homo sapien	205	32	69.6	419	2	08RR24_STRVC	08rr24 streptomyc
133	33	71.7	616	2	09G8H2_9METZ	09g8h2 sycon rapia	206	32	69.6	428	2	081OW3_PLAF7	081ow3 plasmodium
134	33	71.7	616	2	09VXU0_DROME	09vxu0 dirosophila	207	32	69.6	438	2	04SAH0_TETNG	04sah0 tetradon n
135	33	71.7	620	2	07OXQ0_GIALA	07oxq0 giardia lam	208	32	69.6	452	1	IDHP_HUMAN	08sano tetradon n
136	33	71.7	633	2	09CNC49_PASMU	09cnc49 pasteurella	209	32	69.6	452	2	053GL5_HUMAN	P48735 homo sapien
137	33	71.7	641	2	07KM17_DROME	07km17 dirosophila	210	32	69.6	452	2	04RS02_MACFA	05915 homo sapien
138	33	71.7	652	2	06C9T1_YAXLI	06c9t1 yarrowia li	211	32	69.6	454	2	07SYW4_XENLA	04502 macaca fasc
139	33	71.7	656	1	KCNAS_DROME	P08810 dirosophila	212	32	69.6	455	2	06GLF0_XENTR	07syw4 xenopus lae
140	33	71.7	683	2	04IL13_GIBZE	04il13 gibberella	213	32	69.6	457	2	07W42_BORER	O6g1fo xenopus tro
141	33	71.7	683	2	09Y0Z6_DROME	09y0z6 dirosophila	214	32	69.6	482	2	07QPX3_GIALA	07wj42 bordetella
142	33	71.7	787	1	R1R1_BHVIC	P50646 bovine hezp	215	32	69.6	494	2	082GQ2_STRAM	082gq2 streptomyc
143	33	71.7	800	2	06XZ51_9ALPH	06xz51 bovine hezp	216	32	69.6	504	2	04IKZ7_GIBZE	04ikz7 gibberella
144	33	71.7	808	1	PLDAl_PIMBR	05bub8 aspergillus	217	32	69.6	515	2	04RNM4_TETNG	04rnm4 tetradon n
145	33	71.7	818	2	05BBU8_EMENTI	05bub8 aspergillus	218	32	69.6	553	2	08ZXT1_PYRAF	08zxt1 pyrobaculum
146	33	71.7	824	2	065XR9_ORYSA	065xtr9 oryza sativ	219	32	69.6	566	2	074BC4_GEOSL	074bc4 geobacter s
147	33	71.7	858	2	06FN07_CANGA	06fn07 candida gla	220	32	69.6	590	2	05L1P3_GEOKA	05l1f3 geobacillus
148	33	71.7	901	2	08PEV9_XANCA	08pev9 xanthomonas	221	32	69.6	610	2	05WUK5_LEGPA	05wuk5 legionella
149	33	71.7	925	2	055X41_CRYNE	055x41 cryptococcu	222	32	69.6	612	2	05X346_LEGPA	05x346 legionella
150	33	71.7	925	2	05KMU1_CRYNE	05kmu1 cryptococcu	223	32	69.6	612	2	05ZTC5_LEGPH	05ztc5 legionella
151	33	71.7	1001	2	05TR64_ANOGA	05ctr64 anopheles g	224	32	69.6	633	2	04K5A5_PSEPF	04k5a5 pseudomonas
152	33	71.7	1117	2	08UVU2_9VIRU	08jvc2 penicillium	225	32	69.6	664	2	09R0U8_TREDE	09r0u8 treponema d
153	33	71.7	1218	2	061CUC_CABER	06lcus caenorhabdi	226	32	69.6	682	2	073PF7_TREDE	073pf7 treponema d
154	33	71.7	1220	2	044985_CABEL	044985 caenorhabdi	227	32	69.6	776	2	06BXF0_DEBHA	06bxf0 debaryomyce
155	33	71.7	1262	2	0939Z3_ACTIM	0939z3 acinetobact	228	32	69.6	826	2	06MEVA_PARUN	06meva paracalamyd
156	33	71.7	1505	2	070623_ANOGA	07qg23 anopheles g	229	32	69.6	832	2	04TLD9_9EPHN	04tld9 erythrobact
157	33	71.7	1518	2	096316_SCHWA	096316 schistosoma	230	32	69.6	842	2	0572G5_PHYIN	0572g5 phythothor
158	33	71.7	1609	2	0869H1_LYNST	0869h1 lymphaea sta	231	32	69.6	896	1	APCE_SYNY4	002907 phynechoyst
159	33	71.7	2141	2	08659H2_LYNST	08659h2 lymphaea sta	232	32	69.6	896	2	055544_SYNY3	055544 synechoyst
160	33	71.7	2196	2	P91744_LOJBL	P91744 loliyoa blee	233	32	69.6	914	2	04Y4N3_PLACH	04y4n3 plasmodium
161	33	71.7	2203	2	096318_SCHWA	096318 schistosoma	234	32	69.6	1007	2	09YF24_AERPE	09yf24 aeropyrum p
162	32	70.7	401	2	04YO16_PLACH	04yo16 plasmodium	235	32	69.6	1042	2	0746B7_THET2	0746b7 thermus the
163	32	70.7	430	2	04XZB6_PLACH	04xzbe plasmodium	236	32	69.6	1060	2	07RJ92_PLAYO	07rj92 plasmodium
164	32	69.6	61	2	09G019_9CAUD	09g019 bacterioph	237	32	69.6	1210	2	07SE24_NEUCR	07se24 neurospora
165	32	69.6	111	2	08CE31_MOUSE	08ce31 mus musculu	238	32	69.6	1279	2	069AB7_HELAN	069ab7 helianthusa
166	32	69.6	142	2	08ABU5_BACTN	08abj5 bacteroides	239	32	69.6	1340	2	04UAB5_THEAN	04uab5 theileria a
167	32	69.6	144	2	05ASMB_EMENTI	05asm8 aspergillus	240	32	69.6	1513	2	061567_HOMAN	061567 homarus ame
168	32	69.6	147	2	05YZX6_NOCFA	05yzx6 nocardia fa	241	32	69.6	1515	2	07P6J5_ANOGA	07p6j5 anopheles g
169	32	69.6	150	2	06CDH2_YAXLI	06cdh2 yarrowia li	242	32	69.6	2262	2	04RPA6_TETNG	04rpa6 tetradon n
170	32	69.6	151	2	063UV3_BURPS	063uv3 burkholderi	243	31	67.4	81	1	YMDA_ECOLI	P70306 escherichia
171	32	69.6	151	2	062AS9_BURMA	062as9 burkholderi	244	31	67.4	81	2	08FHS7_ECOLI	08fhs7 escherichia
172	32	69.6	161	2	088469_BURMA	088469 zea mays (m	245	31	67.4	81	2	08X7F7_ECOL7	08x7f7 escherichia
173	32	69.6	163	2	071SA6_LILLO	071sae lillium long	246	31	67.4	111	2	091539_XENLA	091539 xenopus lae
174	32	69.6	191	2	0419S6_GIBZE	0419s6 gibberella	247	31	67.4	111	2	091600_XENLA	091600 xenopus lae
175	32	69.6	192	2	0526S5_MAGGR	0526s5 magnaporthe	248	31	67.4	119	2	08SCN7_9CAUD	08scn7 pseudomonas
176	32	69.6	203	2	05K4L8_CRAGI	05k4l8 crassostrea	249	31	67.4	136	2	05JUNG_PYRKO	05jng6 pyrococcus
177	32	69.6	234	2	05WHY4_BACSK	05why4 bacillus cl	250	31	67.4	140	2	088ML7_PSEPK	088ml7 pseudomonas

251	31	67.4	151	2	Q6BPM8	DEBHA	Q6Bpm8	debaromyce	324	31	67.4	345	2	Q95565	RAT	Q95565	rattus norv
252	31	67.4	151	2	Q5E127	GECJA	Q5e127	gecko japon	325	31	67.4	345	2	Q9QYQ1	RAT	Q9QYQ1	rattus norv
253	31	67.4	153	2	Q83B47	COXBU	Q83b47	coxiella bu	326	31	67.4	345	2	Q9TP50	RAT	Q9TP50	rattus norv
254	31	67.4	154	2	Q8XKC9	CLOPE	Q8xkc9	clostridium	327	31	67.4	345	2	Q6JMOS	ANAPL	Q6JMOS	anas platyr
255	31	67.4	159	2	Q9EPB0	RAT	Q9epb0	rattus norv	328	31	67.4	346	2	Q31204	MOUSE	Q31204	mus musculu
256	31	67.4	167	2	Q4NKC0	9M1CC	Q4nkc0	arthrobacte	329	31	67.4	349	2	Q6BSL7	DEBHA	Q6BSL7	debaromyce
257	31	67.4	189	2	Q9HRE7	HALSA	Q9hre7	halobacteri	330	31	67.4	349	2	Q23920	DICDI	Q23920	dictyosteli
258	31	67.4	195	2	Q9L265	STRCO	Q9l265	streptomyce	331	31	67.4	349	2	Q5SCA0	DICDI	Q5SCA0	dictyosteli
259	31	67.4	195	2	Q71A87	9N1CL	Q71a87	namestra co	332	31	67.4	356	2	Q6CS81	KULIA	Q6CS81	kluveromyc
260	31	67.4	195	2	Q8J30	NAMESTRA	Q8j30	namestra co	333	31	67.4	356	2	Q86XG6	HUMAN	Q86XG6	homo sapien
261	31	67.4	195	2	Q8Q1A9	NEPMC	Q8q1a9	manestra co	334	31	67.4	358	2	Q6UPV1	DROMO	Q6UPV1	drosophila
262	31	67.4	196	2	Q7P7B9	FUSNV	Q7p7b9	fusobacteri	335	31	67.4	358	2	Q6UPV4	DROMO	Q6UPV4	drosophila
263	31	67.4	202	2	Q8UHF7	AGRT5	Q8uhf7	agrobacteri	336	31	67.4	358	2	Q6UPV5	DROMO	Q6UPV5	drosophila
264	31	67.4	204	2	Q676H7	9RAIZ	Q676h7	agrobacteri	337	31	67.4	358	2	Q6UPV8	DROMO	Q6UPV8	drosophila
265	31	67.4	204	2	Q6AMC5	DESPS	Q6amc5	desulfotale	338	31	67.4	358	2	Q6UPZ9	DROMO	Q6UPZ9	drosophila
266	31	67.4	206	2	Q86EN1	SCHJA	Q86en1	schistosoma	339	31	67.4	358	2	Q6UQ01	PROCA	Q6UQ01	proca
267	31	67.4	217	2	Q89VF9	BRALJA	Q89vf9	bradyrhizob	340	31	67.4	358	2	Q4ZR60	PEBAY	Q4ZR60	pseudomonas
268	31	67.4	218	2	Q73PR5	TRIDE	Q73pr5	treponema d	341	31	67.4	359	2	Q8C1B9	MOUSE	Q8C1B9	mus musculu
269	31	67.4	229	2	Q5X7D9	LEGPA	Q5x7d9	legionella	342	31	67.4	363	2	Q87277	PEBEM	Q87277	pseudomonas
270	31	67.4	236	2	Q974Y5	SULTO	Q974y5	sulfolobus	343	31	67.4	369	2	Q9JHM2	RAT	Q9JHM2	rattus norv
271	31	67.4	237	2	Q5ZXW6	LEGPH	Q5zxw6	legionella	344	31	67.4	373	2	Q31267	RAT	Q31267	rattus norv
272	31	67.4	239	2	Q607Z9	MENCA	Q607z9	methylcoccc	345	31	67.4	377	2	Q31265	RAT	Q31265	rattus norv
273	31	67.4	241	2	Q9XTQ2	DROST	Q9xtq2	drosophila	346	31	67.4	380	2	Q5LDV0	BACFN	Q5LDV0	bacteroides
274	31	67.4	243	2	Q8TMU7	METAC	Q8tmu7	methanosarc	347	31	67.4	380	2	Q64U22	BACFR	Q64U22	bacteroides
275	31	67.4	247	2	Q5L2C2	STR11	Q5l2c2	streptococc	348	31	67.4	384	1	NACH	DROVI	NACH	drosophila
276	31	67.4	247	2	Q5M3X4	STR12	Q5m3x4	streptococc	349	31	67.4	385	2	Q6MSW4	MYCMS	Q6MSW4	mycoplasma
277	31	67.4	248	2	Q6LZB7	METMP	Q6lzb7	methanococc	350	31	67.4	388	2	Q6BD16	HUMAN	Q6BD16	homo sapien
278	31	67.4	248	2	Q6VEL9	DROMI	Q6vel9	drosophila	351	31	67.4	388	2	Q9GN75	DROMA	Q9GN75	drosophila
279	31	67.4	248	2	Q8VEK9	MOUSE	Q8vek9	mus musculu	352	31	67.4	388	2	Q9GNJ8	DROJE	Q9GNJ8	drosophila
280	31	67.4	259	2	Q80XC0	MOUSE	Q80xc0	mus musculu	353	31	67.4	389	2	Q7JTN8	MYCFA	Q7JTN8	mycobacteri
281	31	67.4	259	2	Q9CXC0	MOUSE	Q9cxc0	mus musculu	354	31	67.4	392	2	Q8E972	SHEON	Q8E972	sheanella
282	31	67.4	262	2	Q6C074	YARLI	Q6c074	yarrowia li	355	31	67.4	396	2	Q7XWQ4	ORYSA	Q7XWQ4	oryza sativ
283	31	67.4	262	2	Q7T196	CHICK	Q7t196	gallus gall	356	31	67.4	396	2	Q4RWL5	TEITNG	Q4RWL5	tetradon n
284	31	67.4	278	2	Q5HN04	STRAP	Q5hn04	staphylococ	357	31	67.4	402	2	Q4SGS6	TEITNG	Q4SGS6	tetradon n
285	31	67.4	278	2	Q8CRS4	STRAP	Q8crs4	staphylococ	358	31	67.4	402	2	Q8TX87	METKA	Q8TX87	methanopyru
286	31	67.4	279	2	Q4W117	ASFPV	Q4w117	aspergillus	359	31	67.4	407	2	Q9NL43	CIOIN	Q9NL43	clona intes
287	31	67.4	287	2	Q4U2A2	AZQVI	Q4u2a2	azotocacter	360	31	67.4	407	2	Q4RQ01	TEITNG	Q4RQ01	tetradon n
288	31	67.4	289	2	Q96Z24	SULTO	Q96z24	sulfolobus	361	31	67.4	412	2	Q8GM97	STRTR	Q8GM97	streptococ
289	31	67.4	291	2	Q971H6	CLOAB	Q971h6	clostridium	362	31	67.4	420	1	Q8K3B	HUMAN	Q8K3B	homo sapien
290	31	67.4	297	1	YDDE	ECOS7	P54292	escherichia	363	31	67.4	420	1	Q8K3B	MOUSE	Q8K3B	mouse
291	31	67.4	297	1	YDDE	ECOL1	P37757	escherichia	364	31	67.4	420	1	Q8K3B	RAT	Q8K3B	rattus norv
292	31	67.4	297	1	YDDE	SALTY	P40788	salmonella	365	31	67.4	420	1	Q6F127	HUMAN	Q6F127	homo sapien
293	31	67.4	297	2	Q5P7P6	SALCH	Q5p7p6	salmonella	366	31	67.4	420	2	Q5YJC2	SPECT	Q5YJC2	speromphili
294	31	67.4	297	2	Q5BPH1	SALPA	Q5bph1	salmonella	367	31	67.4	420	2	Q5XU03	MOUSE	Q5XU03	mus musculu
295	31	67.4	297	2	Q8FHI5	ECOL6	Q8fhi5	escherichia	368	31	67.4	420	2	Q91627	XENIA	Q91627	xenopus lae
296	31	67.4	297	2	Q8E7J3	SALTI	Q8e7j3	salmonella	369	31	67.4	420	2	Q91757	XENIA	Q91757	xenopus lae
297	31	67.4	299	2	Q4RIH2	TEITNG	Q4rih2	tetradon n	370	31	67.4	421	2	Q9IBD2	BRARE	Q9IBD2	brachydanio
298	31	67.4	300	2	Q6C807	YARLI	Q6c807	yarrowia li	371	31	67.4	421	2	Q9YH60	BRARE	Q9YH60	brachydanio
299	31	67.4	300	2	Q5YR8	NOCFA	Q5yr8	nocardia fa	372	31	67.4	423	2	Q8YKR6	VIBPA	Q8YKR6	vibrio para
300	31	67.4	304	2	Q6W9J6	MOUSE	Q6w9j6	mus musculu	373	31	67.4	423	2	Q4RSF6	TEITNG	Q4RSF6	tetradon n
301	31	67.4	307	2	Q8KCQ7	CHLITE	Q8kcq7	chlorobium	374	31	67.4	425	2	Q4RMW9	TEITNG	Q4RMW9	tetradon n
302	31	67.4	313	2	Q974F0	SULTO	Q974f0	sulfolobus	375	31	67.4	427	2	Q4KZ30	BCODI	Q4KZ30	bacteroides
303	31	67.4	314	2	Q4U2A6	AZQVI	Q4u2a6	azotocacter	376	31	67.4	435	2	Q9IBD3	BRARE	Q9IBD3	brachydanio
304	31	67.4	315	2	Q52443	PEBSP	Q52443	pseudomonas	377	31	67.4	438	1	U1B3	DROME	U1B3	drosophila
305	31	67.4	326	2	Q7O5Y3	ANOGA	Q7o5y3	anopheles g	378	31	67.4	440	2	Q9YH61	BRARE	Q9YH61	brachydanio
306	31	67.4	326	2	Q6DFU4	XENIA	Q6dfu4	xenopus lae	379	31	67.4	444	2	Q97ZV2	SULTO	Q97ZV2	sulfolobus
307	31	67.4	326	2	Q6IRDO	XENIA	Q6ird0	xenopus lae	380	31	67.4	446	2	Q5LYA5	STR12	Q5LYA5	streptococ
308	31	67.4	327	1	VP826	HUMAN	Q75436	homo sapien	381	31	67.4	446	2	Q5M2W0	STR12	Q5M2W0	streptococ
309	31	67.4	327	1	VP826	MOUSE	P40336	mus musculu	382	31	67.4	462	2	Q7NB81	MYCDA	Q7NB81	mycoplasma
310	31	67.4	327	2	Q6AYH6	RAT	Q6ayh6	rattus norv	383	31	67.4	465	2	Q7SY03	BRARE	Q7SY03	brachydanio
311	31	67.4	327	2	Q6TNP8	BRARE	Q6tnp8	brachydanio	384	31	67.4	474	2	Q9YOC1	PYRAB	Q9YOC1	pyrococcus
312	31	67.4	327	2	Q7ZUB5	BRARE	Q7zubs	brachydanio	385	31	67.4	476	2	Q08635	BOVIN	Q08635	bos taurus
313	31	67.4	328	2	Q4S0Z5	TEITNG	Q4s0z5	tetradon n	386	31	67.4	478	1	VP826	DROME	VP826	drosophila
314	31	67.4	330	2	Q30633	HELIPY	Q30633	helicobacte	387	31	67.4	483	1	Q4QOB4	DROME	Q4QOB4	drosophila
315	31	67.4	330	2	Q25530	HELIPY	Q25530	helicobacte	388	31	67.4	483	1	Q8K3A	HUMAN	Q8K3A	homo sapien
316	31	67.4	343	2	Q6W9J7	MOUSE	Q6w9j7	mus musculu	389	31	67.4	483	1	Q8K3A	RAT	Q8K3A	rattus norv
317	31	67.4	343	2	Q6W9J8	MOUSE	Q6w9j8	mus musculu	390	31	67.4	484	2	Q7Z9M2	TRIRE	Q7Z9M2	trichoderma
318	31	67.4	343	2	Q6W9J9	MOUSE	Q6w9j9	mus musculu	391	31	67.4	485	2	Q90YV3	XENIA	Q90YV3	xenopus lae
319	31	67.4	343	2	Q6W9K2	9MURI	Q6w9k2	mus musculu	392	31	67.4	488	2	Q8XSR9	RALSO	Q8XSR9	ralstonia s
320	31	67.4	343	2	Q6W9K6	MOUSE	Q6w9k6	mus musculu	393	31	67.4	489	2	Q91781	XENIA	Q91781	xenopus lae
321	31	67.4	343	2	Q6W9L1	MOUSE	Q6w9l1	mus musculu	394	31	67.4	494	2	Q91830	ONCXY	Q91830	oncothymchu
322	31	67.4	343	2	Q6W9K4	MOUSE	Q6w9k4	mus musculu	395	31	67.4	495	1	KCNAL	HUMAN	KCNAL	homo sapien
323	31	67.4	344	2	Q6W9J5	RAT	Q6w9j5	rattus norv	396	31	67.4	495	1	KCNAL	MOUSE	KCNAL	mouse

397	31	67.4	495	1	KCNAL_RAT	P10499	rattus norv	470	31	67.4	1184	2	OSAMV6	CANAL	OSAMV6	candida alb
398	31	67.4	495	2	OCAS5_MOUSE	OCAS5	mus musculi	471	31	67.4	1211	1	ARG26	PICPA	ARG26	pachia past
399	31	67.4	496	2	QASOH_TERNG	QASOH	tetradon n	472	31	67.4	1266	2	OCAR3_YARLI		OCAR3	yarrowia li
400	31	67.4	498	2	QNM28_ARATH	QNM28	arabidopsis	473	31	67.4	1266	2	OC2AV7_BURMA		OC2AV7	burma
401	31	67.4	498	1	QAR1H_TERNG	QAR1H	tetradon n	474	31	67.4	1286	2	OC9AB3_HELAN		OC9AB3	helian
402	31	67.4	499	1	KCNV2_HUMAN	P16389	homo sapien	475	31	67.4	1297	2	QAP193_USTMA		QAP193	ustma
403	31	67.4	499	1	KCNV2_MOUSE	P63141	mus musculi	476	31	67.4	1319	2	OC1EX3_CAEBR		OC1EX3	caenorhabdi
404	31	67.4	499	1	KCNV2_RAT	P63142	rattus norv	477	31	67.4	1322	2	QAVK27_CAEBR		QAVK27	caenorhabdi
405	31	67.4	499	1	KCNV2_XENLA	P22739	xenopus lae	478	31	67.4	1386	2	OC2791_CAEBL		OC2791	caenorhabdi
406	31	67.4	499	2	QNMV3_RABIT	QNMV3	oryctolagus	479	31	67.4	1496	2	OC23X5_MAGGR		OC23X5	magnaporthe
407	31	67.4	499	2	QOY17_IDILO	QOY17	idionotus	480	31	67.4	1500	2	OC3JUT5_BURPS		OC3JUT5	burps
408	31	67.4	499	2	Q7T1AO_CHICK	Q7T1AO	gallus galli	481	31	67.4	1563	2	OC4H31_DICD1		OC4H31	dicd1
409	31	67.4	499	2	Q98TW4_XENLA	Q98TW4	xenopus lae	482	31	67.4	1601	2	OC5HP7_CRYHO		OC5HP7	cryho
410	31	67.4	514	1	G6PD_HUMAN	P11413	homo sapien	483	31	67.4	1607	2	OC5M59_CRYPV		OC5M59	crpv
411	31	67.4	516	2	Q28656_RABIT	Q28656	oryctolagus	484	31	67.4	1634	2	OC87X3_PESPM		OC87X3	pespm
412	31	67.4	518	1	G6PD_DROYA	Q27638	drosophila	485	31	67.4	1674	2	Q7RMJ3_NEUCR		Q7RMJ3	neucr
413	31	67.4	522	2	OC1335_PANIN	OC1335	panulirus i	486	31	67.4	1701	2	Q8WZX8_NEUCR		Q8WZX8	neucr
414	31	67.4	523	1	KCNV3_HUMAN	P22001	homo sapien	487	31	67.4	1930	2	Q51CV9_9CLOS		Q51CV9	9clos
415	31	67.4	524	1	G6PD_DROME	P12646	drosophila	488	31	67.4	1980	2	Q6FWE0_CANGA		Q6FWE0	canga
416	31	67.4	524	2	Q7T198_CHICK	Q7T198	gallus galli	489	31	67.4	2117	2	Q5SM60_CRYNE		Q5SM60	crvne
417	31	67.4	525	1	KCNV3_RAT	P15384	rattus norv	490	31	67.4	2117	2	Q5KBA5_CRYNE		Q5KBA5	crvne
418	31	67.4	525	2	Q4RW80_TERNG	Q4RW80	tetradon n	491	31	67.4	2198	2	Q6UY70_9YIRU		Q6UY70	9yiru
419	31	67.4	528	2	KCNV3_MOUSE	P16390	mus musculi	492	31	67.4	2370	2	Q4UJ22_THEAN		Q4UJ22	thean
420	31	67.4	530	2	Q821G6_STRAW	Q821G6	strepcomyce	493	31	67.4	2435	2	Q51CWO_9CLOS		Q51CWO	9clos
421	31	67.4	532	2	Q591A7_CANAL	Q591A7	candida alb	494	31	67.4	2835	2	Q4G363_LEIMA		Q4G363	leima
422	31	67.4	533	2	Q86MA6_LIMPO	Q86MA6	limulus pol	495	31	67.4	4796	2	Q4Q363_LEIMA		Q4Q363	leima
423	31	67.4	537	2	Q4WET6_ASFPU	Q4WET6	aspeygiillus	496	31	67.4	5037	2	Q5AMF4_CANAL		Q5AMF4	candal
424	31	67.4	543	2	Q4SRT0_TERNG	Q4SRT0	tetradon n	497	31	66.3	516	2	Q5DFZ0_SCHJA		Q5DFZ0	schja
425	31	67.4	550	2	Q4PH28_USTMA	Q4PH28	ustilago ma	498	31	65.2	41	2	Q9X111_THEMA		Q9X111	thema
426	31	67.4	554	2	Q5W6Z9_BACSK	Q5W6Z9	bacillus ci	499	31	65.2	69	1	Y420_ARCFU		Y420	arcfu
427	31	67.4	557	2	Q6P2D3_HUMAN	Q6P2D3	homo sapien	500	31	65.2	71	2	Q4NRU9_9DEL7		Q4NRU9	9del7
428	31	67.4	571	2	Q6EVT9_YERPS	Q6EVT9	yerinia ps	501	31	65.2	73	2	Q9PID9_HUMAN		Q9PID9	human
429	31	67.4	575	2	Q5VMN2_HUMAN	Q5VMN2	homo sapien	502	31	65.2	77	2	Q98317_RHIL0		Q98317	rhil0
430	31	67.4	580	2	Q7T195_CHICK	Q7T195	gallus galli	503	31	65.2	78	2	Q812V3_BACCR		Q812V3	baccr
431	31	67.4	582	2	Q8D2Y2_WIEBR	Q8D2Y2	wiggleswort	504	31	65.2	78	2	Q812V3_BACCR		Q812V3	baccr
432	31	67.4	608	2	Q4WA38_ASFPU	Q4WA38	aspeygiillus	505	31	65.2	78	2	Q81IV8_ENTFA		Q81IV8	entfa
433	31	67.4	608	2	Q5ZX65_LIEGPH	Q5ZX65	legionella	506	31	65.2	110	2	Q6PUC0_ANOGA		Q6PUC0	anoga
434	31	67.4	608	2	Q5XK65_LIEGPA	Q5XK65	legionella	507	31	65.2	111	2	Q6TJU9_DROSI		Q6TJU9	drosi
435	31	67.4	608	2	Q5WY40_LIEGPL	Q5WY40	legionella	508	31	65.2	113	2	Q8JMG0_9NUCL		Q8JMG0	9nucl
436	31	67.4	633	2	Q6LR70_PHOPR	Q6LR70	photobacter	509	31	65.2	122	2	Q9TGK4_ECHGR		Q9TGK4	echgr
437	31	67.4	633	2	Q4SHG0_TERNG	Q4SHG0	tetradon n	510	31	65.2	122	2	Q7Q1S7_ANOGA		Q7Q1S7	anoga
438	31	67.4	635	2	Q48484_KLEPN	Q48484	klebsiella	511	31	65.2	123	2	Q61K33_DROME		Q61K33	drome
439	31	67.4	660	2	Q93HG7_STRAW	Q93HG7	strepcomyce	512	31	65.2	125	2	Q95122_GADMO		Q95122	gadmo
440	31	67.4	675	2	Q61DK9_CAEBR	Q61DK9	caenorhabdi	513	31	65.2	128	2	Q95121_GADMO		Q95121	gadmo
441	31	67.4	677	2	Q98TW3_XENLA	Q98TW3	xenopus lae	514	31	65.2	130	1	R88_IDILO		R88	idilo
442	31	67.4	678	2	Q5TT73_ANOGA	Q5TT73	xenopus lae	515	31	65.2	132	1	R88_ADICA		R88	adica
443	31	67.4	697	2	Q8UG57_XENLA	Q8UG57	xenopus lae	516	31	65.2	132	1	R88_ADICA		R88	adica
444	31	67.4	701	2	Q8LJ37_9ACTO	Q8LJ37	strepcomyce	517	31	65.2	132	2	Q6HTH4_BACCE		Q6HTH4	bacce
445	31	67.4	709	2	Q9A1T1_STEPT	Q9A1T1	strepcomyce	518	31	65.2	132	2	Q6HEH9_BACCH		Q6HEH9	bacch
446	31	67.4	729	1	S15A2_MOUSE	Q9E007	mus musculi	519	31	65.2	132	2	Q731X9_BACCI		Q731X9	bacci
447	31	67.4	729	1	S15A2_MOUSE	Q63424	rattus norv	520	31	65.2	132	2	Q635U2_BACCE		Q635U2	bacce
448	31	67.4	740	2	Q5U401_RAT	Q5U401	rattus norv	521	31	65.2	132	2	Q5OLO9_ORYSA		Q5OLO9	orysa
449	31	67.4	740	2	Q9JMD3_MOUSE	Q9JMD3	mus musculi	522	31	65.2	133	2	Q55116_GADMO		Q55116	gadmo
450	31	67.4	743	2	Q89C74_BRAJA	Q89C74	bradyrhizob	523	31	65.2	133	2	Q55116_GADMO		Q55116	gadmo
451	31	67.4	764	1	ACOC_CUCMC	Q94269	cucumis mel	524	31	65.2	134	2	Q5QY47_IDILO		Q5QY47	idilo
452	31	67.4	787	2	Q9DECH_ONCMY	Q9DECH	oncoyrnchn	525	31	65.2	151	2	Q5QY47_IDILO		Q5QY47	idilo
453	31	67.4	788	2	Q61CH5_CAEBL	Q61CH5	caenorhabdi	526	31	65.2	157	2	Q67LE7_SYTHI		Q67LE7	sythi
454	31	67.4	789	2	Q9U2M6_CAEBL	Q9U2M6	caenorhabdi	527	31	65.2	161	2	Q8VMG8_PSEPU		Q8VMG8	psepu
455	31	67.4	803	2	Q51L74_MAGGR	Q51L74	magnaporthe	528	31	65.2	169	2	Q5AK59_CANAL		Q5AK59	canal
456	31	67.4	831	2	Q75OR9_ASHGO	Q75OR9	ashbya gos	529	31	65.2	169	2	Q5AK59_CANAL		Q5AK59	canal
457	31	67.4	833	2	Q7Q818_ANOGA	Q7Q818	anopheles g	530	31	65.2	170	2	Q5V921_PROMA		Q5V921	proma
458	31	67.4	848	2	Q8VZH3_ARATH	Q8VZH3	arabidopsis	531	31	65.2	172	2	Q59254_PYRHO		Q59254	pyrho
459	31	67.4	848	2	Q9S1UJ_ARATH	Q9S1UJ	arabidopsis	532	31	65.2	172	2	Q16773_CAEBL		Q16773	caeb
460	31	67.4	856	2	Q4PEW4_USTMA	Q4PEW4	ustilago ma	533	31	65.2	174	2	Q5C3M2_SCHJA		Q5C3M2	schja
461	31	67.4	889	2	Q9F2N5_STRICO	Q9F2N5	strepcomyce	534	31	65.2	175	2	Q9GN96_CHRBE		Q9GN96	chrbe
462	31	67.4	898	2	ACOC_ARATH	Q42560	arabidopsis	535	31	65.2	175	2	Q9GSM1_CHRBE		Q9GSM1	chrbe
463	31	67.4	898	2	Q81396_CITRI	Q81396	citrus limo	536	31	65.2	184	2	Q5TY72_ANOGA		Q5TY72	anoga
464	31	67.4	902	2	Q6YNR9_PUUV	Q6YNR9	prunus aviu	537	31	65.2	186	2	Q4R6F1_NACFA		Q4R6F1	nacfa
465	31	67.4	938	2	Q5CLYO_CRYHO	Q5CLYO	cryptospori	538	31	65.2	187	2	Q5N147_FRATY		Q5N147	fraty
466	31	67.4	950	2	Q4I1N2_GIBZE	Q4I1N2	gibberella	539	31	65.2	191	2	Q4NYO2_9BELT		Q4NYO2	9belt
467	31	67.4	954	1	GCSP_STNEL	Q8d13	synecococc	540	31	65.2	197	2	Q8EBV2_SHEON		Q8EBV2	sheon
468	31	67.4	969	2	Q4TUF8_9SEPHN	Q4TUF8	erythrobact	541	31	65.2	200	2	Q72702_9VIRU		Q72702	9viru
469	31	67.4	1032	2	Q8MXL1_LEIMA	Q8MXL1	leishmania	542	31	65.2	200	2	Q73536_RVFN		Q73536	rvfn

543	30	65.2	200	2	073537	RVEV	073537	rife	valley	616	30	65.2	310	2	05WK07	BACSK	05WK07	bacillus	cl
544	30	65.2	200	2	073538	RVEV	073538	rife	valley	617	30	65.2	310	2	08TLW2	METAC	08TLW2	mechanosarc	
545	30	65.2	200	2	073540	RVEV	073540	rife	valley	618	30	65.2	313	2	06VE12	ANOMOL	06VE12	siphonodact	
546	30	65.2	200	2	073541	RVEV	073541	rife	valley	619	30	65.2	316	2	026480	METTH	026480	methanobact	
547	30	65.2	200	2	073542	RVEV	073542	rife	valley	620	30	65.2	317	2	088368	PSEBM	088368	pseudomonas	
548	30	65.2	200	2	073543	RVEV	073543	rife	valley	621	30	65.2	318	2	051906	ENTHI	051906	entamoeba	h
549	30	65.2	200	2	073544	RVEV	073544	rife	valley	622	30	65.2	319	2	082HD4	STRAW	082HD4	streptomyces	
550	30	65.2	200	2	073545	RVEV	073545	rife	valley	623	30	65.2	320	2	0937N3	PHOLU	0937N3	photobacilli	
551	30	65.2	200	2	073546	RVEV	073546	rife	valley	624	30	65.2	320	2	07MZP3	PHOLU	07MZP3	photobacilli	
552	30	65.2	200	2	073548	RVEV	073548	rife	valley	625	30	65.2	321	2	09K3S7	STRKO	09K3S7	streptococcus	
553	30	65.2	200	2	073549	RVEV	073549	rife	valley	626	30	65.2	324	2	07QHK0	ANODA	07QHK0	anophelies	g
554	30	65.2	200	2	076F4	RVEV	076F4	rife	valley	627	30	65.2	325	1	IF32	BOVIN	05S966	bos	taurus
555	30	65.2	200	2	076F5	RVEV	076F5	rife	valley	628	30	65.2	325	1	IF32	HUMAN	013347	homo	sapien
556	30	65.2	200	2	08JUF9	RVEV	08JUF9	rife	valley	629	30	65.2	325	1	IF32	MOUSE	09QZD9	mus	musculi
557	30	65.2	204	2	05OV95	ENTHI	05OV95	entamoeba	h	630	30	65.2	325	2	05TDD7	HUMAN	05DHU7	homo	sapien
558	30	65.2	204	2	098TJ2	PLAF6	098TJ2	platichtys		631	30	65.2	325	2	053HUT	HUMAN	053HUT	homo	sapien
559	30	65.2	206	2	07MKP7	PORGI	07MKP7	potphyromon		632	30	65.2	325	2	05R7R2	PONPY	0571R2	pongo	pygma
560	30	65.2	211	2	0776K8	SULTO	0776K8	sulfobacter		633	30	65.2	325	2	05EBB8	XENTR	05EBB8	xenopus	tro
561	30	65.2	211	2	06LM86	PHOPR	06LM86	photobacter		634	30	65.2	325	2	066J51	XENLA	066J51	xenopus	lae
562	30	65.2	212	2	06VZH7	CNPF	06VZH7	canarypox	v	635	30	65.2	325	2	07ZV55	BRARE	07ZV55	brachydanto	
563	30	65.2	216	2	073PH5	TREDE	073PH5	treponema	d	636	30	65.2	325	2	04SIM1	TETNG	04SIM1	tetradon	n
564	30	65.2	219	2	092FHS	LISIN	092FHS	listeria	in	637	30	65.2	326	2	087524	9LACT	087524	lactococcus	
565	30	65.2	224	2	044474	CABEL	044474	caenorhabdi		638	30	65.2	326	2	09S6S4	9LACT	09S6S4	lactococcus	
566	30	65.2	225	2	093MM2	LACSK	093MM2	lactobacilli		639	30	65.2	326	2	074AW0	GEOSL	074AW0	geobacter	s
567	30	65.2	235	2	05TMM3	ANOGA	05TMM3	anopheles	g	640	30	65.2	326	2	09CE66	LACLA	09CE66	lactococcus	
568	30	65.2	236	2	081IP4	PLAF7	081IP4	plasmodium		641	30	65.2	327	2	06J184	LISMO	06J184	listeria	mo
569	30	65.2	236	2	08DNM3	STRB6	08DNM3	streptococc		642	30	65.2	327	2	067164	AQUAE	067164	aquifex	aeo
570	30	65.2	236	2	097P21	STRPN	097P21	streptococc		643	30	65.2	327	2	071WV0	LISMP	071WV0	listeria	mo
571	30	65.2	237	2	074IA3	LACCO	074IA3	lactobacilli		644	30	65.2	327	2	08Y4G6	LISMO	08Y4G6	listeria	mo
572	30	65.2	244	2	071W42	LISMF	071W42	listeria	mo	645	30	65.2	328	2	08SXU1	DROME	08SXU1	drosophila	
573	30	65.2	244	2	08Y3V9	LISMO	08Y3V9	listeria	in	646	30	65.2	328	2	06VIP3	DROME	06VIP3	drosophila	
574	30	65.2	244	2	0927B9	LISIN	0927B9	listeria	in	647	30	65.2	328	2	05EBV7	VIBF1	05EBV7	vibrio	fisc
575	30	65.2	246	2	093IL8	NOSPU	093IL8	nostoc	punc	648	30	65.2	328	2	0928B6	LISIN	0928B6	listeria	in
576	30	65.2	252	2	094IL90	DUCIN	094IL90	ducheanea	i	649	30	65.2	329	2	08R8R8	THETN	08R8R8	thermannae	
577	30	65.2	252	2	094IL68	POTAN	094IL68	potentilla		650	30	65.2	329	2	0836N9	ENTFA	0836N9	enterococc	
578	30	65.2	252	2	094IL84	HORCU	094IL84	horkelia	cu	651	30	65.2	329	2	097E25	CIOAB	097E25	clostridium	
579	30	65.2	252	2	094IL67	POTRIL	094IL67	potentilla		652	30	65.2	332	2	095158	GADMO	095158	gadus	morthu
580	30	65.2	252	2	094IL89	DUCIN	094IL89	ducheanea	i	653	30	65.2	330	2	08VM02	STRTR	08VM02	streptococc	
581	30	65.2	252	2	094IL88	DUCIN	094IL88	ducheanea	i	654	30	65.2	330	2	048728	9LACT	048728	lactococcus	
582	30	65.2	252	2	094IL69	POTAN	094IL69	potentilla		655	30	65.2	330	2	06X495	STRAG	06X495	streptococc	
583	30	65.2	256	2	072CP6	DESVA	072CP6	desulfovibr		656	30	65.2	330	2	05M4A0	STRF2	05M4A0	streptococc	
584	30	65.2	260	2	05WE00	BACSK	05WE00	bacillus	cl	657	30	65.2	330	2	0830U9	ENTFA	0830U9	enterococc	
585	30	65.2	262	2	092HB4	STRPN	092HB4	streptococc		658	30	65.2	331	1	GALE	LACCA	084903	lactobacilli	
586	30	65.2	262	2	097PG0	STRPN	097PG0	streptococc		659	30	65.2	331	2	088YF0	LACPL	088YF0	lactobacilli	
587	30	65.2	265	1	VNST	RVEVZ	P21698	rift	valley	660	30	65.2	331	2	08DXC8	STRAS	08DXC8	streptococc	
588	30	65.2	266	2	08CMP9	STRB6	08CMP9	streptococc		661	30	65.2	331	2	08E352	STRAS	08E352	streptococc	
589	30	65.2	269	2	04TSB9	9SPHN	04TSB9	erythrobact		662	30	65.2	333	2	05IHB1	RABIT	05IHB1	oryctolagus	
590	30	65.2	271	2	07VG03	HELHP	07VG03	heliobact		663	30	65.2	333	2	088CU9	PSEPK	088CU9	pseudomonas	
591	30	65.2	280	1	DAPE	ARCFU	029511	archaeoglob		664	30	65.2	333	2	065CW8	BACID	065CW8	bacillus	li
592	30	65.2	280	2	05E7U1	VIBF1	05E7U1	vibrio	fisc	665	30	65.2	334	2	088SE9	LACPL	088SE9	lactobacilli	
593	30	65.2	281	2	08YU08	ANASP	08YU08	anabaena	sp	666	30	65.2	336	2	07OBH3	ANODA	07OBH3	anophelies	g
594	30	65.2	284	2	08TLX0	METAC	08TLX0	methanosarc		667	30	65.2	337	2	06N2O9	RHOFA	06N2O9	rhodospseudo	
595	30	65.2	291	2	082IK8	SALTI	082IK8	salimoneila		668	30	65.2	339	2	030424	CALJA	030424	caldoceillum	
596	30	65.2	293	2	0953M6	ECHGR	0953M6	echinococcu		669	30	65.2	340	2	089HQ9	BRALJ	089HQ9	bradyrhizob	
597	30	65.2	293	2	0958U5	ECHGR	0958U5	echinococcu		670	30	65.2	342	2	092S70	RIIME	092S70	rhizobium	m
598	30	65.2	293	2	04SS17	TETNG	04SS17	tetradon	n	671	30	65.2	342	2	08B7V3	MOUSE	08B7V3	mus	musculi
599	30	65.2	295	2	05ONP4	ENTHI	05ONP4	entamoeba	h	672	30	65.2	343	2	04KBE2	PSEB5	04KBE2	pseudomonas	
600	30	65.2	296	2	05WCT8	BACSK	05WCT8	bacillus	cl	673	30	65.2	343	2	08UHX8	AGRT5	08UHX8	agrobacteri	
601	30	65.2	298	2	06CUM6	KIOLA	06CUM6	kluyveromyc		674	30	65.2	345	2	07VCJ3	HELHP	07VCJ3	heliobact	
602	30	65.2	298	2	065MA8	BACID	065MA8	bacillus	li	675	30	65.2	348	1	MO25L	ARATH	0672V9	arabidopsis	
603	30	65.2	299	2	04MXW8	BACCE	04MXW8	bacillus	ce	676	30	65.2	348	1	05XO67	9ARCH	05XO67	uncultured	
604	30	65.2	299	2	06HG09	BACHK	06HG09	bacillus	th	677	30	65.2	351	2	0647V3	9ARCH	0647V3	uncultured	
605	30	65.2	299	2	0734H4	BACCI	0734H4	bacillus	ce	678	30	65.2	351	2	064BV4	9ARCH	064BV4	uncultured	
606	30	65.2	299	2	081AX3	BACCR	081AX3	bacillus	ce	679	30	65.2	351	2	064D31	9ARCH	064D31	uncultured	
607	30	65.2	299	2	081WV2	BACAN	081WV2	bacillus	an	680	30	65.2	352	2	06A1E1	CIOGA	06A1E1	ciona	savig
608	30	65.2	300	2	0638F7	BACAZ	0638F7	bacillus	ce	681	30	65.2	353	2	09TZ26	CABEL	09TZ26	caenorhabdi	
609	30	65.2	302	1	RR30	SPICL	P19954	splanactia	ol	682	30	65.2	353	2	08CE74	MOUSE	08CE74	mus	musculi
610	30	65.2	304	2	096N12	HUMAN	096N12	homo	sapien	683	30	65.2	354	1	LEU3	BACAN	073B59	bacilli	an
611	30	65.2	305	2	08TIS6	METAC	08TIS6	mechanosarc		684	30	65.2	354	2	06HLR2	BACCK	06HLR2	bacillus	ce
612	30	65.2	305	2	09APB9	9BACT	09APB9	uncultured		685	30	65.2	354	2	063DX7	BACCE	063DX7	bacillus	ce
613	30	65.2	308	2	05UIE4	PYRKO	05UIE4	pyrococcus		686	30	65.2	354	2	075BN3	ASHGO	075BN3	aebhya	goss
614	30	65.2	309	2	086GB8	CABEL	086GB8	caenorhabdi		687	30	65.2	356	2					
615	30	65.2								688	30	65.2							

689	30	65.2	356	2	Q513M8_ECOLI	Q513m8 escherichia	762	30	65.2	508	2	Q4VMW8_PROS1	Q4vmw8 bridelia in
690	30	65.2	364	2	Q4J934_SULAC	Q4j934 sulfobus	763	30	65.2	514	2	Q57655_FUGR1	Q57655 fugu rubrip
691	30	65.2	364	2	Q8RC66_ECOL6	Q8rc66 escherichia	764	30	65.2	514	2	Q4G339_9PERB	Q4g339 rhodobacteru
692	30	65.2	365	2	Q8ZV82_PYRAB	Q8zv82 pyrobaculum	765	30	65.2	516	2	Q4RVY1_METNG	Q4rvy1 terradon n
693	30	65.2	366	2	Q60B63_METCA	Q60b63 methylococc	766	30	65.2	527	2	Q4LPY5_9BURK	Q4lpy5 burkholderi
694	30	65.2	369	2	Q7NMF8_CHRVO	Q7nmf8 chromobacte	767	30	65.2	528	2	Q8DDP8_VIBVU	Q8ddp8 vibrio vuln
695	30	65.2	371	2	Q4WRP6_ASPFU	Q4wrp6 aspergillus	768	30	65.2	530	1	G6PDP_FUGRU	P5496 fugu rubrip
696	30	65.2	371	2	Q6H073_FREDI	Q6h073 fremyella d	769	30	65.2	538	2	Q9KZL5_STRCO	Q9kzl5 streptomyce
697	30	65.2	375	2	Q8U2H3_PYRFB	Q8u2h3 pyrococcus	770	30	65.2	538	2	Q82DD5_STRAW	Q82dd5 streptomyce
698	30	65.2	375	2	Q9V027_PYRAB	Q9v027 pyrococcus	771	30	65.2	546	2	Q7M034_VIBVU	Q7m034 vibrio vuln
699	30	65.2	375	2	Q58739_PYRHO	Q58739 pyrococcus	772	30	65.2	546	2	Q9C4Q4_METMP	Q9c4q4 methanococc
700	30	65.2	376	1	RUVB_GIOVI	Q7mp9 glaucobacter	773	30	65.2	546	2	Q6LWN4_METMP	Q6lwn4 methanococc
701	30	65.2	381	2	Q89Q09_BRAJA	Q89q09 bradyrhizob	774	30	65.2	548	1	WRK72_ARATH	Q91xg8 arabidopsis
702	30	65.2	382	2	Q98MH8_RHIO	Q98mh8 rhizobium l	775	30	65.2	550	2	Q6A0A4_DESPS	Q6aq4 desulfofata
703	30	65.2	383	2	Q8LER4_ARATH	Q8ler4 arabidopsis	776	30	65.2	556	1	SYO_NITEU	Q81z87 nitrosomona
704	30	65.2	387	2	Q8ZLR9_STRAM	Q8zlr9 streptomyce	777	30	65.2	557	1	SYD_MGCPN	P75068 mycoplasma
705	30	65.2	390	2	Q7MMG3_PORGI	Q7mmg3 porphyromon	778	30	65.2	558	1	SYO_BRAJA	Q83x6 bradyrhizob
706	30	65.2	394	2	Q6Z3Y1_ORYSA	Q6z3y1 oryza sativ	779	30	65.2	560	1	SYO_CHRVO	Q7rx86 chitrobacte
707	30	65.2	397	2	Q8D6E7_VIBVU	Q8d6e7 vibrio vuln	780	30	65.2	560	2	Q6N5R6_RHOPA	Q6n5r6 rhodospseudo
708	30	65.2	397	2	Q7MDA0_VIBVU	Q7mda0 vibrio vuln	781	30	65.2	562	1	SYO_BUCAP	Q8x9e1 buchnera ap
709	30	65.2	401	2	Q9L1T4_STRCO	Q9l1t4 streptomyce	782	30	65.2	562	2	Q4WR58_ASPFU	Q4wr58 aspergillus
710	30	65.2	402	2	Q25357_HELPY	Q25357 hellicobacte	783	30	65.2	562	2	Q6AUX3_DESPS	Q6a1j3 desulfofata
711	30	65.2	402	2	Q9ZLJ6_HELPJ	Q9zlj6 hellicobacte	784	30	65.2	562	2	Q8DXU5_STRAS	Q8dxj5 streptococc
712	30	65.2	405	2	Q4TEP5_TETNG	Q4tep5 tetradon n	785	30	65.2	570	2	Q727A5_DESVH	Q727a5 desulfovibr
713	30	65.2	406	2	Q4TNU3_9EBHN	Q4tnu3 erythrobact	786	30	65.2	584	1	Y742_STRCO	Q9zn80 streptomyce
714	30	65.2	407	2	Q72AK9_DESVH	Q72ak9 desulfovibr	787	30	65.2	587	2	Q8ZG34_YERPE	Q8zg34 yersinia ps
715	30	65.2	408	2	Q4JVR3_CORJK	Q4jvr3 corynebacte	788	30	65.2	587	2	Q66CA4_YERPS	Q66ca4 yersinia ps
716	30	65.2	408	2	Q5QVB2_IDILO	Q5qvb2 idiomarina	789	30	65.2	590	2	Q6CVY1_KUTUA	Q6cvy1 kluveromyc
717	30	65.2	409	2	Q6MPF3_BDBLA	Q6mpf3 bdellovibr	790	30	65.2	591	2	Q4VUH3_STRMU	Q4vuh3 streptococc
718	30	65.2	413	2	Q6BT53_DEBBA	Q6bt53 debaryomyce	791	30	65.2	599	2	Q4SWM3_TETNG	Q4swm3 tetradon n
719	30	65.2	415	1	DCDA_HABIN	Q9ff93 arabidopsis	792	30	65.2	603	3	Q9XWN3_CABEL	Q9xwn3 caenorhadi
720	30	65.2	415	1	Q9FF93_ARATH	Q9ff93 arabidopsis	793	30	65.2	605	1	SYD_SYNEL	Q8d3j8 synechococc
721	30	65.2	416	1	RFL_HAISA	Q8yh00 halobacteri	794	30	65.2	610	2	Q7O3B7_ANOGA	Q73b77 anopheles g
722	30	65.2	416	2	Q8SY00_DROME	Q8sy00 drosophila	795	30	65.2	630	2	Q4A840_KLEPN	Q4a840 klebsiella
723	30	65.2	419	2	Q519W5_CANPA	Q519w5 canis famli	796	30	65.2	631	2	Q76ZK8_KLEPN	Q76zk8 klebsiella
724	30	65.2	420	2	Q87E31_XYLFT	Q87e31 xyella fas	797	30	65.2	632	2	Q5KRS1_CRYNE	Q5krs1 cryptococcu
725	30	65.2	420	2	Q9PE12_XYLFA	Q9pe12 xyella fas	798	30	65.2	634	2	Q9CNH8_PASMO	Q9cnh8 pasteurella
726	30	65.2	426	2	Q7Q2S4_ANOGA	Q7q2s4 anopheles g	799	30	65.2	638	2	Q6D719_ERWCT	Q6d719 erwinta car
727	30	65.2	434	2	Q8L393_9BACT	Q8l393 uncultured	800	30	65.2	642	2	Q5HT76_CAMJR	Q5ht76 campylobact
728	30	65.2	441	2	Q4UAF3_THERAN	Q4uaf3 theileria a	801	30	65.2	645	2	Q75DY6_ASHGO	Q75dy6 ashbya goss
729	30	65.2	442	2	Q83N60_TROMT	Q83n60 tropheryma	802	30	65.2	645	2	Q87F67_XYLFT	Q87f67 xyella fas
730	30	65.2	442	2	Q83FG0_TROMT	Q83fg0 tropheryma	803	30	65.2	645	2	Q9PH53_XYLFA	Q9ph53 xyella fas
731	30	65.2	445	2	Q9VKF2_DROME	Q9vkf2 dirosophila	804	30	65.2	660	2	Q4VOA0_XANCP	Q4voa0 xanthomonas
732	30	65.2	447	2	Q29393_ARCFU	Q29393 archaeoglob	805	30	65.2	660	2	Q8PE06_XANCP	Q8pe06 xanthomonas
733	30	65.2	447	2	Q6B105_DEBBA	Q6b105 debaryomyce	806	30	65.2	663	2	Q8ZXX0_PYRAB	Q8zxx0 pyrobaculum
734	30	65.2	447	2	Q4J3Z1_GIBZE	Q4j3z1 gibberella	807	30	65.2	667	2	Q54Z32_STRNG	Q54z32 streptococc
735	30	65.2	448	2	Q6CM15_KTULA	Q6cm15 kluveromyc	808	30	65.2	671	2	Q5GUT1_XANOR	Q5gut1 xanthomonas
736	30	65.2	451	2	Q8XSE8_RALSO	Q8xse8 ralstonia s	809	30	65.2	672	2	Q8PQX4_XANAC	Q8pqx4 xanthomonas
737	30	65.2	454	2	Q5ISW3_MAGGR	Q5isw3 magaporthe	810	30	65.2	676	2	Q5Z0A6_NOCFA	Q5z0a6 nocardia fa
738	30	65.2	454	2	Q4POPI_USITMA	Q4popi ustilago ma	811	30	65.2	681	2	Q9VAS4_DROME	Q9vas4 dirosophila
739	30	65.2	458	2	Q5YXK8_NOCFA	Q5yxk8 nocardia fa	812	30	65.2	690	2	Q8U3I8_PYRFT	Q8u3i8 pyrococcus
740	30	65.2	461	2	Q4N069_THERPA	Q4n069 theileria p	813	30	65.2	714	2	Q4SMPI_METNG	Q4smfi terradon n
741	30	65.2	467	2	Q6C6M3_YARLI	Q6c6m3 yarrowia l1	814	30	65.2	718	2	Q4PCY5_USITMA	Q4pcy5 ustilago ma
742	30	65.2	470	2	Q76BC9_POLOR	Q76bc9 polypteris	815	30	65.2	722	2	Q4KM02_HUMAN	Q4kmg2 homo sapien
743	30	65.2	470	2	Q76BF8_ORYIA	Q76bf8 oryzaia lat	816	30	65.2	723	2	Q8LHU0_ORYSA	Q8lhu0 oryza sativ
744	30	65.2	470	2	Q76BH2_LEBPA	Q76bh2 lepidosiren	817	30	65.2	724	2	Q9HFO3_CRYNE	Q9hfo3 cryptococcu
745	30	65.2	471	2	Q9IADI_GUTLE	Q9iad1 pimphales	818	30	65.2	726	2	Q55Z33_CRYNE	Q55z33 cryptococcu
746	30	65.2	471	2	Q677Z3_GYIRU	Q677z3 lymphocysti	819	30	65.2	726	2	Q5KMR9_CRYNE	Q5kme9 cryptococcu
747	30	65.2	472	2	Q76BD6_ACTIB	Q76bd6 acipenser b	820	30	65.2	730	2	Q5VRS3_ORYSA	Q5vrs3 oryza sativ
748	30	65.2	472	2	Q76BFI_LEPOS	Q76bfi lepiosteus	821	30	65.2	758	2	Q7YU49_DROME	Q7yu49 dirosophila
749	30	65.2	472	2	Q76BH9_PROAN	Q76bh9 protopetereus	822	30	65.2	762	2	Q756T4_ASHGO	Q756t4 ashbya goss
750	30	65.2	477	2	Q4ROI8_TETNG	Q4roi8 tetradon n	823	30	65.2	762	2	Q86ZAS_COCHC	Q86zas cohillobolu
751	30	65.2	479	2	Q5KG75_CRYNE	Q5kg75 cryptococcu	824	30	65.2	769	2	Q6BVR3_DEBBA	Q6bvr3 debaryomyce
752	30	65.2	481	1	AKT2_HUMAN	P31751 homo sapien	825	30	65.2	792	2	Q4WRB0_ASPFU	Q4wrb0 aspergillus
753	30	65.2	481	1	AKT2_MOUSE	Q60823 mus musculu	826	30	65.2	793	2	Q7Y0G7_ARATH	Q7y0g7 arachis hyp
754	30	65.2	481	1	AKT2_RAT	P47197 rattus norv	827	30	65.2	796	2	Q8X212_TALEM	Q8x212 talarayces
755	30	65.2	481	2	Q30031_ARCFU	Q30031 archaeoglob	828	30	65.2	797	2	Q92458_TRIRE	Q92458 trichoderma
756	30	65.2	483	2	Q5TU76_ANOGA	Q5tu76 anopheles g	829	30	65.2	799	2	Q6KHP9_MYCMO	Q6khp9 mycoplasma
757	30	65.2	484	2	Q4TEV9_GIBZE	Q4tev9 gibberella	830	30	65.2	807	2	Q9XFX7_CRAPL	Q9xfx7 crataeoslig
758	30	65.2	486	2	Q516D9_ENTHI	Q516d9 entamoeba h	831	30	65.2	808	1	PIDAI1_RICCO	P41142 ricinus com
759	30	65.2	492	2	Q868S5_ANOGA	Q868s5 anopheles g	832	30	65.2	808	1	PIDAI1_TOBAC	P93400 nicotiana t
760	30	65.2	504	2	Q75BD0_ASHGO	Q75bd0 ashbya goss	833	30	65.2	809	2	Q9AWC0_LYCSES	Q9awc0 lycopersico
761	30	65.2	507	2	Q25192_HELPY	Q25192 hellicobacte	834	30	65.2	809	2	Q9SDZ6_LYCSES	Q9sdz6 lycopersico

835	30	65.2	831	2	Q4ZXZ4_PSESY	Q4zxz4 pseudomonas	908	29	63.0	87	2	Q8PBL7_XANCP	Q8pbl7 xanthomonas
836	30	65.2	833	1	DL_DROME	P10041 dirosophila	909	29	63.0	89	2	Q9UYT7_PYRAB	Q9uyt7 pyrococcus
837	30	65.2	860	2	Q5EAM4_XENIA	O5eaa4 xenopus lae	910	29	63.0	89	2	Q8D2X9_WIGGR	Q8d2x9 wigglewort
838	30	65.2	861	1	GCR3_YEAST	P34160 saccharomyc	911	29	63.0	90	2	Q97B89_THENO	Q97b89 thermo
839	30	65.2	889	2	Q8RZJ2_ORYSA	O8rjz2 oryza sativ	912	29	63.0	96	2	Q50NH7_ENTHI	Q50nh7 entameoba
840	30	65.2	890	2	O8IBFI_PLAF7	O8ibfi plasmodium	913	29	63.0	101	2	Q6EB67_CAMJE	Q6eb67 campylobact
841	30	65.2	903	2	Q6ZJL7_ORYSA	Q6zjl7 oryza sativ	914	29	63.0	103	2	Q74B42_GEOGL	Q74b42 geobacter s
842	30	65.2	911	2	Q7RJD2_PLAYO	Q7rjd2 plasmodium	915	29	63.0	103	2	Q9J888_9NUCL	Q9j888 spodoptera
843	30	65.2	914	1	GUX2_CLOSR	P50900 clostridium	916	29	63.0	106	2	Q8SD12_9CAUD	Q8sd12 pseudomonas
844	30	65.2	922	2	Q4I2N6_GIBZE	Q4i2n6 gibberella	917	29	63.0	122	2	Q4X7T6_PLACH	Q4x7t6 plasmodium
845	30	65.2	928	2	Q5URJ1_ORYSA	O5urj1 oryza sativ	918	29	63.0	123	2	Q6ZNP8_HUMAN	Q6znp8 homo sapien
846	30	65.2	938	2	Q7YYA2_CRYPV	Q7yya2 cryptospori	919	29	63.0	124	2	Q5YUJ3_NOCFA	Q5yuj3 nocardia fa
847	30	65.2	949	1	GCSF_BACTN	O8aam0 bacteroides	920	29	63.0	126	2	Q5DDY2_SCHJA	Q5ddy2 schistosoma
848	30	65.2	950	2	Q5PWC6_CHICK	O9pwc6 gallus gall	921	29	63.0	128	2	Q707H0_ECOLI	Q707h0 escherichia
849	30	65.2	962	2	Q5PBU1_AZOSB	O5pui1 azocars sp	922	29	63.0	130	1	R58_PHOPR	Q61va2 photobacter
850	30	65.2	964	2	O6BGS6_PARTE	O6bgs6 parametium	923	29	63.0	132	1	R58_BARRB	O62z2x bartonella
851	30	65.2	1002	1	EPHBS_CHICK	O07977 gallus gall	924	29	63.0	132	1	R58_BAROU	Q6z2d6 bartonella
852	30	65.2	1039	2	Q4FXD7_LEIMA	Q4fxd7 leishmania	925	29	63.0	132	2	Q4UWG7_XANCP	Q4uwg7 xanthomonas
853	30	65.2	1053	2	Q6AQX5_DESPS	O6aqx5 deesulitotale	926	29	63.0	132	2	Q8P7N3_XANCP	Q8p7n3 xanthomonas
854	30	65.2	1063	1	PDR1_YEAST	P12383 saccharomyc	927	29	63.0	135	2	Q5V739_HALMA	Q5v739 haloarcula
855	30	65.2	1074	2	Q7UOP5_RHOBA	Q7uop5 rhodospirell	928	29	63.0	139	2	Q8UOT5_PYRFU	O8uot5 pyrococcus
856	30	65.2	1088	2	Q9FZ59_ARATH	Q9fz59 arabidopsis	929	29	63.0	139	2	Q9VOC7_PYRAB	Q9voc7 pyrococcus
857	30	65.2	1095	2	Q41GT2_GIBZE	Q41gt2 gibberella	930	29	63.0	139	2	Q59043_PYRHO	O59043 pyrococcus
858	30	65.2	1101	2	Q54HP5_DICDI	O54hp5 dictyosteli	931	29	63.0	141	2	Q8DAR6_VIBVO	Q8dar6 vibrio vuln
859	30	65.2	1150	2	Q5VBX4_DROME	O5vbx4 dirosophila	932	29	63.0	144	2	Q89G84_BRUJA	Q89g84 bradyrhizob
860	30	65.2	1171	2	Q7VIM5_PROMP	Q7vims prochloroco	933	29	63.0	145	2	Q9HAT4_HUMAN	Q9hat4 homo saplen
861	30	65.2	1192	2	Q8H6B2_MAIZE	Q8hb22 zea mays (m	934	29	63.0	146	2	Q9E2L8_CYTJO	Q9e2l8 cytophaga j
862	30	65.2	1214	2	Q9LD60_ARATH	Q9ld60 arabidopsis	935	29	63.0	147	2	Q4SIU5_TETNG	Q4siu5 tetradon n
863	30	65.2	1231	2	Q4N305_THERP	Q4n305 thelteria p	936	29	63.0	150	2	Q7OLF0_PYTIRU	Q7olf0 acidianus f
864	30	65.2	1241	2	Q5CT95_CRYPV	Q5ct95 cryptospori	937	29	63.0	151	2	Q67ZG8_ARATH	Q67zg8 arabidopsis
865	30	65.2	1268	2	Q7WJN5_BORBR	Q7wn5 bordetella	938	29	63.0	151	2	Q9LRY6_ARATH	Q9lry6 streptomyce
866	30	65.2	1294	2	O8ZSS1_PYRAF	O8zss1 pyrobaculum	939	29	63.0	152	1	Q60GK6_STRLA	O60gk6 streptomyce
867	30	65.2	1304	2	Q6BHA1_DEBHA	Q6bha1 debaryomyc	940	29	63.0	153	2	SPRL_BACCR	O81ic2 bacillus ce
868	30	65.2	1310	2	Q5BSV8_EMENT	O5bsv8 aspergillus	941	29	63.0	153	2	Q7M144_VIRBY	Q7m144 vibrio vuln
869	30	65.2	1333	2	PUR4_DROME	P35421 dirosophila	942	29	63.0	154	2	Q8Z087_STRAN	Q8z087 streptomyce
870	30	65.2	1354	1	Q6NNY9_DROME	O6nny9 dirosophila	943	29	63.0	159	2	Q6NMD4_ARATH	Q6nmd4 arabidopsis
871	30	65.2	1373	2	Q69A94_LEUME	O69a94 leucocostoc	944	29	63.0	162	1	Y1432_METUA	Q58824 methanococ
872	30	65.2	1454	1	GTRC_STRMU	P13470 streptococc	945	29	63.0	163	2	Q87WL7_PSE9M	Q87wl7 pseudomonas
873	30	65.2	1455	1	Q9LCH3_STROR	Q9lch3 streptococc	946	29	63.0	162	2	Q6LWCI_PHOPR	O6lwc1 photobacter
874	30	65.2	1496	2	Q92626_HUMAN	Q92626 homo saplen	947	29	63.0	164	2	Q8DXF1_STRAS	Q8dxf1 streptococc
875	30	65.2	1520	2	Q665A3_YERPS	Q665a3 yerersinia ps	948	29	63.0	164	2	Q8E373_STRAS	Q8e373 streptococc
876	30	65.2	1543	2	Q9W406_DROME	Q9w406 dirosophila	949	29	63.0	165	2	Q4TRM5_PSPHN	Q4trm5 erythrobact
877	30	65.2	1553	1	TOP2A_CHICK	Q42130 gallus gall	950	29	63.0	169	2	Q746R2_GEOBL	Q746r2 geobacter s
878	30	65.2	1577	2	Q54178_STRGN	Q54178 streptococc	951	29	63.0	175	1	Y6ZG_YEAST	P53045 saccharomyc
879	30	65.2	1586	2	Q9DFB7_CHICK	Q9dfb7 gallus gall	952	29	63.0	176	2	Q96ZT8_SULJO	Q96zt8 sulfotoba h
880	30	65.2	1587	2	Q4ZPR3_PSESY	Q4zpr3 pseudomonas	953	29	63.0	176	2	Q5OU68_ENTHI	Q5ou68 entameoba
881	30	65.2	1631	2	Q7UWMI_RHOBA	Q7uwm1 rhodospirell	954	29	63.0	176	2	Q7NOJ6_CHRYO	Q7nqj6 chromobacte
882	30	65.2	1826	2	Q4SJAV_TETNG	Q4sja7 tetradon n	955	29	63.0	176	2	Q7POR2_CHRYO	Q7por2 chryobacte
883	30	65.2	1830	2	Q4QIK5_LEIMA	Q4qik5 leishmania	956	29	63.0	176	2	Q5UPK6_MIMIV	Q5upk6 mimivirus.
884	30	65.2	1994	2	O8LJX1_SORBI	O8ljx1 sorghum bic	957	29	63.0	182	2	Q8U3V3_PYRFU	Q8u3v3 pyrococcus
885	30	65.2	1998	2	O5CTG1_CRYHO	O5ctg1 cryptospori	958	29	63.0	187	2	Q9HAT3_HUMAN	Q9hat3 homo saplen
886	30	65.2	2025	2	O5CS88_CRYPV	O5cs88 cryptospori	959	29	63.0	187	2	Q6DEMO_BRARE	Q6dem0 brachydanio
887	30	65.2	2055	2	Q4UFU6_THEAN	Q4ufu6 theileria a	960	29	63.0	188	2	Q4N224_THERP	Q4n224 theileria p
888	30	65.2	2184	2	Q7KY09_DROME	Q7ky09 dirosophila	961	29	63.0	188	2	Q4J5N2_AZOVI	Q4j5n2 acrobacter
889	30	65.2	2263	2	Q9W0LO_DROME	Q9w0lo dirosophila	962	29	63.0	192	2	Q9ICD7_9HIV1	Q9icd7 human immun
890	30	65.2	2263	2	Q7KVDI_DROME	Q7kvd1 dirosophila	963	29	63.0	192	2	Q9ICHS_9HIV1	Q9ichs human immun
891	30	65.2	2337	2	O5SDZ2_DICDI	O5sdz2 dictyosteli	964	29	63.0	192	2	Q9J802_9HIV1	Q9j802 human immun
892	30	65.2	2343	2	Q4QIK3_LEIMA	Q4qik3 leishmania	965	29	63.0	192	2	Q9Q6H5_9HIV1	Q9q6h5 human immun
893	30	65.2	2384	2	Q4QIK4_LEIMA	Q4qik4 leishmania	966	29	63.0	193	2	Q4UYC4_XANCP	Q4uyc4 xanthomonas
894	30	65.2	2384	2	Q4PHU0_USTMA	Q4phu0 ustilago ma	967	29	63.0	193	2	Q8P5P7_XANCP	Q8p5p7 xanthomonas
895	30	65.2	2384	2	Q4PHU0_USTMA	Q4phu0 ustilago ma	968	29	63.0	194	2	Q8PH25_XANOR	Q8ph25 xanthomonas
896	30	65.2	3242	2	O6CWS8_KULUA	O6cws8 kluyveromyc	969	29	63.0	194	2	Q5H4A2_XANOR	Q5h4a2 xanthomonas
897	30	65.2	3242	2	O9V4N8_DROME	Q9v4n8 dirosophila	970	29	63.0	200	1	PLI1_TRIPL	Q57690 trimeresuru
898	30	65.2	4488	2	Q7JJD2_DROHY	Q7jjd2 dirosophila	971	29	63.0	202	2	Q8PYL1_METHA	Q8pyl1 methanosa
899	30	65.2	4727	2	O6GR92_MYCNO	O6gr92 mycoplasma	972	29	63.0	202	2	Q9ME56_BETVO	Q9me56 beta vulgar
900	30	65.2	6613	2	Q57UD4_9TRYF	Q57ud4 crypanosoma	973	29	63.0	204	2	Q6F443_PLUXX	Q6f443 pluteia xy
901	29	63.0	61	2	Q6EBJ3_BRARE	Q6ebj3 brachydanio	974	29	63.0	205	2	Q7MZN7_PHOHL	Q7mzn7 photorhabdu
902	29	63.0	71	2	O8KSVI_AZOSB	O8ksvi azospirillum	975	29	63.0	209	2	Q4NCY9_9MICC	Q4ncy9 acrobacter
903	29	63.0	73	2	O7YRZ5_BOSIN	O7yrz5 bos indicus	976	29	63.0	210	2	Q9UND2_SCHPO	Q9und2 schistosac
904	29	63.0	87	2	O7YRZ5_BOSIN	O7yrz5 bos indicus	977	29	63.0	210	2	Q7QRS9_SITALA	Q7qrs9 giardia lam
905	29	63.0	82	2	O7SL84_SUITO	O7sl84 sulfolobus	978	29	63.0	211	2	Q8A617_BACTN	Q8a617 bacteroides
906	29	63.0	87	2	Q4URY2_XANCP	Q4ury2 xanthomonas	979	29	63.0	213	1	KAD_RICPR	Q9zceb6 rickettsia
907	29	63.0	87	2	Q4URY2_XANCP	Q4ury2 xanthomonas	980	29	63.0	213	1	KAD_RICPR	Q9zceb6 rickettsia

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981      29      63.0      213      1      KAD_R1CTY      066w99_rickettsia
982      29      63.0      214      2      Q823T5_CHICV      082315_chlamydia
983      29      63.0      215      2      084255_CHLTR      084255_chlamydia t
984      29      63.0      215      2      Q9PKK1_CHLMU      09pkk1_chlamydia m
985      29      63.0      215      2      Q9Z8E4_CHLPM      09z8e4_chlamydia p
986      29      63.0      217      2      Q4HB28_PDEIO      04hb28_dennococcus
987      29      63.0      218      2      059374_PYRHO      059374_pyrococcus
988      29      63.0      218      2      Q701C9_ANGGA      0701c9_angococcus
989      29      63.0      218      2      Q61KJ3_PHOPR      061kj3_phocobacter
990      29      63.0      219      2      Q9V1X0_PYRAB      09v1x0_pyrococcus
991      29      63.0      219      2      Q9KD05_BACHD      09kd05_bacillus ha
992      29      63.0      224      2      Q583K4_TRYPP      0583k4_trypanosoma
993      29      63.0      226      2      0871F0_VIBPA      0871f0_vibrio para
994      29      63.0      228      2      Q6GA37_STPAR      06ga37_staphylococ
995      29      63.0      228      2      Q6GHR0_STPAR      06ghr0_staphylococ
996      29      63.0      228      2      Q7UMX2_RHOBA      07umx2_rhodospirell
997      29      63.0      228      2      Q7A136_STPAM      07a136_staphylococ
998      29      63.0      228      2      Q7A622_STPAM      07a622_staphylococ
999      29      63.0      228      2      Q99UT5_STPAM      099ut5_staphylococ
1000      29      63.0      229      2      Q51Q48_STILPO      051q48_silicibacter

ALIGNMENTS

RESULT 1
ID      Q8BXJ0_MOUSE PRELIMINARY;      PRT;      596 AA.
AC      Q8BXJ0;
DT      01-MAR-2003 (TrEMBLrel. 23, Created)
DT      01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT      01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE      Mus musculus 10 days neonate medulla oblongata cDNA, RIKEN full-length
DE      enriched library, clone:B830028B07 product:SPlicing FACTOR 3B SUBUNIT
DE      3 (SPlicing FACTOR SFR3B 130 kDa SUBUNIT) homolog.
GN      Name=SF3b3; Synonyms=D8Ert633e;
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC      Muridae; Murinae; Mus.
OX      NCBI_Taxid=10090;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
RC      MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA      Carninci P., Hayashizaki Y.;
RA      "High-efficiency full-length cDNA cloning.";
RA      Meth. Enzymol. 303:19-44(1999).
RN      [2]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
RC      MEDLINE=2108560; PubMed=11217851; DOI=10.1038/35055500;
RA      Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA      Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA      Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA      Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,
RA      Kadota K., Matuda H.A., Ashburner M., Batalov S., Casavant T.,
RA      Fleischmann W., Gaasterland T., Gissi C., King B., Kocula H.,
RA      Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA      Schriml L.M., Stabli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA      Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,
RA      Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA      Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA      Gustincich S., Hill D., Holman M., Hume D.A., Kamaya M., Lee N.H.,
RA      Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombarts P.,
RA      Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA      Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA      Suzuki H., Toyokawa K., Wang K.H., Weitz C., Whitaker C., Willing L.,
RA      Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohseki S.,
RA      Hayashizaki Y.;
RT      "Functional annotation of a full-length mouse cDNA collection.";
RL      Nature 409:685-690(2001).

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RN      [3]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
RC      The FANTOM Consortium;
RA      "The RIKEN Genome Exploration Research Group Phase I & II Team;
RA      "Analysis of the mouse transcriptome based on functional annotation of
RT      60,770 full-length cDNAs.";
RL      Nature 420:563-573(2002).
RN      [4]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
RC      MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA      Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA      Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT      "Normalization and subtraction of cap-trapper-selected cDNAs to
RT      prepare full-length cDNA libraries for rapid discovery of new genes.";
RL      Genome Res. 10:1617-1630(2000).
RN      [5]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
RC      MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA      Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA      Konno H., Akiyama J., Nishi K., Katsunai T., Tashiro H., Itoh M.,
RA      Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA      Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA      Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
RA      Yoneda Y., Iehikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA      Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT      "RIKEN integrated sequence analysis (RISA) system-384-format
RT      sequencing pipeline with 384 multicapillary sequencer.";
RL      Genome Res. 10:1757-1771(2000).
RN      [6]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
RC      Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA      Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA      Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirokane T.,
RA      Horii F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA      Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA      Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA      Nishi K., Nomura K., Nomazaki R., Ono M., Ohsato N., Okazaki Y.,
RA      Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sato H.,
RA      Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA      Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA      Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL      Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AK046845; BAC32894.1; -; mRNA.
DR      WGI; WGI:1289341; SF3B3.
DR      InterPro; IPR003006; IG_MHC.
DR      PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ      SEQUENCE      596 AA;      66023 MW;      3882AF2147258785 CRC64;

Query Match      82.6%;      Score 38;      DB 2;      Length 596;
Best Local Similarity      75.0%;      Pred. No. 46;
Matches      6;      Conservative      2;      Mismatches      0;      Indels      0;      Gaps      0;
Db      324 ERLKTFD 331

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RESULT 2
ID      Q6ZOL0_MOUSE PRELIMINARY;      PRT;      1122 AA.
AC      Q6ZOL0;
DT      05-JUL-2004 (TrEMBLrel. 27, Created)
DT      05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT      05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE      MKIA0017 protein (Fragment).
GN      Name=SF3b3; Synonyms=mkIAA0017;
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

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OC Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryonic tail;
RX PubMed=14621295;
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoaka S.,
RA Suga Y., Nagase T., Ohara O., Koga H.;
RT "Prediction of the coding sequences of mouse homologues of KIAA gene:
RT III. the complete nucleotide sequences of 500 mouse KIAA-homologous
RT cDNAs identified by screening of terminal sequences of cDNA clones
RT randomly sampled from size-fractionated libraries.";
RL DNA Res. 10:167-180(2003).
DR EMBL; AK129035; BAC97845.1; -.
DR MGI; MGI:1289341; Sflb3.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003676; P:nucleic acid binding; IEA.
DR InterPro; IPR004871; CPGS_A.C.
DR Pfam; PF03178; CPGS_A; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT NON TER
SO SEQUENCE 1122 AA; 12533 MW; 1BD89B7D0DB5E20B CRC64;

Query Match 82.6%; Score 38; DB 2; Length 1122;
Best Local Similarity 75.0%; Pred. No. 95;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVRLRYFD 8
DB 324 EIRLRYFD 331

RESULT 3
ID Q4T237.TEING PRELIMINARY; PRT; 1171 AA.
AC Q4T237;
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE Chromosome undetermined SCAF10345, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG0008515001;
OS Tetradon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetradon.
OX NCBI_TaxId=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jallou O., Aury J.M., Brunet F., Petit J.L., Strange-Thomann N.,
RA Mauceli E., Bouteau L., Fischer C., Orouf-Costar C., Bernot A.,
RA Nicud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
RA Biemont C., Shalli Z., Catolico L., Poullain J., De Bernardis V.,
RA Chruad C., Duprat S., Broctier P., Coutanceau J.P., Guzy J.,
RA Parra G., Lartier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Westrov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Landet P., Schachter V., Queller F., Saurin W., Scarpelli C.,
RA Winkler P., Lander E.S., Weissbach J., Roest Crolians H.;
RT "Genome duplication in the teleost fish Tetradon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-951(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope, Whitehead Institute Centre for Genome Research,
RG Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.

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DR EMBL; CAAB01010345; CAP93045.1; -; Genomic_DNA.
FT NON TER 1171 1171
SQ SEQUENCE 1171 AA; 129293 MW; 300B47C84353DC5 CRC64;

Query Match 82.6%; Score 38; DB 2; Length 1171;
Best Local Similarity 75.0%; Pred. No. 99;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVRLRYFD 8
DB 324 EIRLRYFD 331

RESULT 4
SF3B3 HUMAN
ID SF3B3 HUMAN STANDARD; PRT; 1217 AA.
AC Q15993; Q8U029; (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Splicing factor 3B subunit 3 (Spliceosome associated protein 130) (SAP
DE 130) (SF3b130) (pre-mRNA splicing factor SF3b 130 kDa subunit)
DE (S7AF130).
GN Name=SF3B3; Synonyms=KIAA0017, SAP130;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxId=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX MEDLINE=99421963; PubMed=10490618;
RA Das B.K., Xia L., Palandjian L., Gozani O., Chyung Y., Reed R.;
RT "Characterization of a protein complex containing spliceosomal
RT proteins saps 49,130,145 and 155 ";
RL Mol. Cell. Biol. 19:6796-6802(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Bone marrow;
RX MEDLINE=96051387; PubMed=7584026;
RA Nomura N., Miyajima N., Sazuka T., Tanaka A., Kawarabayashi Y.,
RA Sato S., Nagase T., Seki N., Ishikawa K.-I., Tabata S.;
RT "Prediction of the coding sequences of unidentified human genes. I.
RT The coding sequences of 40 new genes (KIAA0001-KIAA0040) deduced by
RT analysis of randomly sampled cDNA clones from human immature myeloid
RL cell line KG-1.";
RL DNA Res. 1:27-35(1994).
RN [3]
RP SEQUENCE REVISION.
RA Nomura N.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP PARTIAL PROTEIN SEQUENCE, AND IDENTIFICATION IN THE STAG COMPLEX WITH
RP SF3B3; GNC5L; KIAA0764; TAF5L; TAF6L; TADA3L; TAF10; TRAP; TAF12 AND
RP TAP9.
RX MEDLINE=21448975; PubMed=11564863;
RX DOI=10.1128/MCB.21.20.6782-6795.2001;
RA Martiniz E., Palhan V.B., Tjernberg A., Lyman E.S., Camper A.M.,
RA Kundu T.K., Chait B.T., Roeder R.G.;
RT "Human STAGA complex is a chromatin-acetylating transcription
RT coactivator that interacts with pre-mRNA splicing and DNA damage-
RT binding factors in vivo.";
RL Mol. Cell. Biol. 21:6782-6795(2001).
RN [5]
RP -1- FUNCTION: Subunit of the splicing factor SF3B required for 'A'
RP complex assembly formed by the stable binding of U2 snRNP to the
RP branchpoint sequence (BPS) in pre-mRNA. Sequence independent
RP binding of SF3A/SF3B complex upstream of the branch site is
RP essential, it may anchor U2 snRNP to the pre-mRNA. May also be
RP involved in the assembly of the 'B' complex. Belongs also to the
RP minor U12-dependent spliceosome, which is involved in the splicing
RP of rare class of nuclear pre-mRNA intron.
CC -1- SUBUNIT: Component of splicing factor SF3B which is composed of
CC four subunits; SF3B4/SAP49, SF3B3/SAP130, SF3B2/SAP145,
CC

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CC SF3B1/SAP155. SF3B associates with the splicing factor SF3A and a
CC 12S RNA unit to form the U2 small nuclear ribonucleoproteins
CC complex (U2 snRNP). Interaction between SF3B3 and SF3B1 is tighter
CC than the interaction between SF3B3 and SF3B2. Component of the
CC STRGA transcription coactivator-HNT complex, at least composed of
CC SF3B3/SAP130, GCN5L2, SYAF5gamma/KIAA0764, TAF5L, TADA3L,
CC TAF10, TAF12, TRRAP and TAF9.
CC -1- INTERACTION:
CC P08633:HCK; NBEXP=1; InAct=EBI-346977, EBI-346340;
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: Belongs to the RSEI family.
CC -----
CC This Swiss-Prot entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL, AJ001443; CAB56791.1; -, mRNA.
CC EMBL, D87686; BAA32662.2; ALT INIT. mRNA.
CC EMBL, D13642; BAA02805.1; -, tRNA.
CC InAct; Q15393; -.
CC DR Ensembl; ENSG00000189091; Homo sapiens.
CC DR HGNC; HGNC:10770; SF3B3.
CC DR H-InvDB; HIX0013202; -.
CC DR Reactome; Q15393; -.
CC MIM; 605523; -.
CC DR GO; GO:0030532; C:small nuclear ribonucleoprotein complex; TAS.
CC DR GO; GO:0005681; C:spliceosome complex; TAS.
CC DR GO; GO:0031202; F:RNA splicing factor activity, transsterifi. .; TAS.
CC DR GO; GO:0006397; F:RNA processing; TAS.
CC DR GO; GO:0006461; P:protein complex assembly; TAS.
CC DR GO; GO:0008380; P:RNA splicing; TAS.
CC DR InterPro; IPR004871; CPSF_A_C.
CC DR Pfam; PF03178; CPSF_A; 1.
CC DR Direct protein sequencing; mRNA processing; mRNA splicing;
CC Nuclear protein; Spliceosome.
CC KW CONFLICT 193 193 G -> D (in Ref. 2).
CC FT CONFLICT 302 302 W -> L (in Ref. 2).
CC FT CONFLICT 193 193 W -> L (in Ref. 2).
CC SQ SEQUENCE 1217 AA; 135592 MW; 9A02875099A03B5E CRC64;

Query Match 82.6%; Score 38; DB 1; Length 1217;
Best Local Similarity 75.0%; Pred. No. 1e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVRLKPYD 8
Db 324 EIRLKPYD 331

RESULT 5
Q6NT18_HUMAN PRELIMINARY; PRT; 1217 AA.
AC Q6NT18;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Splicing factor 3b, subunit 3, 130kDa.
GN Name=SF3B3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBT_TaxID=9606;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carrini P., Prange C.,
RA Rahn S.A., Loguella N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunatirne P.H.,
RA Richards S., Worley D.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.W., Maira M.A.,
RA "Generation and initial analysis of more than 15,000 full-length human
RA and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Skin;
RA Strausberg R.;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC068974; AAH68974.1; -, mRNA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR004871; CPSF_A_C.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF03178; CPSF_A; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 1217 AA; 135516 MW; 8EB34BF1E7D22AA CRC64;
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Query Match 82.6%; Score 38; DB 2; Length 1217;
Best Local Similarity 75.0%; Pred. No. 1e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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QY 1 EVRLKPYD 8
Db 324 EIRLKPYD 331
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RESULT 6
Q5RB15_PONPY PRELIMINARY; PRT; 1217 AA.
AC Q5RB15;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein DKFZp469G1915.
GN Name=DKFZp469G1915;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Pongo.
OX NCBT_TaxID=9600;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RG The German cDNA Consortium;
RA Koehrer K., Beyer A., Mewes H.W., Weill B., Amid C., Oeanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR858662; CAH90875.1; -, mRNA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR004871; CPSF_A_C.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF03178; CPSF_A; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
KW Hypothetical protein.
SQ SEQUENCE 1217 AA; 135503 MW; 8EF13748756F839 CRC64;
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```
Query Match 82.6%; Score 38; DB 2; Length 1217;
Best Local Similarity 75.0%; Pred. No. 1e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 EVRLRYFD 8
 Db 324 EIRLRYFD 331

RESULT 7
 Q921M3_MOUSE PRELIMINARY; PRT; 1217 AA.

Q921M3_MOUSE
 ID Q921M3_MOUSE PRELIMINARY; PRT; 1217 AA.
 AC Q921M3;
 DT 01-DEC-2001 (Tremblrel. 19, last sequence update)
 DT 10-MAY-2005 (Tremblrel. 30, last annotation update)
 DE Splicing factor 3b, subunit 3, 130kDa (Mus musculus 2 days neonate
 DE thymic thymic cells CDNA, RIKEN full-length enriched library,
 DE clone:R430008P19 product:SPICING FACTOR 3B SUBUNIT 3 (SPICEOSOME
 DE ASSOCIATED PROTEIN 130) (SAP 130) (SP3B130) (PRE-MRNA SPLICING FACTOR
 DE SP3B 130 kDa SUBUNIT) homolog).
 GN Name=Sp3b3;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 OX [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FVB/N;
 RC TISSUE=Eye, and
 RC Mammmary tumor. Metallothionien-TGF alpha model. 10 month old virgin
 RC mouse. Taken by biopsy.
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Narusina K., Farmer A.A., Rubin G.W., Hong L.,
 RA Stepleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rata S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,
 RA Villalón D.K., Mazny D.N., Sodergren E.U., Lu X., Gibbs R.A.,
 RA Fahey U., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzyzinski M.T., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FVB/N;
 RC TISSUE=Mammary tumor. Metallothionien-TGF alpha model. 10 month old
 RC virgin mouse. Taken by biopsy.
 RA Director MGC Project;
 RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Eye;
 RA Director MGC Project;
 RL Submitted (JAN-2003) to the EMBL/Genbank/DBJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOD; TISSUE=Thymus;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.,
 RT "High-efficiency full-length cDNA cloning."
 RL Mech. Enzymol. 303:19-44(1999).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOD; TISSUE=Thymus;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.I.,
 RA Saito T., Okazaki Y., Gojobori T., Bond H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi G., King B., Kochwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schmitt L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guernicich S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima Y., Mazzarelli J., Mombauer P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Saeki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kontecki S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOD; TISSUE=Thymus;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaide I., Otsu N., Saito R., Suzuki H., Yamana K.I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schoenbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schmitt L.M., Kanapin A., Matsuda H., Batalov S., Beisels K.W.,
 RA Blake J.A., Brad D., Bruce V., Chochia C., Corbini L.E., Cousins S.,
 RA Dalla E., Dargatz T.A., Fletcher C.F., Forrest A., Fraser K.S.,
 RA Gaasterland T., Gariboldi M., Gissi G., Godzik A., Gough J.,
 RA Grimmond S., Guernicich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lemhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numa K., Okido T., Pavan W.J., Pereira G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sadelain A., Schneider C., Sempile C.A., Setou M., Shimada K.,
 RA Sultana R., Takanaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yaunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.,
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 RN [7]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOD; TISSUE=Thymus;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes."
 RL Genome Res. 10:1617-1630(2000).
 RN [8]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOD; TISSUE=Thymus;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
 RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
 RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunaga S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,

RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT Sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771 (2000).
[9]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOB; TISSUE=Thymus;
RA Adachi J., Alzawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanaoka T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoch H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nihi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Satoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC011412; AAH11412.1; -; mRNA.
DR EMBL; BC042580; AAH42580.1; -; mRNA.
DR EMBL; AK088288; BAC04248.1; -; mRNA.
DR Ensemble; ENSMUSG00000033732; Mus musculus.
DR MGI; MGI:1289341; Sl3b3.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0005676; F:nucleic acid binding; IEA.
DR InterPro; IPR003006; C:PSF_A_C.
DR InterPro; IPR003006; I:PSF_A_C.
DR Pfam; PF03179; C:PSF_A; 1.
DR PROSITE; PS00290; I:G_MHC; UNKNOWN_1.
SQ SEQUENCE 1217 AA; 135549 MW; DD12A12CB8B23A CRC64;

Query Match 82.6%; Score 38; DB 2; Length 1217;
Best Local Similarity 75.0%; Pred. No. 1e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 EVRLRYFD 8
|:|:|:|:
DB 324 EIRLRKTFD 331

RESULT 8
Q8YZM1 ANASP PRELIMINARY; PRT; 470 AA.
AC Q8YZM1-
ID Q8YZM1-
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE A10436 protein.
GN Ordered locus names=alr0436;
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OC NCBI_TaxID=103690;
OK
RN
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Matenabe A., Iriuguchi M., Iehikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuda A., Muraki A.,
RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.,
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:205-213 (2001).
DR EMBL; BA000019; BAB72394.1; -; Genomic_DNA.
DR PIR; AC1861; AC1861.
KW Complete proteome.
SQ SEQUENCE 470 AA; 51599 MW; 838C25EFC05B7B1F CRC64;

Query Match 80.4%; Score 37; DB 2; Length 470;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 VRLRYFD 8

DB 407 VRLRYFD 413
|||||

RESULT 9
Q4SAX2 TETNG
ID Q4SAX2 TETNG PRELIMINARY; PRT; 598 AA.
AC Q4SAX2-
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome 3 SCAFL1679, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG0021223001.
OS Tetradon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthopterygia; Acanthopterygii; Perciformes; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetradon.
OX NCBI_TaxID=99883;
[1]
RP NUCLEOTIDE SEQUENCE.
RA Uallion O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bounneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Niclaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthonard V., Jubin C., Castelli V., Klinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cartolico L., Poulain J., De Bernardis V.,
RA Caraud C., Dupret S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan F., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Lander V., Schachter V., Quetier F., Sakin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.,
RT "Genome duplication in the teleost fish Tetradon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957 (2004).
[2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope, Whitehead Institute Centre for Genome Research;
RL Submitted (Feb-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAE0104679; CAG02210.1; -; Genomic_DNA.
FT NEM TER 598
SQ SEQUENCE 598 AA; 63513 MW; 9BB4F9B11D9C8786 CRC64;

Query Match 80.4%; Score 37; DB 2; Length 598;
Best Local Similarity 77.8%; Pred. No. 76;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 EVRLRYFDV 9
|:|:|:|:
DB 376 EIRLRKTFD 384

RESULT 10
PDDAI_VTGN
ID PDDAI_VTGN STANDARD; PRT; 809 AA.
AC 004865;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Phospholipase D alpha 1 (EC 3.1.4.4) (PLD alpha 1) (Choline
DE phosphatase 1) (Phosphatidylcholine-hydrolyzing phospholipase D 1).
GN Name=PDD1;
OS Vigna unguiculata (Cowpea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC Rosids; eustosids I; Fabales; Fabaceae; Papilionoideae; Phaseolae;
OX NCBI_TaxID=3917;


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RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=cv. Bspace-1; TISSUE=leaf;
RA el Maarouf H., Pham Thi A.T., Garell M., D'Arcy-Lameta A.,
RA Zuliy-Fodil Y.,
RA Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Hydrolyzes glycerol-phospholipids at the terminal
CC phosphodiesteric bond. Plays an important role in various cellular
CC processes.
CC -1- CATALYTIC ACTIVITY: A phosphatidylcholine + H(2)O = choline + a
CC phosphatidate.
CC -1- COFACTOR: Calcium (By similarity).
CC -1- DOMAIN: C2 domain is a calcium-binding fold, and the binding
CC promotes the protein association with membranes. A lower affinity
CC toward calcium can be anticipated for PLD alpha due to the absence
CC of two potential calcium ligands.
CC -1- SIMILARITY: Belongs to the phospholipase D family. C2-PLD
CC subfamily.
CC -1- SIMILARITY: Contains 1 C2 domain.
CC -1- SIMILARITY: Contains 2 PLD phosphodiesterase domains.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL, U92656; AAB51392.1; -; mRNA.
CC PIR, T11695; T11695.
CC InterPro, IPR000008; C2.
CC InterPro, IPR011736; PLD.
CC InterPro, IPR011402; PLD_plant.
CC Pfam, PF00168; C2; 1.
CC PIRSF, PIRSF036470; PLD_plant; 1.
CC SMART, SM00155; PLDC; 2.
CC DR SMART; SM00155; PLDC; 2.
CC DR PROSITE, PSS0004; C2 DOMAIN; FALSE_NEG.
CC DR PROSITE, PSS0035; PLD; 2.
CC KM Calcium, Hydrolase; Lipid degradation; Repeat.
CC FT DOMAIN 1 109 C2.
CC FT DOMAIN 326 365 PLD phosphodiesterase 1.
CC FT DOMAIN 655 682 PLD phosphodiesterase 2.
CC FT ACT_SITE 331 331 Potential.
CC FT ACT_SITE 333 333 Potential.
CC FT ACT_SITE 338 338 Potential.
CC FT ACT_SITE 660 660 Potential.
CC FT ACT_SITE 662 662 Potential.
CC FT ACT_SITE 667 667 Potential.
CC SQ SEQUENCE 809 AA; 91565 MW; 4E9F0B634DD946 CRC64;

Query Match 80.4%; Score 37; DB 1; Length 809;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VRLRYFDV 9
Db 143 VRLQYFDV 150

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RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15746427; DOI=10.1126/science.1107008;
RA Cerdeno-Tarraga A.-M., Patrick S., Crossman L.C., Blakely G.,
RA Abratt V., Lemard N., Foxton I., Duerden B., Harris B., Quail M.A.,
RA Barron A., Clark L., Cotton I., Doggett J., Holden M.T.G., Larke N.,
RA Line A., Lord A., Nodbertczak H., Ormond C., Price C.,
RA Rabinowitsch E., Woodward J., Barrell B.G., Parkhill J.,
RT "Extensive DNA inversions in the B. fragilis genome control variable
RT gene expression".
RL Science 307:1463-1465 (2005).
CC EMBL, CR26927; CH07776.1; -; Genomic_DNA.
CC InterPro, IPR003437; GDC-P.
CC InterPro, IPR01547; Glyco_hydro_5.
CC Pfam, PF02347; GDC-P; 1.
CC TIGRFAMs, TIGR00461; gcvp; 1.
CC DR PROSITE, PSS0659; GLYCOSYL_HYDROL_F5; UNKNOWN_1.
CC KW Complete proteome; Oxidoreductase.
CC SQ SEQUENCE 949 AA; 104591 MW; DFC4995CFE151D CRC64;

Query Match 80.4%; Score 37; DB 2; Length 949;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EVRLRYFD 8
Db 408 EVNLRYFD 415

RESULT 12
ID 064U07 BACFR PRELIMINARY; PRT; 949 AA.
AC 064U07;
DT 25-OCT-2004 (TRENBLrel. 28, Created)
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE Glycine dehydrogenase.
DE Glycine dehydrogenase.
GN Ordered locus names=BF2025;
OS Bacteroides fragilis.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=817;
(1)
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=YCH46;
RX PubMed=15466707; DOI=10.1073/pnas.0404172101;
RA Kuwahara T., Yamashita A., Hitekawa H., Nakayama H., Toh H., Okada N.,
RA Kuhara S., Hattori M., Hayashi T., Ohnishi Y.,
RT "Genomic analysis of Bacteroides fragilis reveals extensive DNA
RT inversions regulating cell surface adaptation".
RL Proc. Natl. Acad. Sci. U.S.A. 101:14919-14924 (2004).
CC EMBL, AP006841; BAD48772.1; -; Genomic_DNA.
CC GO, GO:0005961; C:glycine dehydrogenase complex (decarboxylat. .; IEA.
CC DR GO, GO:0004375; C:glycine dehydrogenase (decarboxylating) act. .; IEA.
CC DR GO, GO:0016491; F:oxidoreductase activity; IEA.
CC DR GO, GO:0006544; P:glycine metabolism; IEA.
CC DR InterPro, IPR003437; Glyco_hydro_5.
CC DR InterPro, IPR001547; GDC-P.
CC DR Pfam, PF02347; GDC-P; 1.
CC DR TIGRFAMs, TIGR00461; gcvp; 1.
CC DR PROSITE, PSS0659; GLYCOSYL_HYDROL_F5; UNKNOWN_1.
CC KW Complete proteome.
CC SQ SEQUENCE 949 AA; 104679 MW; 8826948720335871 CRC64;

Query Match 80.4%; Score 37; DB 2; Length 949;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EVRLRYFD 8
Db 408 EVNLRYFD 415

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RESULT 13
OSJIDS_PYRKO PRELIMINARY; PRT; 331 AA.
ID OSJIDS5;
AC OSJIDS5;
DT 10-MAY-2005 (TREMBlrel. 30, Created)
DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)
DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)
N2, N2-dimethylguanosine tRNA methyltransferase.
GN OrderedCusNames=TK0981;
OS Pyrococcus kodakarensis (Thermococcus kodakarensis).
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Thermococcus.
NCBI_TaxID=69014;
[1]
RP NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA).
RC STRAIN=KOD1;
RX PubMed=15710748; DOI=10.1101/gr.3003105;
RA Fukui T., Atom T., Kanai T., Matsumi R., Fujiwara S., Imanaka T.;
RT "Complete genome sequence of the hyperthermophilic archaeon
Thermococcus kodakarensis KOD1 and comparison with Pyrococcus
genomes.";
RL Genome Res. 15:352-363 (2005).
DR EMBL; AP006878; BAD85170.1; -; Genomic DNA.
DR GO; GO:0003677; F.DNA binding; IEA.
DR GO; GO:0008170; F.N-methyltransferase activity; IEA.
DR GO; GO:0008757; F.S-adenosylmethionine-dependent methyltransf. . .; IEA.
DR GO; GO:0016740; F.transferrase activity; IEA.
DR GO; GO:0006306; P.DNA methylation; IEA.
DR InterPro; IPR005885; CHP117.
DR InterPro; IPR002296; N12M6_mtfase.
DR InterPro; IPR002052; N6_Mtase.
DR InterPro; IPR000241; RNA_methylase.
DR InterPro; IPR000051; SAM_bd.
DR InterPro; IPR004114; THUMP.
DR Pfam; PF02926; THUMP; 1.
DR Pfam; PF01170; UPF0020; 1.
DR PRINTS; PR00507; N12M6MTRFAS.
DR TIGRFAMs; TIGR01177; Cons_hypoch1177; 1.
DR PROSITE; PS00092; N6_MTASE; UNKNOWN 1.
KW Complete proteome; Methyltransferase; Transferrase.
SQ
SEQUENCE 331 AA; 37443 MW; 5DBBEPF57CCG0 CRC64;

Query Match 78.3%; Score 36; DB 2; Length 331;
Best Local Similarity 85.7%; Pred. No. 63;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VRLRYFD 8
Db 139 IRLRYFD 145

RESULT 14
OSLJYO_DROME PRELIMINARY; PRT; 440 AA.
ID OSLJYO;
AC OSLJYO;
DT 01-FEB-2005 (TREMBlrel. 29, Created)
DT 01-FEB-2005 (TREMBlrel. 29, Last sequence update)
DT 01-FEB-2005 (TREMBlrel. 29, Last annotation update)
DE CG40146-PB.3;
GN ORFNames=CG40146;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
[1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426065; PubMed=12537568;
RA Celinker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA Pacled J.W., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svrtkac R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
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RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
[2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426071; PubMed=12537574;
RA Hoskins R.A., Smith C.D., Carlson J.W., Carvalho A.B., Halpern A.,
RA Kaminker J.S., Kennedy C., Mungall C.J., Sullivan B.A., Sutton G.G.,
RA Yasuhara J.C., Wakimoto B.T., Myers E.W., Celinker S.E., Rubin G.M.,
RA Karpen G.H.;
RT "Heterochromatic sequences in a Drosophila whole-genome shotgun
assembly.";
RL Genome Biol. 3:RESEARCH0085.1-RESEARCH0085.16(2002).
[3]
RP NUCLEOTIDE SEQUENCE.
RA Adams M.D., Holt R.A., Evans C.A., Gocayne J.D., Amaratilake P.G.,
RA Li P.W., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D.,
RA Zhang Q., Chen L.X., Brandon R.C., Rogers Y.H., An H.J.,
RA Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Bau A., Baxendale J.,
RA Beasley E.M., Beeson K.Y., Bhandari D., Bolanos R.A., Bousam D.A.,
RA Center A., Chandrasekhar I., Dahlke C., Davenport L.B., Davies P.,
RA Delecher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K.,
RA Doup L.E., Dunn P., Evangelista C.C., Ferreria S., Flanagan M.J.,
RA Foster C., Gabrielian A.E., Garg N.S., Glasser K., Glodex A., Gong F.,
RA Gu Z., Guan P., Halpern A.L., Harris M., Heiman T.J., Houck J.,
RA Hoslin D., Howland T.J., Wei M.H., Idegawa C., Jalali M., Kalush F.,
RA Ke Z., Keichun K.A., Kodira C.D., Kraft C., Kravitz S., Lai Z.,
RA Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X.,
RA Matel B., McIntosh T.C., McPherson D., Merkulov G., Miller J.R.,
RA Milshina N.V., Mobarry C., Moy M., Murphy B., Nelson K.A.,
RA Nuskern D.R., Pittman G.S., Pan S., Pollard J., Puri V., Reinert K.,
RA Remington K., Scheeler F., Shue B.C., Siden-Kiamos I., Simpson M.,
RA Skupski M.P., Smith T., Spier E., Strong R., Sun E., Tector C.,
RA Turner R., Venter E., Wang A.H., Wang X., Wang Z.Y., Williams S.M.,
RA Woodao T., Wu D., Xiao Q.A., Ye J., Zaveri U.S., Zhan M., Zhang G.,
RA Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhu S., Zhu X.,
RA Smith H.O., Myers E.W., Venter J.C.;
RT "Drosophila melanogaster Heterochromatic Scaffold.";
RL Submitted (DEC-2002) to the EMBL/Genbank/DBJ databases.
[4]
RP NUCLEOTIDE SEQUENCE.
RA Smith C.D., Acevedo D., Carlson J.W., Hoskins R.A., Kennedy C.,
RA Mungall C.J., Yandell M.D., Celinker S.E., Karpen G.H.;
RT Submitted (AUG-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL; AABU01002702; BAL24595.1; -; Genomic DNA.
DR GO; GO:0016021; C.integral to membrane; IEA.
DR InterPro; IPR004837; NacCa_Exmemb.
DR Pfam; PF01699; Na_Ca_ex; 2.
SQ
SEQUENCE 440 AA; 48318 MW; D76080E020F36E5 CRC64;

Query Match 78.3%; Score 36; DB 2; Length 440;
Best Local Similarity 87.5%; Pred. No. 87;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EVRLRYFD 8
Db 36 EVSLRYFD 43

RESULT 15
O7PLW4_DROME PRELIMINARY; PRT; 441 AA.
ID O7PLW4;
AC O7PLW4;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE CG40146-PA.3.
GN ORFNames=CG40146;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
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NCBI_TaxId=7227;
[1]
NUCLEOTIDE SEQUENCE.
MEDLINE=22426065; PubMed=12537568;
Celinker S.B., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champagne M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R., Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodegryn E.J., Svirskas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
"Finishing a whole-genome shotgun: release 3 of the Drosophila melanogaster euchromatic genome sequence."
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
[2]
NUCLEOTIDE SEQUENCE.
MEDLINE=22426071; PubMed=12537574;
Hoskins R.A., Smith C.D., Carlson J.W., Carvalho A.B., Halpern A., Kaminker J.S., Kennedy C., Mungall C.J., Sullivan B.A., Sutton G.G., Yasuhara J.C., Wakimoto B.T., Myers E.W., Celinker S.E., Rubin G.M., Karpen G.H.;
"Heterochromatic sequences in a Drosophila whole-genome shotgun assembly."
Genome Biol. 3:RESEARCH0085.1-RESEARCH0085.16(2002).
[3]
NUCLEOTIDE SEQUENCE.
Adams M.D., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Li P.W., Henderson S.N., Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.H., An H.J., Baxendale J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Beasley E.M., Beeson K.Y., Bhandari D., Bolanos R.A., Busam D.A., Center A., Chandrasekhar I., Dahlke C., Davenport L.B., Davies P., Deleter A., Deng Z., Dew I., Dietz S.M., Dodson K., Doup L.E., Dunn P., Evangelista C.C., Ferriera S., Flanigan M.J., Foster C., Gabrielian A.E., Garg N.S., Glasser K., Glodok A., Gong F., Gu Z., Guan P., Halpern A.L., Harris M., Heiman T.J., Houck J., Hostin D., Howland T.J., Wei M.H., Ibegwam C., Jalali M., Kalush F., Ke Z., Ketchum K.A., Kodira C.D., Kraft C., Kravitz S., Lai Z., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Lin X., Mattei B., McIntosh T.C., McPherson D., Merkulov G., Miller J.R., Milshina N.V., Mobarry C., Moy M., Murphy B., Nelson K.A., Nusken D.R., Peltman G.S., Pan S., Pollard J., Puri V., Reinert K., Remington D.R., Scheeler F., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Strong R., Sun E., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.Y., Williams S.M., Woodage T., Wu D., Yao Q.A., Ye J., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhu S., Zhu X., Smith H.O., Myers E.W., Venter J.C.;
"Drosophila melanogaster Heterochromatic Scaffold."
Submitted (DEC-2002) to the EMBL/Genbank/DBJ databases.
[4]
NUCLEOTIDE SEQUENCE.
Smith C.D., Acevedo D., Carlson J.W., Hoskins R.A., Kennedy C., Mungall C.J., Yandell M.D., Celinker S.E., Karpen G.H.;
Submitted (AUG-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL; AABU01002702; EAA46196.1; -; Genomic DNA.
DR Ensembl; CG40146; Drosophila melanogaster.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR004837; NaCa_Exemb.
DR Pfam; PF01699; Na_Ca_ex_2.
SQ SEQUENCE 441 AA; 48389 MW; 111105E629619238 CRC64;
Query Match 78.3%; Score 36; DB 2; Length 441;
Best Local Similarity 87.5%; Pred. No. 87;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 16
Q9U0H5_PLAF7 PRELIMINARY; PRT; 722 AA.
ID Q9U0H5_PLAF7 PRELIMINARY; PRT; 722 AA.

AC Q9U0H5;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein PFD0545w.
GN Name=PFD0545w;
OC Plasmodium falciparum (Isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxId=36329;
[1]
NUCLEOTIDE SEQUENCE.
MEDLINE=22255708; PubMed=12368667; DOI=10.1038/nature01095;
Hall N., Pain A., Berriman M., Churcher C., Harris B., Harris D., Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K., Buckee C.O., Burrows C., Cherevach I., Chillingworth A., Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C., Cronin A., Davies R., Davis P., Dear P., Dearden F., Doggett J., Felwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z., Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P., Humphrey S., Jagels K., James K.D., Johnson D., Kerhornou A., Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N., Line A., Maddison M., McLean J., Mooney P., Moule S., Murphy L., Oliver K., Ormond D., Price C., Quail M.A., Rabinowitsch E., Rajandream M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M., Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens K., Taylor K., Tivey A., Unwin I., Whitehead S., Woodward J., Sulston J.E., Craig A., Newbold C., Barrell B.G.;
"Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13."
Nature 419:527-531(2002).
[2]
NUCLEOTIDE SEQUENCE.
Devlin K., Pain A., Berriman B., Hall N., Bowman S., Churcher C., Harris B., Harris D., Lawson D., Quail M., Barrell B.;
Submitted (FEB-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL; AL035475; CAB62888.1; -; Genomic DNA.
KW Hypothetical protein.
SQ SEQUENCE 722 AA; 86440 MW; C37213DB81C3BC7E CRC64;
Query Match 78.3%; Score 36; DB 2; Length 722;
Best Local Similarity 55.6%; Pred. No. 1.5e+02;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

RESULT 17
RSB1 SCHPO
ID RSB1 SCHPO STANDARD; PRT; 1206 AA.
AC Q9UTJ2;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Pre-mRNA splicing factor rsel (Pre-mRNA processing protein 12) (Spliceosome associated protein 130).
GN Name=prp12; Synonyms=sap130; ORFNames=prp1298.03c; Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxId=4896;
[1]
NUCLEOTIDE SEQUENCE (GENOMIC DNA), FUNCTION, AND SUBCELLULAR LOCATION.
PubMed=11350031;
Habara Y., Urushiyama S., Shibuya T., Ohshima Y., Tani T.;
"Mutation in the prp12+ gene encoding a homolog of SAPI30/SEB130 RT causes differential inhibition of pre-mRNA splicing and arrest of cell cycle progression in Schizosaccharomyces pombe."
RNA 7:671-681(2001).
[2]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=972;

RA MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
RA Wood V., Gilliam R., Rajandream M.A., Lyne M.H., Lyne R., Stewart A.,
RA Sgouras J.G., Peat N., Hayles J., Baker S.G., Basham S., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D.E., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornby T., Howarth S., Huckle E.J., Hunt S., Jagsis K.,
RA James K.D., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney K., Moutle S., Mungall K.L., Murphy L.D., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabbittowles E.,
RA Rutherford K.M., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M.N., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J.R., Volkhardt G., Aert R., Robben J., Gymnopoulos E.,
RA Wellens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Duesterhoeft A., Fritz C., Holzer E., Moestl D.,
RA Hilbert H., Borzym K., Langer I., Beck A., Lehrich H., Reinhardt R.,
RA Pohl T.M., Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreno S., Gloux S., Lelaire V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forstberg S.L.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,
RA "The genome sequence of Schizosaccharomyces pombe.",
RA Nature 415:871-880(2002).
RN [3]
RP FUNCTION.
RP PubMed=9003295;
RA Urushiyama S., Tani T., Ohshima Y.;
RT "Isolation of novel pre-mRNA splicing mutants of Schizosaccharomyces
RT pombe.",
RT Mol. Genet. 253:118-127(1996).
RN [4]
RP MASS SPECTROMETRY, AND IDENTIFICATION IN THE CWF COMPLEX.
RX MEDLINE=2181936; PubMed=11884590;
RX DOI=10.1128/MCB.22.7.2011-2024.2002;
RA Ohl M.D., Link A.J., Ren L., Jennings J.L., McDonald W.H., Gould K.L.;
RT "Proteomic analysis reveals stable multiprotein complexes in both
RT fission and budding yeasts containing Myd-related Cdc5p/Cef1p, novel
RT pre-mRNA splicing factors, and snRNAs.",
RT Mol. Cell. Biol. 22:2011-2024(2002).
CC -1- FUNCTION: Involved in mRNA splicing and G2/M transition.
CC -1- SUBUNIT: Belongs to the 40S Cdc5-associated complex (or cwf
CC complex), spliceosome sub-complex, remnants of a late-stage
CC spliceosome composed of the U2, U5 and U6 snRNAs and at least
CC brr2, cdc5, cwf2, cwf3, cwf4, cwf5, cwf6, cwf7, cwf8, cwf9, cwf10,
CC cwf11, cwf12, cwf13, cwf14, cwf15, cwf16, cwf17, cwf18, cwf19,
CC cwf20, cwf21, cwf22, cwf23, cwf24, cwf25, cwf26, cwf27, cwf28,
CC iet3, iet4, mel1, prp5, prp10, prp12, prp17, prp22, sap61, sap62,
CC sap14, sap145, slt7, smd1, smd1, smd3, smf1, smf1 and syf2.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: Belongs to the RSE1 family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC DR EMBL, AB034966; BAA86918.1; -; Genomic DNA.
CC DR EMBL, AL556333; CAB92100.1; -; Genomic DNA.
CC DR InterAct, Q90TT2; -;
CC DR GeneDB, Spombe; SPAPJ698.03c; -;
CC DR InterPro, IPR004871; CPSP A.C.
CC DR Pfam, PF03178; CPSP A; 1. -;
CC DR Cell cycle: Complete proteome; mRNA processing; mRNA splicing;
CC Nucleic acid; Spliceosome.
CC KW SEQUENCE 1206 AA; 134972 MW; 88AC5252ADB7C47D CRC64;
CC SQ

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVRLRYFD 8
DB 343 EIRLMYFD 350
RESULT 18
ID Q802W7 BRARE PRELIMINARY; PRT; 1217 AA.
AC Q802W7;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Zgc:55440;
GN Name=ef3b3; ORFNames=zgc:55440;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AB; TISSUE=Whole body;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax B.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carlnici P., Prange C.,
RA Raha S.S., Loguelfano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,
RA Villalon D.K., Mizny D.M., Sodergren E.D., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schin J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.",
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AB; TISSUE=Whole body;
RA Strausberg R.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC047171; AAH47171.1; -; mRNA.
DR ZFIN, ZDB-GENE-040426-2901; ef3b3.
DR GO, GO:0005634; C:nucleus; IEA.
DR GO, GO:0003676; F:nucleic acid binding; IEA.
DR InterPro, IPR004871; CPSP A.C.
DR InterPro, IPR003006; IQ_MHC.
DR Pfam, PF03178; CPSP A; 1.
DR PROSITE, PS00290; IQ_MHC; UNKNOWN 1.
SQ SEQUENCE 1217 AA; 135587 MW; 014CA22E4DA8F3C CRC64;
CC

Query Match 78.3%; Score 36; DB 2; Length 1217;
Best Local Similarity 62.5%; Pred. No. 2.7e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVRLRYFD 8
DB 324 EIRLMYFD 331
RESULT 19
ID DARC_Y CHRVO STANDARD; PRT; 79 AA.
ID DARC_Y CHRVO
AC Q7NP06;

DT 13-SEP-2005 (rel. 48, Created)
DT 13-SEP-2005 (rel. 48, Last sequence update)
DT 13-SEP-2005 (rel. 48, Last annotation update)
DE Darcynin.
GN OrderedLocNames=Cv4311.
OS Chromobacterium violaceum.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Chromobacterium.
OX NCBI_TaxID=536;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 12472 / DSM 30191;
RX MEDLINE=22882880; PubMed=14500782; DOI=10.1073/pnas.1832124100;
RA Vasconcelos A.T.R., de Almeida D.F., Hungria M., Guimaraes C.T.,
RA Antonio R.V., Almeida F.C., de Almeida L.G.P., de Almeida R.,
RA Alves-Gomes J.A., Andrade E.M., Araripe J., de Araujo M.F.F.,
RA Astolfi-Filho S., Azevedo V., Baptista A.J., Bataus L.A.M.,
RA Batista J.S., Belo A., van den Berg C., Bogo M., Bonatto S.,
RA Bordignon J., Brígido M.M., Brito C.A., Brocchi M., Burity H.A.,
RA Camargo A.A., Cardoso D.D.P., Carneiro N.P., Carraro D.M.,
RA Carvalho C.M.B., Cascardo J.C.M., Cavada B.S., Chueire L.M.O.,
RA Czerzynski-Pasa T.B., Cunha-Junior N.C., Fagundes N., Falcao C.L.,
RA Fantinatti F., Farias I.P., Felipe M.S.S., Feriari L.P., Ferro J.A.,
RA Ferro M.I.T., Franco G.R., Freitas N.S.A., Furlan L.R.,
RA Gratzinelli R.T., Gomes E.A., Goncalves P.R., Grangefiro T.B.,
RA Gratzinelli R.T., Grisdar E.C., Hanna E.S., Jardim S.N., Laurino J.,
RA Leoi L.C.T., Lima L.F.A., Loureiro M.F., Lyra M.C.C.P.,
RA Madeira H.M.F., Manfio G.P., Maranhao A.Q., Martins W.S.,
RA di Mauro S.M.Z., de Medeiros S.R.B., Weisner R.V., Moreira M.A.M.,
RA Nascimento F.F., Nicolas M.F., Oliveira J.G., Oliveira S.C.,
RA Palciao R.F.C., Parente J.A., Pedrosa F.O., Pena S.D.J., Pereira J.O.,
RA Pereira M., Pinto L.S.R., Pinto L.S., Porto J.I.R., Portrich D.P.,
RA Ramalho-Neto C.E., Reis A.M.M., Rigo L.U., Rondinelli E.,
RA Santos E.B.P., Santos F.R., Schneider M.P.C., Senanez H.N.,
RA Silva A.M.R., da Silva A.L.C., Silva D.W., Silva R., Simoes I.C.,
RA Simon D., Soares C.M.A., Soares R.B.A., Souza E.M., Souza K.R.L.,
RA Souza R.C., Steffens M.B.R., Steindel M., Teixeira S.R., Urmenyi T.,
RA Vettore A., Massen R., Zaha A., Simpson A.J.G.,
RT "The complete genome sequence of Chromobacterium violaceum reveals
RT remarkable and exploitable bacterial adaptability.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:11660-11665(2003).
CC -i- SIMILARITY: Belongs to the darcynin family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AB016925; AA064070.1; -; Genomic_DNA.
KW Complete proteome.
SQ SEQUENCE 79 AA; 9290 MM; 77ECD9EBCB3DC0 CRC64;

Query Match 76.1%; Score 35; DB 1; Length 79;
Best Local Similarity 75.0%; Pred. No. 20;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVRLRYFDV 8
Db 10 EVRLRYFDV 17

RESULT 20
026063_HELPY PRELIMINARY; PRT; 228 AA.
AC 026063;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Hypothetical protein HP1537.
GN OrderedLocNames=HP1537;
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;

OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=26695 / ATCC 700392;
RX MEDLINE=97394467; PubMed=9252185; DOI=10.1038/41483;
RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
RA Fleischmann R.D., Ketchum K.A., Klein H.-P., Gill S.R.,
RA Dougherty B.A., Nelson K.E., Quackenbush J., Zhou L., Kirkness E.F.,
RA Peterson S.N., Loftus B.J., Richardson D.L., Dodson R.J., Khalak H.G.,
RA Glodek A., McKenney K., Fitzgerald L.M., Lee N., Adams M.D.,
RA Hickey E.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D.,
RA Kelley J.M., Cotton M.D., Weidman J.F., Fujii C., Bowman C.,
RA Wathey L., Wallin E., Hayes W.S., Borodovsky M., Karp P.D.,
RA Smith H.O., Fraser C.M., Venter J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter
RT pylori.";
RL Nature 388:539-547(1997).
RT Nature 388:539-547(1997).
DR EMBL; AE000651; AAD08576.1; -; Genomic_DNA.
DR PIR; A64712; A64712.
DR TIGR; HP1537; -;
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 228 AA; 26845 MM; 79CF28899145C741 CRC64;

Query Match 76.1%; Score 35; DB 2; Length 228;
Best Local Similarity 66.7%; Pred. No. 67;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EVRLRYFDV 9
Db 170 EVRLRYFDV 178

RESULT 21
Q77SA9_SNUCL
ID Q77SA9_SNUCL PRELIMINARY; PRT; 242 AA.
AC Q77SA9;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Late expression factor1.
GN Name=Ec-1ef1;
OS Ecotropic obliqua nucleopolyhedrovirus.
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=59376;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Zhang C.-X., Ma X.-C., Xu H.-D.;
RL Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Zhang C., Ma X.-C., Xu H.-D.;
RA Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF107100; AA088177.1; -; Genomic_DNA.
SQ SEQUENCE 242 AA; 28417 MM; 298F8BCB03173559 CRC64;

Query Match 76.1%; Score 35; DB 2; Length 242;
Best Local Similarity 87.5%; Pred. No. 72;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 VRLRYFDV 9
Db 150 VRLRYFDV 157

RESULT 22
074856_SCHPO
ID 074856_SCHPO PRELIMINARY; PRT; 332 AA.
AC 074856;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)

```

DE SPCCL18.06c protein.
CN ORFNames=SPCCL18.06c;
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
RA Wood V., Gilliam R., Rajandream M.A., Lyne M.H., Lyne R., Stewart A.,
RA Sgouros J.G., Peet N., Hayles J., Baker S.G., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins W., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D.E., Hildalgo J., Hodgson G.,
RA Holtroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K.D., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K.L., Murphy L.D., Niblett D., Odeh C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinovitch E.,
RA Rutherford K.M., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M.N., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J.R., Voicakeert G., Aert R., Robben J., Grymoprez B.,
RA Wellens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Duesterhoeft A., Fritz C., Holzer E., Moesli D.,
RA Hilbert H., Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R.,
RA Pohl T.M., Eger P., Zimmermann W., Wedler H., Wambutt R., Punnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Letaud V., Mottier S.,
RA Gilbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armerstrong J., Forsburg S.L.,
RA Ceretti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Batteil B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe."
RL Nature 415:871-880(2002).
DR EMBL: AL013907; CAA21420.1; -; Genomic_DNA.
DR PIR: T41149; T41149.
DR HSP: P39008; IUOC.
DR GeneDB_Spmbe; SPCCL18.06c; -.
DR GO: GO:0005634; C:nucleus; IEA.
DR GO: GO:0016564; P:transcriptional repressor activity; IEA.
DR GO: GO:0016481; P:negative regulation of transcription; IEA.
DR InterPro: IPR012337; RnaeH_fold.
DR InterPro: IPR012337; RnaeH_fold.
DR Pfam: PF04857; CAP1; 1.
DR Complete proteome; Nuclear protein.
SQ SEQUENCE 332 AA; 37230 MW; 5B5525C1A7871E CRC64;

Query Match 76.1%; Score 35; DB 2; Length 332;
Best Local Similarity 75.0%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EVRLRYFD 8
DB 250 EIRSRYFD 257

RESULT 23
044528 CAEEL PRELIMINARY; PRT; 338 AA.
ID 044528 CAEEL PRELIMINARY;
AC 044528
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Seven tm receptor protein 161.
GN Name=scr-161; ORFNames=t08B6.3;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]

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RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology."
RL Science 282:2012-2018(1998).
DR EMBL: AF038623; AAB94157.1; -; Genomic_DNA.
DR PIR: T15074; T15074.
DR Ensembl; T08B6.3; Caenorhabditis elegans.
DR WormBase; WBGene0006206; T08B6.3.
DR WormBep; T08B6.3; CE17224.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0004930; F:G-protein coupled receptor activity; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR InterPro: IPR003002; 7TM_chemreceptl.
DR InterPro: IPR00168; Nm/TM_chemreceptl.
DR Pfam: PF01461; 7tm_4; 1.
DR Complete proteome; Receptor.
SQ SEQUENCE 338 AA; 39044 MW; D4EB6D21D6ED0186 CRC64;

Query Match 76.1%; Score 35; DB 2; Length 338;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EVRLRYFD 8
DB 122 EGRIRYFD 129

RESULT 24
05E419 VIBF1 PRELIMINARY; PRT; 446 AA.
ID 05E419 VIBF1 PRELIMINARY;
AC 05E419
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
GN OrderedCusNames=VFI562;
OS Vibrio fischeri (strain ATCC 700601 / E5114).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrrio.
OX NCBI_TaxID=312309;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15703294; DOI=10.1073/pnas.040990102;
RA Ruby E.G., Urdanowski M., Campbell U., Dunn A., Faini M., Gunsalus R.,
RA Loseroh P., Lupp C., McCann J., Millikan D., Schaefer A., Stabb E.,
RA Stevens A., Vaislik K., Whistler C., Greenberg E.P.;
RT "Complete genome sequence of Vibrio fischeri: a symbiotic bacterium
RT with pathogenic congeners."
RL Proc. Natl. Acad. Sci. U.S.A. 102:3004-3009(2005).
DR EMBL: CP000020; AAW6057.1; -; Genomic_DNA.
DR InterPro: IPR010583; MIPA.
DR Pfam: PF06629; MIPA; 1.
DR Complete proteome; Hypothetical protein.
SQ SEQUENCE 446 AA; 51858 MW; 8933113C15DFEC59 CRC64;

Query Match 76.1%; Score 35; DB 2; Length 446;
Best Local Similarity 75.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 VRLRYFDV 9
DB 101 MRLRYFDL 108

RESULT 25
08SWF5 ENCCU PRELIMINARY; PRT; 496 AA.
ID 08SWF5 ENCCU PRELIMINARY;
AC 08SWF5
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)

```

DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
DE Hypothetical protein EC002_0320.
GN OrderedlocusNames=EC002_0320;
OS Eucephalitozoon cuniculi.
OC Eukaryota; Fungi; Microsporidia; Unikaryonidae; Eucephalitozoon.
OX NCBI_TaxId=6035;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=GB-M1;
RC MEDLINE=21576510; PubMed=11719806; DOI=10.1038/35106579;
RA Katinka M.D., Duprat S., Connillot E., Metenier G., Thomarat F.,
RA Preissier G., Barbe V., Peyretallade B., Broctier P., Winkler P.,
RA Delbac F., El Aloui H., Peyret P., Saurin W., Gouy M.,
RA Weissenbach U., Vivares C.P.;
RT "Genome sequence and gene compaction of the eukaryote parasite
RT Eucephalitozoon cuniculi.";
RL Nature 414:450-453 (2001).
DR BMBJ; AL590442; CAD25063.1; -; Genomic_DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 496 AA; 57568 MW; 975A70FA59F93C3D CRC64;

Query Match 76.1%; Score 35; DB 2; Length 496;
Best Local Similarity 75.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EVRLRYFPD 8
|:|:|:|:|
DB 177 EIRRRYFD 184

RESULT 26
Q9AMB3 ORYSA PRELIMINARY; PRT; 910 AA.
AC Q9AMB3;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DE Nuclear cap-binding protein CBP80.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxId=39947;
RN NUCLEOTIDE SEQUENCE.
RP Deeba M., Kmiecik M., Jarmolowski A.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR HSSP; AY017415; AAG54079.1; -, mRNA.
DR HSSP; Q09161; INS2.
DR Gramene; Q9AMB3; -;
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR InterPro; IPR003890; IF_eIF4G.
DR Pfam; PF02854; MIF4G; 1.
DR SMART; SM00543; MIF4G; 1.
SQ SEQUENCE 910 AA; 103823 MW; 23D62F81E8596F56 CRC64;

Query Match 76.1%; Score 35; DB 2; Length 910;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EVRLRYFPD 8
|:|:|:|:|
DB 452 EIRLRYFD 459

RESULT 27
Q4P102 USTWA PRELIMINARY; PRT; 1010 AA.
AC Q4P102;
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)

DE Hypothetical protein.
GN ORFNames=UW06211.1;
OS Ustilago maydis 521.
OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
OC Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
OX NCBI_TaxId=237631;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=521;
RC Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,
RA Ait-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,
RA Archach H., Armbruster J., Bachantsang P., Baldwin U., Barry A.,
RA Bayul T., Blitshsteyn B., Bloom T., Blye J., Boguslavskiy L.,
RA Borowsky M., Boukhgalter B., Brunache A., Butler J., Calixte N.,
RA Calvo S., Camarata J., Campo K., Chang J., Chehatsang Y., Citron M.,
RA Collymore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,
RA Dorjee K., Dorris L., Dufley N., Dupes A., Ekins T., Engels R.,
RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
RA Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Gnerre S.,
RA Guirke A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
RA Homan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,
RA Jaitte D., Jones C., Kamal M., Kamat A., Kamyselis M., Karlsson E.,
RA Kells C., Kieu A., Kisher P., Kodira C., Kulbokas E., Labutti K.,
RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,
RA Lindblad-toh K., Liu X., Lokitsang T., Lokitsang Y., Lucien O.,
RA Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,
RA Manning J., Marabella R., Maru K., Matthews C., Muccelli E.,
RA McCarthy M., McDonough S., Mcghee T., Meldrum J., Menus L.,
RA Mesirov J., Mihalov A., Minova T., Mikkelsen T., Mlenga V., Moru K.,
RA Mozes J., Multrah L., Munson G., Naylor J., News C., Nguyen C.,
RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizari M., Norbu C.,
RA Norbu N., O'donnell P., Okowo O., O'leary S., Omotosho B.,
RA O'Neill K., Osman S., Parker S., Perrin D., Phunkhang P., Pignani B.,
RA Purcell S., Rachupka T., Ramasamy U., Rambeau R., Ray V., Raymond C.,
RA Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,
RA Rutman M., Schubach R., Seaman C., Settipalli S., Sharpe T.,
RA Sheridan J., Shepa N., Shi J., Smirnov S., Smith C., Sougnez C.,
RA Spencer B., Stalker J., Strange-thomann N., Stavropoulos S.,
RA Stenson K., Stone C., Stone S., Stubbs M., Talmas J., Tchunga P.,
RA Tenzing P., Testaye S., Theodore J., Thoulitsang Y., Topham K.,
RA Towey S., Tsamla T., Tsomo N., Vallee D., Vassiliev H.,
RA Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,
RA Wangdi T., Whitaker C., Wilkinson J., Wu Y., Wymann D., Yadev S.,
RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,
RA Zimmer A., Zody M., Lander E.;

RT "The genome sequence of Ustilago maydis.",
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBJ; AACP01000236; EAK87049.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 1010 AA; 111808 MW; 2DEBD504E4821E79 CRC64;

Query Match 76.1%; Score 35; DB 2; Length 1010;
Best Local Similarity 75.0%; Pred. No. 3.6e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EVRLRYFPD 8
|:|:|:|:|
DB 620 EIRLRYFD 627

RESULT 28
Q70722 ANOGA PRELIMINARY; PRT; 1217 AA.
AC Q70722;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE ENSANGP0000017759.

```
GN ORFNames=ENSG00000015270;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RT "Anopheles gambiae re-annotation.";
RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RL Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AA0801008960; EMBL1859.1; -; Genomic_DNA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR004871; CPGF_A.C.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF03178; CPGF_A; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 1217 AA; 135223 MW; E3B161671881CDB CRC64;

Query Match 76.1%; Score 35; DB 2; Length 1217;
Best Local Similarity 62.5%; Pred. No. 4.4e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVRLRYFD 8
Db 324 EIKLKYFD 331

RESULT 29
OSB186_DROME
ID OSB186_DROME PRELIMINARY; PRT; 1227 AA.
AC OSB186;
DT 10-MAY-2005 (TRENBLrel. 30, Created)
DT 10-MAY-2005 (TRENBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TRENBLrel. 30, Last annotation update)
DE RE01063P.
GN Name=CG13900;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Berkley;
RA Stapleton M., Carlson J., Chavez C., Friese B., George R., Pacleb J.,
RA Park S., Wan K., Yu C., Rubin G.M., Celinker S.;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BT021338; AA033486.1; -; mRNA.
DR InterPro; IPR010819; AGE/RNAP.
DR InterPro; IPR004871; CPGF_A.C.
DR InterPro; IPR010980; Cyt_C_b562.
DR InterPro; IPR011992; EFL-Hand_type.
DR InterPro; IPR001524; Glyco_hydro_6.
DR InterPro; IPR012287; Homeodomain-fel.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR001093; IMPDH/GMPcase.
DR InterPro; IPR010503; LT-IIB.
DR InterPro; IPR004103; Lyase_8_C.
DR InterPro; IPR004094; Pict_in_antistn.
DR InterPro; IPR011991; Wing_hlx_DNA_bd.
DR Pfam; PF03178; CPGF_A; 1.
DR Pfam; PF00478; IMPDH; 1.
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DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 1227 AA; 136581 MW; E41CEDB8413CC96 CRC64;

Query Match 76.1%; Score 35; DB 2; Length 1227;
Best Local Similarity 62.5%; Pred. No. 4.5e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVRLRYFD 8
Db 324 EIKLKYFD 331

RESULT 30
OSB0M7_DROME
ID OSB0M7_DROME PRELIMINARY; PRT; 1227 AA.
AC OSB0M7;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 10-MAY-2005 (TRENBLrel. 30, Last annotation update)
DE CG13900-PA, isoform A (LD01809P).
GN ORFNames=CG13900;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=10731132, DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Goehyne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Chame M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., McKlos G.L.G.,
RA Abiri J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svaitks R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Gibbs R.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).

RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426065; PubMed=12537568;
RA Celinker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Chame M., Dugan S.P., Friese B., Hodgson A.,
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
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RA Pacleeb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svitskas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scher P.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
RT melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J.W., Svitskas R.,
RA Patel S., Friese E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celisner S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomic perspective.";
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Betencourt B.R., Celisner S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RG Berkeley Drosophila Genome Project;
RA Celisner S., Carlson J., Wan K., Pfeiffer B., Friese E., George R.,
RA Hoskins R., Stapleton M., Pacleeb J., Park S., Svitskas R., Smith E.,
RA Yu C., Rubin G.;
RT "Drosophila melanogaster release 4 sequence.";
RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
RN [6]
RP NUCLEOTIDE SEQUENCE.
RG FlyBase;
RL Submitted (MAR-2005) to the EMBL/Genbank/DBJ databases.
RN [7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Berkeley;
RA Stapleton M., Carlson J., Chavez C., Friese E., George R., Pacleeb J.,
RA Park S., Wan K., Yu C., Rubin G.M., Celisner S.;
RL Submitted (MAR-2005) to the EMBL/Genbank/DBJ databases.
DR EMBL: AE003469; AAF47416.2; -; Genomic_DNA.
DR EMBL: BT021424; AAX3572.1; -; mRNA.
DR Ensembl: CG13900; Drosophila melanogaster.
DR FlyBase: FBgn0035162; CG13900.
DR GO: GO:0005634; C:nucleus; IEA.
DR GO: GO:0003676; F:nucleic acid binding; IEA.
DR InterPro: IPR004871; C:SPF_A_C.
DR InterPro: IPR003006; I9_MHC.
DR Pfam: PF03178; C:SPF_A; 1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 1227 AA; 136615 MW; 3E1C4527841321FB CRC64;

Query Match 76.1%; Score 35; DB 2; Length 1227;
Best Local Similarity 62.5%; Pred. No. 4.5e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVRLRYFD 8
|:|:|:|
DB 324 EIKLKFDP 331

RESULT 31
06FST1_CANGA PRELIMINARY; PRT; 149 AA.
AC 06FST1;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
BT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)

DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Ubiquitin-conjugating enzyme (EC 6.3.2.19) (Ubiquitin carrier
DE protein).
GN OrderedLocusNames=CAGL00508063g;
OS Candida glabrata (Yeast) (Torulopsis glabrata).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5478;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 2001 / CBS 138.
RX PubMed=15229592; DOI=10.1038/nature02579;
RA Dujon B., Sherman D., Fischer G., Durand P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Nevegilise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Bockrich J.-M., Beyne E., Bleykasten C.,
RA Boissiere A., Boyer J., Carcolico L., Confalonieri F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Gropi A.,
RA Hantreya F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Kozul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicoud J.-M., Nikolaki M., Ozas S., Olier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.-F., Strub M.-L., Suleau A.,
RA Swennen D., Tekala F., Mesolowski-Louvel M., Westhof E., Wirth B.,
RA Zenou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissenbach J.,
RA Wincker P., Souciet J.-L.;
RT "Genome evolution in yeasts."
RL Nature 430:35-44(2004).
CC -I- CATALYTIC ACTIVITY: ATP + ubiquitin + protein lysine = AMP +
CC -I- diphosphate + protein N-ubiquityllysine.
CC -I- PATHWAY: Ubiquitin conjugation; second step.
CC -I- SIMILARITY: Belongs to the ubiquitin-conjugating enzyme family.
DR EMBL: CR380953; CAG59640.1; -; Genomic_DNA.
DR SRR: 06FST1.2-149
DR GO: GO:0016874; F:ligase activity; IEA;
DR GO: GO:0004840; F:ubiquitin conjugating enzyme activity; IEA.
DR GO: GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO: GO:0006512; P:ubiquitin cycle; IEA.
DR InterPro: IPR00608; UBQ-conjugat_E2.
DR Pfam: PF00179; UO_conj_1.
DR ProDom: PD000461; UBQ_conjugat; 1.
DR SMART: SM00212; UBCC; 1.
DR PROSITE: PS00183; UBQUITTIN_CONJUGAT_1; 1.
DR PROSITE: PS0127; UBQUITTIN_CONJUGAT_2; 1.
KW Complete proteome; ligase; ubl conjugation pathway.
SQ SEQUENCE 149 AA; 16973 MW; 9B19FAC32DBE643 CRC64;

Query Match 73.9%; Score 34; DB 2; Length 149;
Best Local Similarity 77.8%; Pred. No. 68;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EVRLRYFD 9
|:|:|:|
DB 29 EDNLRYFDV 37

RESULT 32
0412KO_GIBZE PRELIMINARY; PRT; 149 AA.
AC 0412KO;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORNames=FG08558.1;
OS Gibberella zeae PH-1.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocryomycetidae; Hypocreales; Nectriaceae; Gibberella.
OX NCBI_TaxID=229533;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PH-1;
RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,

RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavsky L.,
RA Bouhagalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA Choepel Y., Collymore A., Cook A., Cooke P., Corum B., Derrillano K.,
RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA Erickson J., Faro S., Ferreira P., Fitzgerald M., Gage D., Galagan J.,
RA Garcia S., Gierre S., Graham L., Grand-Pierre N., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu A.,
RA Ma L.-J., Mabbitt R., Maclean C., Macdonald P., Major J., Manning J.,
RA Matthews C., Mauceli E., McCarthy M., Meldrum J., Meneses L.,
RA Mihova T., Mianga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,
RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
RA Rachtupka A., Ramasamy U., Raymond C., Retta R., Rice C., Rogov P.,
RA Roman J., Schauer S., Schupack R., Seaman S., Severy P., Smirnov S.,
RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
RA Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,
RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
RA Lander E.,
RT "Fusarium graminearum genome sequence,"
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: AACM01000347; EAA71419.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 149 AA; 16697 MW; 0A52C728DA9AE241 CRC64;

Query Match 73.9%; Score 34; DB 2; Length 149;
Best Local Similarity 77.8%; Pred. No. 68;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EVRLRYFDV 9
| | | | |
Db 28 EDNLRYFDV 36

RESULT 33
Q4WCUI ASPFU PRELIMINARY; PRT; 149 AA.
ID Q4WCUI ASPFU PRELIMINARY;
AC Q4WCUI;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Ubiquitin conjugating enzyme (ubcm), putative.
GN ORFNames=Atu6G02420;
OS Aspergillus fumigatus Af293.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=330879;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AF293;
RA Bierman W., Pain A., Anderson M.J., Wortman J., Kim H., Stanley.,
RA Arroya J., Barriman M., Abe K., Archer D.B., Bermejo C., Bennett J.,
RA Bowyer P., Chen D., Collins M., Collsen R., Davies R., Dyer P.S.,
RA Farman M., Fedorova N., Fedorova N., Feldblyum T.V., Fischer R.,
RA Foster J., Fraser A., Garcia J.L., Garcia M.J., Goble A.,
RA Goldman G.H., Goni K., Griffith-Jones S., Gwilliam R., Haas B.,
RA Haas H., Harris D., Horiuchi H., Huang J., Humphrey S., Jimenez J.,
RA Keller N., Khouri H., Kitamoto K., Kobayashi T., Kulkarni R.,
RA Kumagai T., Lafton A., Latge J.-P., Li W., Lord A., Lu C.,
RA Majors W.H., May G.S., Miller B.L., Mohammad Y., Molina M., Monod M.,
RA Mouyna I., Mulligan S., Murphy L., O'Neill S., Paulsen I.,
RA Penault M.A., Petrea M., Price C., Pritchard B.L., Quail M.A.,
RA Rablunowitsch E., Rawlins N., Rajandream M.-A., Reichard U.,
RA Renauld H., Robson G.D., Rodriguez S.L., Sanchez M., Rodriguez-Pena J.M.,
RA Roming C.M., Rutter S., Salzberg S.L., Squares R., Squares S.,
RA Sanchez-Ferreiro J.C., Saunders D., Seeger K., Squares R.,
RA Takeuchi M., Tekala F., Turner G., Vazquez de Aldana C.R., Weidman J.,
RA White O., Woodward J., Yu J.-H., Fraser C., Galagan J.E., Asai K.,

RA Machida M., Hall N., Barrell B., Denning D.W.,
RT "Genomic sequence of the pathogenic and allergenic filamentous fungus
RT Aspergillus fumigatus,"
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -! CATALYTIC ACTIVITY: ATP + ubiquitin + protein lysine = AMP +
CC diphosphate + protein N-ubiquityllysine.
CC -! PATHWAY: Ubiquitin conjugation; second step.
CC -! SIMILARITY: Belongs to the ubiquitin-conjugating enzyme family.
DR EMBL: AAH0100012; EAL85797.1; -; Genomic_DNA.
DR InterPro: IPR006068; UBG-conjugat_E2.
DR Pfam: PF00179; UQ_con; 1.
DR ProDom: PD000461; UBO_conjugat; 1.
DR SMART: SM00212; UBCC; 1.
DR PROSITE: PS00183; UBIQUITIN_CONJUGAT_1; 1.
DR PROSITE: PS00127; UBIQUITIN_CONJUGAT_2; 1.
KW Ligase; Ubl conjugation pathway.
SQ SEQUENCE 149 AA; 16992 MW; CD362B9D1481E0D2 CRC64;

Query Match 73.9%; Score 34; DB 2; Length 149;
Best Local Similarity 77.8%; Pred. No. 68;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EVRLRYFDV 9
| | | | |
Db 28 EDNLRYFDV 36

RESULT 34
O51MH3 MAGGR PRELIMINARY; PRT; 150 AA.
ID O51MH3 MAGGR PRELIMINARY;
AC O51MH3;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=MG02568.4;
OS Magnaporthe oryzae 70-15.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
OX NCBI_TaxID=242507;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=70-15;
RA Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,
RA Ait-Zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,
RA Arachchi H., Armbruster J., Bachantang P., Baldwin J., Barry A.,
RA Bayul T., Blitshteyn B., Bloom T., Blye J., Boguslavsky L.,
RA Borowsky M., Bouhagalter B., Brunache A., Butler J., Calixte N.,
RA Calvo S., Camarata J., Campo K., Chang J., Cheahsang Y., Citroen M.,
RA Callymore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,
RA Dorjee K., Dorris L., Dufey N., Dupes A., Elkins T., Engels R.,
RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
RA Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Gierre S.,
RA Gnirke A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
RA Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,
RA Jaffe D., Jones C., Kamal M., Kamat A., Kawysselis M., Karlsson E.,
RA Kells C., Kieu A., Klsner P., Kodira C., Kulbokas E., Labutli K.,
RA Lama D., Landers T., Leeger J., Levine S., Lewis D., Lewis T.,
RA Lindblad-Toh K., Liu X., Lokysang T., Lokysang Y., Lucien O.,
RA Lui A., Ma L.-J., Mabbitt R., Macdonald P., Maclean C., Major J.,
RA Manning J., Marabelli R., Maru K., Matthews C., Mauceli E.,
RA McCarthy M., McDonough S., McGhee T., Meldrum J., Meneses L.,
RA Mesirov J., Mhallev A., Mihova T., Mikkelsen T., Mianga V., Moru K.,
RA Mozes J., Mulrain L., Munson G., Naylor J., Neves C., Nguyen C.,
RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizazi M., Norbu C.,
RA Norbu N., O'Donnell P., Okawo O., O'Leary S., Omotombo B.,
RA O'Neill K., Osman K., Parker S., Perrin D., Phunkhang P., Pigani B.,
RA Purcell S., Rachtupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,

RA Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,
 RA Ruman M., Schupbach R., Seaman C., Settipalli S., Sharpe T.,
 RA Sheridan J., Shepa N., Shi J., Smirnov S., Smith C., Sougenz C.,
 RA Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,
 RA Steenson K., Stone C., Stone S., Stubbs M., Talamas J., Tchinga P.,
 RA Tensing P., Testise S., Theodore J., Thoulutsang Y., Topham K.,
 RA Towey S., Tsamla T., Tsomo N., Vallee D., Vassiliev H.,
 RA Venkateraman V., Vinson J., Vo A., Wade C., Wang S., Wanchuk T.,
 RA Wangdi T., Whitaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,
 RA Yang S., Yang X., Yeager S., Yee E., Young G., Zairoun J., Zembeck L.,
 RA Zimmer A., Zody M., Zander E.;
 RT "The genome sequence of *Magnaporthe oryzae*."
 RL Submitted (Oct-2003) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=70-15;
 RA Dean R., Mitchell T., Brown D., Pan H., Thon M.;
 RL Submitted (Oct-2003) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=70-15;
 RA Zhu H., Blackmon B.;
 RL Submitted (Oct-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 CC -!- CATALYTIC ACTIVITY: ATP + ubiquitin + protein lysine = AMP +
 diphosphate + protein N-ubiquityllysine.
 CC -!- PATHWAY: Ubiquitin conjugation; second step.
 CC -!- SIMILARITY: Belongs to the ubiquitin-conjugating enzyme family.
 DR EMBL; AAC01001519; EAA47325.1; -; Genomic_DNA.
 DR SMR; Q51MH3; 2-147.
 DR InterPro; IPR000608; Ubq-conjugat_E2.
 DR Pfam; PF00179; Ubq_con; 1.
 DR ProDom; PD000461; Ubq_conjugat; 1.
 DR SMART; SM00212; UBCC1; 1.
 DR PROSITE; PS00183; UBIQUITIN CONJUGAT 1; 1.
 DR PROSITE; PS0127; UBIQUITIN CONJUGAT 2; 1.
 KW Hypothetical protein; ligase; Ub1 conjugation pathway.
 SQ SEQUENCE 150 AA; 16882 MW; 813AA52393ADFA7 CRC64;

Query Match 73.9%; Score 34; DB 2; Length 150;
 Best Local Similarity 77.8%; Pred. No. 68;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EVRLRYPDV 9
 Db 28 EDNLRYPDV 36

RESULT 35
 Q7SDM1 NEUCR PRELIMINARY; PRT; 151 AA.
 AC Q7SDM1;
 DT 01-MAR-2004 (TREMBlrel. 26, Created)
 DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Hypothetical protein.
 GN Name=NCU02113.1;
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
 OX NCBI_TaxID=5141;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=OR74A;
 RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
 RA Jaffe D., Fitzhugh W., Ma L.-D., Smirnov S., Purcell S., Rehman B.,
 RA Elkins T., Engle S., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
 RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
 RA Selitrenikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
 RA Kothe G.O., Jedd G., Mewes W., Steben C., Marcotte E., Greenberg D.,
 RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,

RA Kamal M., Kamysseilis M., Manceli E., Biele C., Rudd S., Fishman D.,
 RA Kryzotova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,
 RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmi S.A.,
 RA Desguza C.C., Glass L., Orbach M.J., Béglund J., Voelker R.,
 RA Yarden O., Plamann L., Seiler S., Dunlap J., Radford A., Aramayo R.,
 RA Yavlen D.O., Alex L.A., Mannhaupt G., Ebohe D.J., Freitag M.,
 RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.;
 RT "The Genome Sequence of the Filamentous Fungus *Neurospora crassa*."
 RL Nature 0:0-0(2003).
 CC -!- CATALYTIC ACTIVITY: ATP + ubiquitin + protein lysine = AMP +
 diphosphate + protein N-ubiquityllysine.
 CC -!- PATHWAY: Ubiquitin conjugation; second step.
 CC -!- SIMILARITY: Belongs to the ubiquitin-conjugating enzyme family.
 CC -!- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 CC EMBL; AABX0100048; EAA34871.1; -; Genomic_DNA.
 DR HSSP; P52490; IJAT.
 DR SMR; Q7SDM1; 2-147.
 DR GO; GO:0016874; F:ligase activity; IEA.
 DR GO; GO:0004840; F:ubiquitin conjugating enzyme activity; IEA.
 DR GO; GO:0006512; F:ubiquitin cycle; IEA.
 DR InterPro; IPR000608; Ubq-conjugat_E2.
 DR Pfam; PF00179; Ubq_con; 1.
 DR ProDom; PD000461; Ubq_conjugat; 1.
 DR PROSITE; PS00183; UBIQUITIN CONJUGAT 1; 1.
 DR PROSITE; PS0127; UBIQUITIN CONJUGAT 2; 1.
 KW Hypothetical protein; ligase; Ub1 conjugation pathway.
 SQ SEQUENCE 151 AA; 16981 MW; 1865B115EBE14BE CRC64;

Query Match 73.9%; Score 34; DB 2; Length 151;
 Best Local Similarity 77.8%; Pred. No. 69;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EVRLRYPDV 9
 Db 28 EDNLRYPDV 36

RESULT 36
 Q74ZS7 ASHGO PRELIMINARY; PRT; 154 AA.
 ID Q74ZS7 ASHGO
 AC Q74ZS7;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Ubiquitin-conjugating enzyme (EC 6.3.2.19) (Ubiquitin carrier
 protein).
 GN Name=AGR121C;
 OS *Asbya gossypii* (Yeast) (Eremothecium *gossypii*).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetidae; Saccharomycetaceae; Eremothecium.
 OX NCBI_TaxID=33169;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=ATCC 10895;
 RX PubMed=15001715; DOI=10.1126/science.1095781;
 RA Dietrich F.S., Voegelé S., Brachat S., Lerch A., Gates K., Steiner S.,
 RA Mohr C., Pohlmann R., Luedi P., Choi S., Wing R.A., Flavier A.,
 RA Gatiney T.D., Philippsen P.;
 RT "The *Asbya gossypii* genome as a tool for mapping the ancient
 Saccharomycetes cerevisiae genome."
 RL Science 304:304-307(2004).
 CC -!- CATALYTIC ACTIVITY: ATP + ubiquitin + protein lysine = AMP +
 diphosphate + protein N-ubiquityllysine.
 CC -!- PATHWAY: Ubiquitin conjugation; second step.
 CC -!- SIMILARITY: Belongs to the ubiquitin-conjugating enzyme family.
 DR EMBL; AE016820; AAS54611.1; -; Genomic_DNA.
 DR HSSP; P06104; IAYZ.
 DR SMR; Q74ZS7; 4-149.
 DR AGD; AGR121C; -;
 DR GO; GO:0016874; F:ligase activity; IEA.
 DR GO; GO:0004840; F:ubiquitin conjugating enzyme activity; IEA.

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DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0006512; P:ubiquitin cycle; IEA.
DR InterPro; IPR000608; UBG-conjugat_E2.
DR Pfam; PF00179; UQ_con; 1.
DR ProDom; PD000461; UBG_conjugat; 1.
DR SMART; SM00212; UBCC; 1.
DR PROSITE; PS00183; UBIQUITIN_CONJUGAT_1; 1.
DR PROSITE; PS50127; UBIQUITIN_CONJUGAT_2; 1.
DR Complete proteome; ligase; ubi conjugation pathway.
SQ SEQUENCE 154 AA; 17377 MW; 8E153E7B09800335 CRC64;

Query Match 73.9%; Score 34; DB 2; Length 154;
Best Local Similarity 77.8%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EVRLRYFDV 9
Db 29 EDNLRYFDV 37

RESULT 37
Q4P877 USTWA PRELIMINARY; PRT; 168 AA.
ID Q4P877 USTWA PRELIMINARY; PRT; 168 AA.
AC Q4P877;
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DE Hypothetical protein.
GN ORFNames=UM03686.1;
OS Ustilago maydis 521.
OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
OC Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
OK NCBI_TaxID=237631;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Birren B., Nussbaum C., Abebe A., Abouelleil A., Adkoya E.,
RA Ait-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,
RA Archenci H., Armbruster J., Bachantsang P., Baldwin U., Barry A.,
RA Bayul T., Blitsheteyn B., Bloom D., Blaye J., Boguslavskiy L.,
RA Borowsky M., Bouhgalter B., Brumache A., Butler J., Calixte N.,
RA Calvo S., Camarata J., Campo K., Chang J., Cheshtsang Y., Citroen M.,
RA Collimore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,
RA Dorjee K., Dorris L., Dufley N., Dupes A., Elkins T., Engels R.,
RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
RA Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Guerre S.,
RA Gutke A., Goyette A., Graham J., Grandbois E., Gyaltzen K., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
RA Homan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,
RA Jaffe C., Jones C., Kamal M., Kamat A., Kamyssele M., Karlsson E.,
RA Kells C., Klein A., Klsner P., Kodira C., Kulbokas E., Labutti K.,
RA Lamm D., Landers T., Legier J., Levine S., Lewis D., Lewis T.,
RA Lindblad-Toh K., Liu X., Lokysang T., Lokysang Y., Lucien O.,
RA Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,
RA Manning J., Marabelli R., Maru K., Matthews C., Maucelli E.,
RA McCarthy M., McDonough S., Mcghee T., Meldrum J., Menus L.,
RA Mesirov J., Mihalav A., Mihova T., Mikelsen T., Miera V., Moru K.,
RA Mostov J., Mulrain L., Munson G., Naylor J., News C., Nguyen C.,
RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizari M., Norbu C.,
RA O'Neill K., O'donnell P., Okawa O., O'leary S., Omotosho B.,
RA Pirelli S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,
RA Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,
RA Rutman M., Schupbach R., Seaman C., Settipalli S., Sharpe T.,
RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sounguez C.,
RA Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,
RA Stenson K., Stone C., Stone S., Stubbs M., Talmas J., Tchunga P.,
RA Tenzing P., Tesfaye S., Theodore J., Thoultsang Y., Topham K.,
RA Towey S., Tsamla T., Tsomo N., Vallee D., Vassiliev H.,
RA Venkataraman V., Vinson D., Vo A., Wade C., Wang S., Wangchuk T.,
RA Wangdi T., Whitaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,
RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembek L.,

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RA Zimmer A., Zody M., Lander E.;
RT "the genome sequence of Ustilago maydis";
RL Submitted (Feb-2004) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -! CATALYTIC ACTIVITY: ATP + ubiquitin + protein lysine = AMP +
CC diphosphate + protein N-ubiquityllysine.
CC -! PATHWAY: Ubiquitin conjugation; second step.
CC -! SIMILARITY: Belongs to the ubiquitin-conjugating enzyme family.
DR EMBL; AACP0100124; EAK8484.1; -; Genomic_DNA.
DR InterPro; IPR000608; UBG-conjugat_E2.
DR Pfam; PF00179; UQ_con; 1.
DR ProDom; PD000461; UBG_conjugat; 1.
DR SMART; SM00212; UBCC; 1.
DR PROSITE; PS00183; UBIQUITIN_CONJUGAT_1; 1.
DR PROSITE; PS50127; UBIQUITIN_CONJUGAT_2; 1.
DR Hypothetical protein; ligase; ubi conjugation pathway.
SQ SEQUENCE 168 AA; 19171 MW; 3DFCAE9FE10BA4F1 CRC64;

Query Match 73.9%; Score 34; DB 2; Length 168;
Best Local Similarity 77.8%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EVRLRYFDV 9
Db 28 EDNLRYFDV 36

RESULT 38
MATWC SCHKA STANDARD; PRT; 181 AA.
ID MATWC SCHKA STANDARD; PRT; 181 AA.
AC O6WRX5;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Mating-type M-specific polypeptide Mc (mat-Mc).
GN Name=matMc;
GN Schizosaccharomyces kambucha (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetiales; Schizosaccharomycetaceae;
OX NCBI_TaxID=204045;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA PubMed-14618565; DOI=10.1002/yea.1042;
RA Singh G., Klar A.J.S.;
RT "DNA sequence of the mat2,3 region of Schizosaccharomyces kambucha
RT shares high homology with the corresponding sequence from Sz. pombe.";
RL Yeast 20:1273-1278(2003).
CC -! FUNCTION: Positive regulator of MPM genes. The HMG box recognizes
CC the DNA sequence 5'-ACCAAG-3'. Cell type in fission yeast is
CC determined by the mating-type components mat1, mat2-p and mat-3M.
CC Cell type is determined by the alternate allele present in mat1,
CC either p in an h+ or m in an h- cell. Mat2-p and mat3-M serves as
CC donor of information that is transposed to mat1 during a switch of
CC mating type (BY similarity).
CC -! SUBCELLULAR LOCATION: Nuclear (potential).
CC -! SIMILARITY: Contains 1 HMG box DNA-binding domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC EMBL; AY271822; AAC082722.1; -; Genomic_DNA.
DR InterPro; IPR000910; HMG_12_box.
DR Pfam; PF00505; HMG_box; 1.
DR SMART; SM00398; HMG; 1.
DR PROSITE; PS50118; HMG_BOX_2; 1.
DR DNA-binding; Fertilization; Nuclear protein; Transcription;
KW Transcription regulation.

```

```
FT DNA BIND 103 171 HMG box.
SQ SEQUENCE 181 AA; 21030 MW; 6D8EEF06081AEC715 CRC64;

Query Match
Best Local Similarity 85.7%; Score 34; DB 1; Length 181;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 EVRLRYF 7
   |||:|
Db 147 EVRLRYF 153

RESULT 39
MATWC SCHPO STANDARD; PRT; 181 AA.
AC P10840.03URE1;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Mating-type M-specific polypeptide Mc (mat-MC).
GN Name=matMca; Synonyms=matMc; ORFNames=SPBC23G7.09;
   and
GN Name=matWcb; Synonyms=matWc; ORFNames=SPBC1711.02;
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
   Schizosaccharomycetales; Schizosaccharomycetaceae;
   Schizosaccharomycetes.
CX NCBI_TaxID=4896;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=88312604; PubMed=2900761;
RT Kelly M., Burke J., Smith K., Klar A., Beach D.;
   "Four mating-type genes control sexual differentiation in the fission
   yeast."; 7:1537-1547(1988).
RL [2]
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
   STRAIN=972;
RA Wood V., Gwilliam R., Rajadream M.A., Lyne M.H., Lyne R., Stewart A.,
   Sgouros J.G., Peat N., Hayles J., Baker S.G., Basham D., Bowman S.,
   Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
   Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
   Gentles S., Goble A., Hamlin N., Harris D.E., Hidalgo J., Hodgson G.,
   Holroyd S., Hornby T., Howarth S., Huckle E.J., Hunt S., Jagsels K.,
   James K.D., Jones L., Jones M., Leacher S., McDonald S., McLean J.,
   Mooney P., Moule S., Mungall K.L., Murphy L.D., Niblett D., Odell C.,
   Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinovitch E.,
   Rutherford K.M., Rutter S., Saunders D., Seeger K., Sharp S.,
   Skelton J., Simmonds M.N., Squares R., Squares S., Stevens K.,
   Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
   Woodward J.R., Voicakeit G., Aert R., Robben J., Gymnopoulos B.,
   Welljens I., Vansteleels E., Rieger M., Schaefer M., Mueller-Auer S.,
   Gabel C., Fuchs M., Duesterhoeft A., Fritzc C., Holzer E., Moestl D.,
   Hilbert H., Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R.,
   Pohl T.M., Eger P., Zimmermann W., Medler H., Wambutt R., Purnelle B.,
   Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mortier S.,
   Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
   Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Thode G.,
   Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Bento J.,
   Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
   Centuri L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
   Shpakovski D.V., Ussery D., Barrett B.G., Nurse P.;
   "The genome sequence of Schizosaccharomyces pombe.";
   Nature 415:871-880(2002).
RL Nature 415:871-880(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE OF 100-181.
RX MEDLINE=94043341; PubMed=8227043;
RT Doolies D., van de Wetering M., Knippels L., Clevers H.;
   "The Schizosaccharomyces pombe mating-type gene mat-Mc encodes a
   sequence-specific DNA-binding high mobility group box protein.";
   J. Biol. Chem. 268:24813-24817(1993).
RL [1]
CX -1- FUNCTION: Positive regulator of MFM genes. The HMG box recognizes
```

```
CC the DNA sequence 5'-AACAAAG-3'. Cell type in fission yeast is
CC determined by the mating-type components mat1, mat2-P and mat3-M.
CC Cell type is determined by the alternate allele present in mat1,
CC either P in an h+ or M in an h- cell. Mat2-P and mat3-M serves as
CC donor of information that is transposed to mat1 during a switch of
CC mating type.
CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -1- INDUCTION: By nitrogen starvation.
CC -1- SIMILARITY: Contains 1 HMG box DNA-binding domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL, X07642; CAA30481.1; -; Genomic DNA.
CC EMBL, AL035065; CAA22625.1; -; Genomic DNA.
CC EMBL, AL353012; CAB88232.1; -; Genomic DNA.
CC PIR, S00555; S00555.
CC HSP, Q05066; 1J46.
CC TRANSFAC, T01275; -.
CC GeneDB, Spombe; SPBC1711.02; -.
CC GeneDB, Spombe; SPBC23G7.09; -.
CC InterPro; IPR000910; HMG_12_box.
CC Pfam; PF00505; HMG_box; 1.
CC SMART; SM00398; HMG; 1.
CC PROSITE; PS50118; HMG_BOX_2; 1.
CC Complete proteome; DNA-binding; Fertilization; Nuclear protein;
CC Transcription; Transcription regulation.
CC DNA BIND 103 171
FT CONFLICT 174 174 Missing (in Ref. 3).
SQ SEQUENCE 181 AA; 21003 MW; 9301E076BD12016F CRC64;
```

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Query Match
Best Local Similarity 85.7%; Score 34; DB 1; Length 181;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 EVRLRYF 7
   |||:|
Db 147 EVRLRYF 153

RESULT 40
O7MF27_VIBVY PRELIMINARY; PRT; 272 AA.
ID O7MF27_VIBVY
AC O7MF27;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Hypothetical protein VVA0493.
GN OrderedLocustNames=VVA0493;
OS Vibrio vulnificus (strain YJ016).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
   Vibrionaceae; Vibrio.
CX NCBI_TaxID=196600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14656965; DOI=10.1101/gr.1295503;
RA Chao C.-Y., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C.,
   Liao T.-L., Liu Y.-M., Chen H.-J., Chen A.B.-T., Li J.-C., Su T.-L.,
   Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-F.;
   "Comparative genome analysis of Vibrio vulnificus, a marine
   pathogen.";
   Genome Res. 13:2577-2587(2003).
RL Genome Res. 13:2577-2587(2003).
DR EMBL; BA000038; BAC96519.1; -; Genomic DNA.
KV Complete proteome; Hypothetical protein.
SQ SEQUENCE 272 AA; 30615 MW; 9C73CA374B189D34 CRC64;
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Oy      1 EVRLRYFDV 9
       :|||:|
Db      100 QVRLRYFV 108

RESULT 41
Q72EA3 DESVH PRELIMINARY; PRT; 273 AA.
ID Q72EA3 DESVH PRELIMINARY; PRT; 273 AA.
AC Q72EA3 DESVH PRELIMINARY; PRT; 273 AA.
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Amino acid ABC transporter, periplasmic amino acid-binding protein.
DE OrderedLocNames=DVU0675;
OS Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB 8303).
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobacteriales;
OC Desulfobacteriaceae; Desulfobacteriales;
OC Desulfobacteriaceae; Desulfobacteriales;
OX NCBI_TaxID=882;

[1]
NUCLEOTIDE SEQUENCE.
RP PubMed:15077118; DOI=10.1038/nbt959;
RA Heidelberg J.F., Seshadri R., Haveman S.A., Hemme C.L., Paulsen I.T.,
RA Kolonay J.F., Eisen J.A., Ward N.L., Methe B.A., Brinkac L.M.,
RA Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Madupu R.,
RA Nelson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J.,
RA Peterson J.D., Davidson T.M., Zafar N., Zhou L., Kadane D.,
RA Dimitrov G., Hance W., Tran K., Knouri H.M., Gill J., Uitterlinden T.R.,
RA Feldblyum T.V., Wall J.D., Voordouw G., Frazer C.M.;
RT "The genome sequence of the anaerobic, sulfate-reducing bacterium
RT Desulfovibrio vulgaris Hildenborough.";
RL Nat. Biotechnol. 22:554-559(2004).
DR EMBL: AE017311; AAS95156.1; -; Genomic_DNA.
DR TIGR: DVU0675; -;
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.
DR GO: GO:0005234; F:glutamate-gated ion channel activity; IEA.
DR GO: GO:0004970; F:ionotropic glutamate receptor activity; IEA.
DR GO: GO:0005215; F:transporter activity; IEA.
DR GO: GO:0006810; F:transport; IEA.
DR InterPro: IPR001320; Ion glu receptor.
DR InterPro: IPR001311; SBP/glu receptor.
DR InterPro: IPR001638; SBP bac_3.
DR Pfam: PF00497; SBP bac_3; 1.
DR SMART: SM00062; PBPB; 1.
DR SMART: SM00079; PBPB; 1.
DR PROSITE: PS01039; SBP_BACTERIAL_3; UNKNOWN_1.
DR Complete proteome.
KW Complete proteome.
SQ SEQUENCE 273 AA; 30217 MW; 13FD2DE673A97502 CRC64;

Query Match 73.9%; Score 34; DB 2; Length 273;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy      1 EVRLRYFDV 9
       :|||:|
Db      172 KARLRYFD 179

RESULT 42
Q4ZLT8 PSBSY PRELIMINARY; PRT; 313 AA.
ID Q4ZLT8 PSBSY PRELIMINARY; PRT; 313 AA.
AC Q4ZLT8 PSBSY PRELIMINARY; PRT; 313 AA.
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=Payr_4857;
OS Pseudomonas syringae pv. syringae B728a.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=205918;

```

```

RN      [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B728a;
RG DOE Joint Genome Institute;
RA Chain P., Larimer F., DiBartolo G., Copeland A., Lykidis A., Trong S.,
RA Nolan M., Goltsman E., Thiel J., Malfatti S., Lapidis A., Detter J.C.,
RA Land M., Richardson P.M., Kyriades N.C., Ivanova N.;
RT "Comparison of two complete genome sequences of Pseudomonas syringae
RT pv. syringae B728a and pv. tomato DC3000.";
RL Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2005).
RN      [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B728a;
RG Loper J.;
RA Submitted (May-2005) to the EMBL/GenBank/DBJ databases.
RN      [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B728a;
RA Fell H., Fell W.S., Lindow S.E.;
RL Submitted (May-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL: CP000075; AAY39884.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 313 AA; 35023 MW; F6179B2F6296FDD6 CRC64;

Query Match 73.9%; Score 34; DB 2; Length 313;
Best Local Similarity 75.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy      1 EVRLRYFDV 8
       :|||:|
Db      299 ELRLRYFD 306

RESULT 43
Q4IAY3 GIBZE PRELIMINARY; PRT; 349 AA.
ID Q4IAY3 GIBZE PRELIMINARY; PRT; 349 AA.
AC Q4IAY3 GIBZE PRELIMINARY; PRT; 349 AA.
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=FG05655.1;
OS Gibberella zeae PH-1.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocricetidae; Hypocricetidae; Nectriaceae; Gibberella.
OX NCBI_TaxID=229533;

[1]
NUCLEOTIDE SEQUENCE.
RP STRAIN=PH-1;
RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavsky L.,
RA Boukhgelter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA Choquet Y., Collymore A., Cook A., Cooke P., Corum B., DeArillano K.,
RA Diaz U.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA Erickson J., Faro S., Ferreira P., Fitzgerald M., Gage D., Galagan J.,
RA Gardy J.S., Gierke S., Graham L., Grand-Pierre N., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas S.,
RA Kells C., Landers T., Levine R., Linblad-Toh K., Liu G., Lui A.,
RA Ma L.-O., Mabbitt R., Maclean C., Macdonald P., Major U., Manning J.,
RA Matthews C., Mauceli E., McCarthy M., Meldrum J., Menus L.,
RA Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,
RA Oliver J., Peterson K., Punukhang P., Pierre N., Purcell S.,
RA Rachupka A., Ramasamy U., Raymond C., Rette R., Rise C., Rogov P.,
RA Roman J., Schauer S., Schupbach R., Seaman S., Severy P., Shtrom S.,
RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
RA Talamas J., Tesfaye S., Theodore J., Topham K., Travers N.,
RA Vasilev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA Wu X., Wyman D., Young G., Zainoun J., Zemlek L., Zimmer A., Zody M.,
RA Lander E.;
RT "Pisarium graminearum genome sequence.";
RL Submitted (Feb-2004) to the EMBL/GenBank/DBJ databases.

```

CC -! CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.

DR EMBL; AACM01000231; EAA75226.1; -; Genomic_DNA.
KM Hypothetical protein
SQ SEQUENCE 349 AA; 39501 MW; 69CD772AC4CBC6F3 CRC64;

Query Match 73.9%; Score 34; DB 2; Length 349;
Best Local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EVRLRYFDV 9
|:|:|:|:
DB 113 EAGLRVFDI 121

RESULT 44
087UJ7_PSESM
ID 087UJ7_PSESM PRELIMINARY; PRT; 356 AA.

AC 087UJ7;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
GN Hypothetical protein.
DE OrderedlocusNames=PSPT05299;
OS Pseudomonas syringae (pv. tomato).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
NCBI_TaxID=323;
RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=DC3000;
RX MEDLINE=22834015; PubMed=12928499; DOI=10.1073/pnas.171982100;
RA Buell C.R., Joardar V., Lindeberg M., Selengut J., Paulsen I.T.,
Gwin M.L., Dodson R.J., Deboy R.T., Durkin A.S., Kolonay J.F.,
Madupu R., Daugherty S.C., Brinkac L.M., Beanan M.J., Haft D.H.,
Nelson W.C., Davidson T.C., Zafar N., Zhou L., Liu J., Yuan Q.,
Khouri H.M., Fedorova N.B., Tran B., Russell D., Berry K.J.,
Rau Uterback T.R., Van Aken S.E., Feldblyum T.V., D'Ascenzo M.,
Deng W.-L., Ramos A.R., Alfano J.R., Carlinhour S., Chatterjee A.K.,
Delaney T.P., Lazrowitz S.G., Martin G.B., Schneider D.J., Tang X.,
Bender C.L., White O., Fraser C.M., Collier A.;
RT "The complete genome sequence of the Arabidopsis and tomato pathogen
Pseudomonas syringae pv. tomato DC3000."
RL Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186 (2003).
DR EMBL; AE016853; AAO58725.1; -; Genomic_DNA.
DR TIGR; PSPT05299; -;
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0006725; P:aromatic compound metabolism; IEA.
DR InterPro; IPR000073; A/b hydrolase.
DR InterPro; IPR003089; AB hydrolase.
DR InterPro; IPR000379; Set_estrs.
DR Pfam; PF00561; Abhydrolase_1; 1.
DR PRINTS; PR00111; ABHYDROLASE.
KM Complete proteome; Hypothetical protein.
SQ SEQUENCE 356 AA; 39276 MW; AB95F26CF1CC878E CRC64;

Query Match 73.9%; Score 34; DB 2; Length 356;
Best Local Similarity 75.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EVRLRYFDV 8
|:|:|:|:
DB 342 ELRVRVFD 349

RESULT 45
P96988 RHOMR PRELIMINARY; PRT; 412 AA.

AC P96988;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

DE Xylanase (Fragment).
OS Rhodothermus marinus (Rhodothermus obamensis).
OC Bacteria; Bacteroidetes; Sphingobacteriales;
OC Creontichaceae; Rhodothermus.
NCBI_TaxID=29549;
RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=DSM 4252;
RA Norbert Karlsson E.M.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; X87417; CAA60868.2; -; Genomic_DNA.
DR PDB; 1K42; NMR; A=-.

DR PDB; 1K45; NMR; A=-.

DR GO; GO:0004553; F:hydrolase activity; hydrolyzing O-glycosyl . . .; IEA.

DR GO; GO:0005975; P:carbohydrate metabolism; IEA.

DR InterPro; IPR01000; Glyco_hydro_10.

DR Pfam; PF00331; Glyco_hydro_10; 1.

DR SMART; SM00633; Glyco_10; 1.

FT Xylan degradation.

FT NON TER

SQ SEQUENCE 412 AA; 46981 MW; EBA74A6812B43625 CRC64;

Query Match 73.9%; Score 34; DB 2; Length 412;
Best Local Similarity 77.8%; Pred. No. 2.1e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EVRLRYFDV 9
|:|:|:|:
DB 353 EVRLQVFDV 361

RESULT 46

088EC2_PSEPK

ID 088EC2_PSEPK PRELIMINARY; PRT; 414 AA.

AC 088EC2;

DT 01-JUN-2003 (TREMBLrel. 24, Created)

DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)

DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)

GN Hypothetical protein.

DE OrderedlocusNames=PP4544;

OS Pseudomonas putida (strain KT2440).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

OC Pseudomonadaceae; Pseudomonas.

NCBI_TaxID=160488;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC MEDLINE=22423060; PubMed=12534463;

RX DOI=10.1046/j.1462-2920.2002.00366.x;

RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,

RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,

RA Brinkac L.M., Beanan M.J., Deboy R.T., Daugherty S.C., Kolonay J.F.,

RA Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,

RA Hance I., Chris Lee P., Holtzaple E.K., Scanlan D., Tran K.,

RA Moazzez A., Uterback T.R., Rizzo M., Lee K., Kosack D., Mostl D.,

RA Medler H., Lauber J., Stjepandic D., Høheisel J., Straetz M., Heim S.,

RA Kiewitz C., Eissen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.,

RA Fraser C.M.;

RT "Complete genome sequence and comparative analysis of the

metabolically versatile Pseudomonas putida KT2440."

RL Environ. Microbiol. 4:799-808 (2002).

DR EMBL; AE016791; AAN70117.1; -; Genomic_DNA.

DR TIGR; PP4544; -.

KM Complete proteome; Hypothetical protein.

SQ SEQUENCE 414 AA; 45300 MW; 3725653CE960646 CRC64;

Query Match 73.9%; Score 34; DB 2; Length 414;
Best Local Similarity 77.8%; Pred. No. 2.1e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EVRLRYFDV 9
|:|:|:|:
DB 88 DVRLRYFDV 96

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RESULT 47
REF_HAUMA STANDARD; PRT; 418 AA.
AC 05JYX3;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Peptide chain release factor subunit 1 (translation termination factor
arfl1).
GN Name=prfl1; OrderedLocustNames=trnAC3164;
OS Halobacterium marismortui (Halobacterium marismortui).
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC Halobacteriaceae; Haloarcula.
NC NCBITaxID=2238;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 43049;
RX PubMed=15520287; DOI=10.1101/gr.2700304;
RA Baliga N.S., Bonneau R., Facciotti M.T., Pan M., Glusman G.,
RA Deutsch E.W., Shannon P., Chiu Y., Weng R.S., Gan R.R., Hung P.,
RA Date S.V., Marcotte E., Hood L., Ng W.V.;
"Genome sequence of Halobacterium marismortui: a halophilic archaeon from
the Dead Sea.";
Genome Res. 14:2221-2234(2004).
CC -!- FUNCTION: Directs the termination of nascent peptide synthesis
(translaction) in response to the termination codons UAA, UAG and
UGA (by similarity).
CC -!- SUBUNIT: Heterodimer of two subunits, one of which binds GTP (by
similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -!- SIMILARITY: Belongs to the eukaryotic release factor 1 family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC -----
DR EMBL, AY596297; AAV47870.1; -; Genomic_DNA.
DR HAMAP, MF_00424; -; 1.
DR InterPro, IPR004403; eRF1.
DR InterPro, IPR005140; eRF1.1.
DR InterPro, IPR005141; eRF1.2.
DR InterPro, IPR005142; eRF1.3.
DR PANTHER, PTHR10113; eRF1.1.
DR Pfam, PF03463; eRF1_1; 1.
DR Pfam, PF03464; eRF1_2; 1.
DR Pfam, PF03465; eRF1_3; 1.
DR TIGRFAMs, TIGR00108; eRF.1.
KW Complete proteome; Protein biosynthesis.
SQ SEQUENCE 418 AA; 46641 MW; 0F9A77B9817455A6 CRC64;

Query Match 73.9%; Score 34; DB 1; Length 418;
Best Local Similarity 85.7%; Pred. No. 2.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 RLRYPDV 9
| | | | |
Db 81 RLRYDV 87

RESULT 48
ID Q7AAU7_ECO57 PRELIMINARY; PRT; 433 AA.
AC Q7AAU7;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Putative adherence factor.
GN OrderedLocustNames=EC83860;
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

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OC Enterobacteriaceae; Escherichia.
OX NCBITaxID=83334;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=O157:H7 / Sakai / RIMD 0509952 / EHEC;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohnishi E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasaki K., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohemorrhagic Escherichia coli
O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
DR EMBL; BA000007; BAB37283.1; -; Genomic DNA.
SQ SEQUENCE 433 AA; 50207 MW; D73BAE17082A0E8C CRC64;

Query Match 73.9%; Score 34; DB 2; Length 433;
Best Local Similarity 75.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EVRLRYPD 8
| | | | |
Db 47 EARLRFPD 54

RESULT 49
ID Q8XEH7_ECO57 PRELIMINARY; PRT; 433 AA.
AC Q8XEH7;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Putative cytochrome.
GN OrderedLocustNames=z4332;
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBITaxID=83334;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;
RX MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Postel G., Hackert J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobbeck E.J., Davis N.W., Lim A., DiMaiano E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin X., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533(2001).
DR EMBL; AE005174; AAG58116.1; -; Genomic_DNA.
DR PIR; H85956; H85956.
KW Complete proteome.
SQ SEQUENCE 433 AA; 50203 MW; D73BAB03082A0E8C CRC64;

Query Match 73.9%; Score 34; DB 2; Length 433;
Best Local Similarity 75.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EVRLRYPD 8
| | | | |
Db 47 EARLRFPD 54

RESULT 50
ID Q7T199_CHICK PRELIMINARY; PRT; 516 AA.
AC Q7T199;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Shaker subfamily potassium channel KCNA10.
OS Gallus gallus (Chicken).

```


OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxId=9031;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=14969738; DOI=10.1016/j.molbrainres.2003.10.022;
 RA Duzhy D.E., Sakai Y., Sokolowski B.H.;
 RT "Cloning and developmental expression of Shaker potassium channels in
 the cochlea of the chicken.";
 RL Brain Res. Mol. Brain Res. 121:70-85(2004).
 DR EMBL; AY329362; AAP94024.1; -; mRNA.
 DR HSSP; Q9VMZ5; 1H02.
 DR SMR; O7T199; 91-189.
 DR Ensembl; ENSGALG0000000441; Gallus gallus.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0008076; C:voltage-gated potassium channel complex; IEA.
 DR GO; GO:0005515; F:protein binding; IEA.
 DR GO; GO:0005249; F:voltage-gated potassium channel activity; IEA.
 DR GO; GO:0006813; P:cation transport; IEA.
 DR GO; GO:0006813; P:potassium ion transport; IEA.
 DR InterPro; IPR000210; BTB_POZ.
 DR InterPro; IPR005821; Ion_trans.
 DR InterPro; IPR001622; K+channel_pore.
 DR InterPro; IPR003968; Kv_channel.
 DR InterPro; IPR003091; K_channel.
 DR InterPro; IPR003131; K_tetra.
 DR InterPro; IPR005820; M+channel_nlg.
 DR InterPro; IPR003972; Shaker_channel.
 DR Pfam; PF00520; Ion_trans; 1.
 DR Pfam; PF02214; K_tetra; 1.
 DR PRINTS; PR00169; KCHANNEL.
 DR PRINTS; PR01491; KCHANNEL.
 DR PRINTS; PR01496; SHAKERCHANNEL.
 DR SMART; SM00225; BTB; 1.
 KM Ion transport; Ionic channel; Transmembrane; Transport.
 SQ SEQUENCE 516 AA; 58983 MW; 8DDF48AA407B9153 CRC64;

Query Match 73.9%; Score 34; DB 2; Length 516;

Best Local Similarity 75.0%; Pred.No. 2.8e+02;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 EVRLRYFD 8
 | | | | |
 Db 121 EKRMRYFD 128

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 Job time : 135.286 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 4, 2006, 13:09:53 ; Search time 20.2857 Seconds
(without alignments)
36.680 Million cell updates/sec

Title: US-10-700-632-3

Perfect score: 46

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Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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4: /cgn2_6/prodata/1/1aa/BCTUS.COMB.pep:*
5: /cgn2_6/prodata/1/1aa/RB.COMB.pep:*
6: /cgn2_6/prodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	35	76.1	143	2	US-09-069-628-11
3	35	76.1	474	2	US-09-270-767-43583
4	34	73.9	812	1	US-08-446-794A-2
5	34	73.9	812	1	US-08-446-794A-4
6	34	73.9	812	1	US-08-750-007-3
7	34	73.9	812	1	US-08-945-024-2
8	33	71.7	127	2	US-09-270-767-60383
9	33	71.7	150	1	US-08-606-143-29
10	33	71.7	151	2	US-09-134-000C-4110
11	33	71.7	152	1	US-08-606-143-21
12	33	71.7	311	2	US-09-252-991A-28792
13	33	71.7	403	2	US-09-270-767-44912
14	33	71.7	563	2	US-09-270-957-6
15	33	71.7	563	2	US-09-270-957-21
16	33	71.7	616	2	US-09-275-252A-4
17	32	69.6	62	2	US-09-248-796A-24375
18	32	69.6	114	2	US-09-865-483-8
19	32	69.6	114	2	US-10-726-555-8
20	32	69.6	137	2	US-08-466-151-7
21	32	69.6	137	2	US-08-466-163B-7
22	32	69.6	137	2	US-09-802-096-7
23	32	69.6	137	2	US-09-802-077-7
24	32	69.6	137	2	US-09-925-179-7
25	32	69.6	385	2	US-09-134-000C-5159
26	32	69.6	412	2	US-08-765-907A-13
27	32	69.6	412	2	US-09-987-614A-13

28	32	69.6	452	1	US-08-984-171-3	Sequence 3, Appl
29	31	67.4	94	2	US-09-270-767-31984	Sequence 31984, A
30	31	67.4	94	2	US-09-270-767-47201	Sequence 47201, A
31	31	67.4	152	1	US-08-606-143-5	Sequence 5, Appl
32	31	67.4	152	1	US-08-606-143-6	Sequence 6, Appl
33	31	67.4	152	1	US-08-606-143-7	Sequence 7, Appl
34	31	67.4	152	1	US-08-606-143-9	Sequence 9, Appl
35	31	67.4	152	1	US-08-606-143-10	Sequence 10, Appl
36	31	67.4	152	1	US-08-606-143-11	Sequence 11, Appl
37	31	67.4	152	1	US-08-606-143-12	Sequence 12, Appl
38	31	67.4	152	1	US-08-606-143-15	Sequence 15, Appl
39	31	67.4	152	1	US-08-606-143-16	Sequence 16, Appl
40	31	67.4	152	1	US-08-606-143-18	Sequence 18, Appl
41	31	67.4	152	1	US-08-606-143-20	Sequence 20, Appl
42	31	67.4	152	1	US-08-606-143-25	Sequence 25, Appl
43	31	67.4	152	1	US-08-606-143-28	Sequence 28, Appl
44	31	67.4	152	1	US-08-606-143-30	Sequence 30, Appl
45	31	67.4	152	1	US-08-606-143-32	Sequence 32, Appl
46	31	67.4	166	2	US-09-902-540-16140	Sequence 16140, A
47	31	67.4	207	2	US-09-248-796A-16052	Sequence 16052, A
48	31	67.4	269	2	US-09-328-352-5849	Sequence 5849, Ap
49	31	67.4	279	2	US-09-134-001C-4707	Sequence 4707, Ap
50	31	67.4	290	2	US-09-489-039A-12135	Sequence 12135, A
51	31	67.4	314	2	US-09-252-991A-18599	Sequence 18599, A
52	31	67.4	327	1	US-08-926-724-1	Sequence 1, Appl
53	31	67.4	327	2	US-08-926-724-3	Sequence 3, Appl
54	31	67.4	327	2	US-08-904-032-3	Sequence 3, Appl
55	31	67.4	327	2	US-09-949-016-6562	Sequence 6562, Ap
56	31	67.4	351	2	US-09-916-109-7	Sequence 7, Appl
57	31	67.4	351	2	US-10-211-412B-7	Sequence 8077, Ap
58	31	67.4	353	2	US-09-949-016-8077	Sequence 3, Appl
59	31	67.4	361	2	US-09-916-109-3	Sequence 6, Appl
60	31	67.4	361	2	US-10-211-412B-3	Sequence 6, Appl
61	31	67.4	387	2	US-09-916-109-6	Sequence 6, Appl
62	31	67.4	387	2	US-10-211-412B-6	Sequence 6, Appl
63	31	67.4	394	2	US-09-916-109-2	Sequence 2, Appl
64	31	67.4	407	2	US-09-489-039A-10871	Sequence 10871, A
65	31	67.4	420	1	US-08-602-168A-14	Sequence 14, Appl
66	31	67.4	420	2	US-09-335-038-1	Sequence 1, Appl
67	31	67.4	420	2	US-09-916-109-1	Sequence 1, Appl
68	31	67.4	420	2	US-10-211-412B-1	Sequence 1, Appl
69	31	67.4	420	2	US-09-538-092-1163	Sequence 1163, Ap
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71	31	67.4	447	2	US-10-211-412B-5	Sequence 5, Appl
72	31	67.4	452	2	US-09-270-767-45514	Sequence 45514, A
73	31	67.4	483	2	US-09-916-109-4	Sequence 4, Appl
74	31	67.4	483	2	US-10-211-412B-4	Sequence 4, Appl
75	31	67.4	483	2	US-09-538-092-1162	Sequence 1162, Ap
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77	31	67.4	523	2	US-09-949-016-6195	Sequence 6195, Ap
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97	30	65.2	203	1	US-08-346-126-3	Sequence 3, Appl
98	30	65.2	203	2	US-08-893-828-3	Sequence 3, Appl
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103	30	65.2	236	2	US-09-583-110-3029	Sequence 3029, Ap	176	29	63.0	232	2	US-08-437-642B-28	Sequence 28, Appl
104	30	65.2	236	2	US-09-195-524-4	Sequence 4, Appli	177	29	63.0	232	2	US-08-437-642B-29	Sequence 29, Appl
105	30	65.2	241	2	US-09-107-433-4815	Sequence 4815, Ap	178	29	63.0	232	2	US-08-437-642B-31	Sequence 31, Appl
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115	30	65.2	480	2	US-09-526-043-13	Sequence 13, Appl	188	29	63.0	232	4	PCT-US93-07832-26	Sequence 26, Appl
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117	30	65.2	586	2	US-09-252-991A-11011	Sequence 31011, A	190	29	63.0	232	4	PCT-US93-07832-28	Sequence 28, Appl
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122	30	65.2	649	2	US-09-270-767-61886	Sequence 61886, A	195	29	63.0	232	4	PCT-US93-07832-35	Sequence 34, Appl
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124	30	65.2	703	2	US-10-048-621-6	Sequence 6, Appli	197	29	63.0	232	4	PCT-US93-07832-37	Sequence 36, Appl
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126	30	65.2	808	1	US-08-471-251A-2	Sequence 2, Appli	199	29	63.0	232	4	PCT-US93-07832-39	Sequence 38, Appl
127	30	65.2	830	2	US-08-872-855-11	Sequence 11, Appl	200	29	63.0	233	1	US-09-543-681A-8209	Sequence 8209, Ap
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249	29	63.0	464	2	US-09-056-783-2	Sequence 2	322	28	60.9	198	2	US-09-252-901A-11000	Sequence 11000, A
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253	29	63.0	469	2	US-09-705-686-23	Sequence 23, Appl	326	28	60.9	214	2	US-09-328-352-6025	Sequence 6025, Ap
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263	29	63.0	613	2	US-09-949-016-9735	Sequence 9735, Ap	336	28	60.9	289	2	US-10-723-061-22	Sequence 22, Appl
264	29	63.0	614	2	US-10-104-047-3276	Sequence 3276, Ap	337	28	60.9	295	2	US-09-902-540-10320	Sequence 10320, Ap
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267	29	63.0	628	2	US-09-333-636-6	Sequence 6, Appl	340	28	60.9	313	1	US-08-592-411-15	Sequence 15, Appl
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276	29	63.0	729	2	US-10-170-217-2	Sequence 2	349	28	60.9	346	1	US-09-153-559A-10	Sequence 10, Appl
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306	28	60.9	148	2	US-09-733-210-440	Sequence 440, App	379	28	60.9	461	2	US-09-967-952A-4	Sequence 4, Appl
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394	28	60.9	604	2	US-09-862-027-17	Sequence 17, Appl	467	27	58.7	156	2	US-09-248-786A-19980	Sequence 19980, A
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404	28	60.9	868	2	US-09-800-729-106	Sequence 106, App	477	27	58.7	203	1	US-08-684-024-8	Sequence 8, Appli
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410	28	60.9	1475	2	US-09-740-274-2	Sequence 2, Appli	483	27	58.7	205	2	US-09-145-668-7	Sequence 7, Appli
411	28	60.9	2262	2	US-09-269-446D-44	Sequence 44, Appl	484	27	58.7	205	2	US-09-234-245-7	Sequence 7, Appli
412	28	60.9	2265	1	US-08-148-097D-35	Sequence 35, Appl	485	27	58.7	205	2	US-09-234-245-6	Sequence 9, Appli
413	28	60.9	2509	1	US-08-148-097D-35	Sequence 35, Appl	486	27	58.7	212	2	US-09-234-245-6	Sequence 6, Appli
414	28	60.9	2546	2	US-09-949-016-9500	Sequence 9500, Ap	487	27	58.7	212	2	US-09-234-245-8	Sequence 8, Appli
415	28	60.9	2546	2	US-09-949-016-9501	Sequence 9501, Ap	488	27	58.7	218	2	US-09-942-937-2	Sequence 2, Appli
416	28	60.9	3072	2	US-09-413-814-93	Sequence 93, Appl	489	27	58.7	221	2	US-09-348-352-5680	Sequence 5680, Ap
417	28	60.9	3079	2	US-09-413-814-80	Sequence 80, Appl	490	27	58.7	221	2	US-09-949-016-10176	Sequence 10176, A
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423	27	58.7	17	2	US-09-490-070A-211	Sequence 211, App	496	27	58.7	235	2	US-09-583-110-0362	Sequence 3626, Ap
424	27	58.7	17	2	US-09-490-153-211	Sequence 211, App	497	27	58.7	238	2	US-09-583-110-0362	Sequence 3626, Ap
425	27	58.7	17	2	US-09-490-324-211	Sequence 211, App	498	27	58.7	243	2	US-10-159-901-44	Sequence 44, Appl
426	27	58.7	20	1	US-08-057-162B-4	Sequence 7, Appli	499	27	58.7	243	2	US-10-159-901-44	Sequence 44, Appl
427	27	58.7	24	2	US-08-986-837-7	Sequence 7, Appli	500	27	58.7	266	2	US-09-248-796A-19900	Sequence 19900, A
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429	27	58.7	29	2	US-09-868-864A-2	Sequence 2, Appli	502	27	58.7	271	2	US-08-467-285-2	Sequence 2, Appli
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431	27	58.7	68	2	US-09-107-532A-4596	Sequence 4596, Ap	504	27	58.7	271	2	US-09-375-907-1	Sequence 1, Appli
432	27	58.7	70	2	US-09-328-352-8126	Sequence 8126, Ap	505	27	58.7	271	2	US-09-543-681A-4346	Sequence 4346, Ap
433	27	58.7	70	2	US-09-543-681A-5149	Sequence 5149, Ap	506	27	58.7	271	2	US-09-538-092-1298	Sequence 1298, Ap
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435	27	58.7	78	2	US-09-270-767-52831	Sequence 52831, A	508	27	58.7	280	2	US-09-270-767-50774	Sequence 40774, A
436	27	58.7	79	2	US-09-513-999C-4530	Sequence 4530, Ap	509	27	58.7	280	2	US-09-270-767-55990	Sequence 55990, A
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439	27	58.7	97	2	US-09-543-681A-7909	Sequence 7909, Ap	512	27	58.7	295	2	US-09-830-280A-562	Sequence 562, App
440	27	58.7	111	2	US-08-881-037-14	Sequence 14, Appl	513	27	58.7	303	2	US-09-489-039A-7927	Sequence 7927, App
441	27	58.7	111	2	US-08-881-037-15	Sequence 15, Appl	514	27	58.7	308	2	US-09-710-219-578	Sequence 578, App
442	27	58.7	111	2	US-08-881-037-16	Sequence 16, Appl	515	27	58.7	310	2	US-09-252-991A-25022	Sequence 25022, A
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464	27	58.7	153	1	US-08-606-143-31	Sequence 31, Appl	537	27	58.7	369	2	US-09-352-990-6	Sequence 3, Appli
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573	27	58.7	612	2	US-08-762-500-79	Sequence 2, Appli	646	26	56.5	59	1	US-08-633-879C-18	Sequence 18, Appli
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595	27	58.7	777	2	US-10-012-064A-310	Sequence 310, App	668	26	56.5	109	2	US-09-270-767-5367	Sequence 5367, A
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694	26	56.5	155	1	US-08-606-143-23	Sequence 23, Appl	767	26	56.5	336	2	US-09-81-212-165	Sequence 165, Ap
695	26	56.5	158	2	US-09-605-703B-2516	Sequence 2516, Ap	768	26	56.5	336	2	US-09-713-601A-165	Sequence 165, Ap
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697	26	56.5	168	2	US-09-053-197A-20	Sequence 20, Appl	770	26	56.5	338	2	US-09-777-430C-48	Sequence 48, Appl
698	26	56.5	168	2	US-09-085-761A-20	Sequence 20, Appl	771	26	56.5	339	2	US-09-187-999-15	Sequence 15, Appl
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701	26	56.5	173	2	US-09-270-767-56556	Sequence 56556, A	774	26	56.5	346	2	US-09-489-039A-10342	Sequence 10342, A
702	26	56.5	174	2	US-09-543-681A-4727	Sequence 4727, Ap	775	26	56.5	347	2	US-08-749-816-3	Sequence 3, Appl
703	26	56.5	175	2	US-09-303-518D-524	Sequence 524, Ap	776	26	56.5	347	2	US-09-144-914-6	Sequence 6, Appl
704	26	56.5	176	2	US-09-270-767-40471	Sequence 40471, A	777	26	56.5	347	2	US-09-270-767-46821	Sequence 46821, A
705	26	56.5	176	2	US-09-270-767-55687	Sequence 55687, A	778	26	56.5	351	2	US-09-489-039A-1599	Sequence 7599, Ap
706	26	56.5	177	2	US-09-902-540-11502	Sequence 11502, A	779	26	56.5	352	1	US-08-483-926A-11	Sequence 11, Appl
707	26	56.5	191	2	US-08-936-165A-1525	Sequence 6235, App	780	26	56.5	352	1	US-08-733-045-12	Sequence 12, Appl
708	26	56.5	191	2	US-09-134-000C-6235	Sequence 6235, Ap	781	26	56.5	352	1	US-09-771-161A-157	Sequence 157, Ap
709	26	56.5	192	2	US-09-309-572-18	Sequence 18, Appl	782	26	56.5	355	2	US-09-270-767-45567	Sequence 45567, A
710	26	56.5	192	2	US-09-319-588C-8	Sequence 8, Appl	783	26	56.5	357	2	US-09-489-039A-10510	Sequence 10510, A
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712	26	56.5	203	2	US-09-902-540-9766	Sequence 9766, Ap	785						

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832	26	56.5	479	2	US-09-771-161A-248	Sequence 248, App	905	26	56.5	757	2	US-09-902-340-11380	Sequence 11380, A
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834	26	56.5	480	2	US-09-590-740-2	Sequence 2, Appli	907	26	56.5	766	1	US-08-951-648-2	Sequence 2, Appli
835	26	56.5	480	2	US-09-538-092-1053	Sequence 6, Appli	908	26	56.5	766	2	US-09-174-437-2	Sequence 2, Appli
836	26	56.5	480	2	US-09-205-658-157	Sequence 1053, Ap	909	26	56.5	766	2	US-09-686-055A-2	Sequence 2, Appli
837	26	56.5	480	2	US-09-526-043-14	Sequence 14, Appl	910	26	56.5	779	1	US-08-951-648-6	Sequence 6, Appli
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839	26	56.5	481	2	US-08-976-063E-38	Sequence 38, Appl	912	26	56.5	779	2	US-09-686-055A-6	Sequence 6, Appli
840	26	56.5	486	2	US-09-949-016-6790	Sequence 6790, Ap	913	26	56.5	779	2	US-09-420-190-1	Sequence 1, Appli
841	26	56.5	498	2	US-09-438-185A-600	Sequence 600, App	914	26	56.5	803	1	US-08-951-648-4	Sequence 4, Appli
842	26	56.5	499	2	US-09-270-767-57610	Sequence 57610, A	915	26	56.5	803	2	US-09-174-437-4	Sequence 4, Appli
843	26	56.5	509	2	US-08-688-988-40	Sequence 40, Appl	916	26	56.5	803	2	US-09-686-055A-4	Sequence 4, Appli
844	26	56.5	510	2	US-09-198-452A-639	Sequence 639, App	917	26	56.5	825	2	US-09-540-082A-26	Sequence 26, Appl
845	26	56.5	510	2	US-10-028-180-94	Sequence 94, Appl	918	26	56.5	839	2	US-10-202-481-4	Sequence 4, Appli
846	26	56.5	513	2	US-09-068-804-14	Sequence 14, Appl	919	26	56.5	849	2	US-09-081-385-152	Sequence 152, App
847	26	56.5	520	2	US-09-902-540-14226	Sequence 14226, A	920	26	56.5	849	2	US-09-752-639-152	Sequence 152, App
848	26	56.5	527	1	US-08-592-126-145	Sequence 145, App	921	26	56.5	849	2	US-09-712-813-152	Sequence 152, App
849	26	56.5	527	1	US-08-687-080-48	Sequence 48, App	922	26	56.5	849	2	US-09-700-354A-152	Sequence 152, App
850	26	56.5	527	1	US-09-168-595-145	Sequence 145, App	923	26	56.5	871	2	US-09-252-91A-29422	Sequence 29422, A
851	26	56.5	528	2	US-09-270-767-42914	Sequence 42914, A	924	26	56.5	876	1	US-08-785-071A-2	Sequence 2, Appli
852	26	56.5	529	2	US-09-949-016-6196	Sequence 6196, Ap	925	26	56.5	880	2	US-09-012-872-2	Sequence 2, Appli
853	26	56.5	533	2	US-09-907-794A-332	Sequence 332, App	926	26	56.5	881	2	US-09-700-487-3	Sequence 3, Appli
854	26	56.5	533	2	US-09-905-125A-332	Sequence 332, App	927	26	56.5	893	2	US-10-771-708-12	Sequence 12, Appl
855	26	56.5	533	2	US-09-902-775A-332	Sequence 332, App	928	26	56.5	893	2	US-09-328-352-6626	Sequence 6626, Ap
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857	26	56.5	533	2	US-09-903-603A-332	Sequence 332, App	930	26	56.5	898	2	US-09-489-039A-10322	Sequence 10322, A
858	26	56.5	533	2	US-09-904-920A-332	Sequence 332, App	931	26	56.5	919	2	US-08-985-916-16	Sequence 16, Appl
859	26	56.5	533	2	US-09-905-064-332	Sequence 332, App	932	26	56.5	927	2	US-09-252-91A-16765	Sequence 16765, A
860	26	56.5	533	2	US-09-906-618-332	Sequence 332, App	933	26	56.5	942	2	US-09-657-931A-9	Sequence 9, Appli
861	26	56.5	533	2	US-09-906-646-332	Sequence 332, App	934	26	56.5	1031	2	US-09-252-91A-11865	Sequence 11865, A
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863	26	56.5	533	2	US-09-902-736A-332	Sequence 332, App	936	26	56.5	1098	2	US-10-202-481-2	Sequence 2, Appli
864	26	56.5	533	2	US-09-906-722A-332	Sequence 332, App	937	26	56.5	1116	2	US-09-252-91A-24374	Sequence 24374, A
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866	26	56.5	537	1	US-08-643-879C-2	Sequence 2, Appli	939	26	56.5	1362	2	US-09-134-001C-4955	Sequence 4955, Ap
867	26	56.5	538	2	US-09-949-016-8017	Sequence 8017, Ap	940	26	56.5	1433	2	US-09-710-079-2052	Sequence 8, Appli
868	26	56.5	544	2	US-09-198-452A-380	Sequence 380, App	941	26	56.5	1402	2	US-09-106-968E-8	Sequence 8, Appli
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870	26	56.5	557	2	US-08-336-618-42	Sequence 2, Appli	943	26	56.5	1433	2	US-09-252-91A-21268	Sequence 21268, A
871	26	56.5	557	2	US-09-438-185A-365	Sequence 365, App	944	26	56.5	1433	2	US-09-916-964B-184	Sequence 184, App
872	26	56.5	557	2	US-09-949-016-7931	Sequence 7931, Ap	945	26	56.5	1577	1	US-08-793-824-2	Sequence 2, Appli
873	26	56.5	558	2	US-09-134-000C-4456	Sequence 4456, Ap	946	26	56.5	1681	2	US-10-037-417-20	Sequence 20, Appl
874	26	56.5	559	2	US-09-134-000C-4516	Sequence 4516, Ap	947	26	56.5	1637	2	US-10-037-417-18	Sequence 18, Appl
875	26	56.5	559	2	US-09-134-000C-4516	Sequence 4516, Ap	948	26	56.5	1728	2	US-09-919-497-98	Sequence 98, Appl
876	26	56.5	559	2	US-09-134-000C-4516	Sequence 4516, Ap	949	26	56.5	1736	2	US-09-949-016-9470	Sequence 9470, Ap
877	26	56.5	559	2	US-09-134-000C-4516	Sequence 4516, Ap	950	26	56.5	2336	2	US-09-268-163-10	Sequence 10, Appl
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880	26	56.5	559	2	US-09-134-000C-4516	Sequence 4516, Ap	953	26	56.5	2418	2	US-09-207-363-1	Sequence 1, Appli
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979 25 54.3 50 2 US-09-270-767-62096 Sequence 62096, A
980 25 54.3 58 1 US-08-086-328C-28 Sequence 28, App1
981 25 54.3 58 1 US-08-086-328C-42 Sequence 42, App1
982 25 54.3 58 1 US-08-086-328C-84 Sequence 84, App1
983 25 54.3 58 1 US-08-086-328C-207 Sequence 207, App
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988 25 54.3 61 1 US-08-829-876-222 Sequence 222, App
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995 25 54.3 61 2 US-10-076-604-222 Sequence 222, App
996 25 54.3 62 2 US-09-134-000C-5557 Sequence 5557, App
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998 25 54.3 63 2 US-09-248-786A-25210 Sequence 25210, A
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1000 25 54.3 65 2 US-09-107-532A-5827 Sequence 5827, App

ALIGNMENTS

RESULT 1
US-09-311-021-22
Sequence 22, Application US/09311021
Patent No. 6706869
GENERAL INFORMATION:
APPLICANT: Wong, Gordon G.
APPLICANT: Clark, Hilary
APPLICANT: Fechtel, Kim
APPLICANT: Agostino, Michael J.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: GI 6300-11A
CURRENT APPLICATION NUMBER: US/09/311, 021
CURRENT FILING DATE: 1999-05-13
NUMBER OF SEQ ID NOS: 268
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 22
LENGTH: 933
TYPE: PRT
ORGANISM: Homo sapiens
US-09-311-021-22

Query Match 82.6%; Score 38; DB 2; Length 933;
Best Local Similarity 75.0%; Pred. No. 25;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVRLRYFD 8
Db 40 EIRLKTFD 47

RESULT 2
US-09-069-628-11
Sequence 11, Application US/09069628B
Patent No. 6913756
GENERAL INFORMATION:
APPLICANT: Kearney, John F.
TITLE OF INVENTION: Monoclonal Antibodies Specific for Anthrax Spores
TITLE OF INVENTION: and Peptides Derived from the Antibodies Thereof
FILE REFERENCE: D6086
CURRENT APPLICATION NUMBER: US/09/069, 628B
CURRENT FILING DATE: 1998-04-29
NUMBER OF SEQ ID NOS: 31
SEQ ID NO 11

LENGTH: 143
TYPE: PRT
ORGANISM: Mus musculus
FEATURE:
OTHER INFORMATION: Sequence of framework three (FR3) region in hybridoma
Patent No. 6913756
OTHER INFORMATION: a07 incorporating VH7183.6 heavy chain gene from the
OTHER INFORMATION: VH7183 (MORC21) family
US-09-069-628-11

Query Match 76.1%; Score 35; DB 2; Length 143;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EVRLRYFDV 9
Db 92 EVTLRYFDV 100

RESULT 3
US-09-270-767-43583
Sequence 43583, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 43583
LENGTH: 474
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-270-767-43583

Query Match 76.1%; Score 35; DB 2; Length 474;
Best Local Similarity 62.5%; Pred. No. 49;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVRLRYFD 8
Db 318 EIRLKTFD 325

RESULT 4
US-08-446-794A-2
Sequence 2, Application US/08446794A
Patent No. 5747327
GENERAL INFORMATION:
APPLICANT: UEKI, JUN
APPLICANT: MORIOKA, SHINTI
TITLE OF INVENTION: PHOSPHOLIPASE D GENE ORIGINATED FROM
TITLE OF INVENTION: PLANT
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: P.O. BOX 747
CITY: FALUS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446, 794A
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:

NAME: MURPHY JR, GERALD M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 0760-0203P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 812 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-446-794A-2

Query Match 73.9%; Score 34; DB 1; Length 812;
Best Local Similarity 75.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 VLRLYFDV 9
|:|:|:|:|
Db 147 VKLQYFDV 154

RESULT 5
US-08-446-794A-4
Sequence 4, Application US/08446794A
Patent No. 5747327
GENERAL INFORMATION:

APPLICANT: Ueki, JUN
APPLICANT: MORIOKA, SHINJI
TITLE OF INVENTION: PHOSPHOLIPASE D GENE ORIGINATED FROM
TITLE OF INVENTION: PLANT
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: P.O. BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,794A
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 0760-0203P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8050
TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 812 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-446-794A-4

Query Match 73.9%; Score 34; DB 1; Length 812;
Best Local Similarity 75.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 VLRLYFDV 9
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Db 147 VKLQYFDV 154

RESULT 6
US-08-750-007-3
Sequence 3, Application US/08750007
Patent No. 5801016
GENERAL INFORMATION:

APPLICANT: MORIOKA, SHINJI
APPLICANT: Ueki, JUN
TITLE OF INVENTION: DNA FRAGMENT, RECOMBINANT VECTOR
TITLE OF INVENTION: CONTAINING THE SAME AND METHOD FOR EXPRESSING FOREIGN
TITLE OF INVENTION: GENES USING THE SAME
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,007
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: MURPHY JR, GERALD M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 0760-221P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 812 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-750-007-3

Query Match 73.9%; Score 34; DB 1; Length 812;
Best Local Similarity 75.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 VLRLYFDV 9
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Db 147 VKLQYFDV 154

RESULT 7
US-08-945-024-2
Sequence 2, Application US/08945024
Patent No. 5973226
GENERAL INFORMATION:

APPLICANT: MORIOKA, SHINJI
APPLICANT: Ueki, JUN
TITLE OF INVENTION: METHOD FOR CHANGING COMPOSITION OF
TITLE OF INVENTION: PHOSPHOLIPIDS PRODUCED BY ORGANISM AND RECOMBINANT VECTOR
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

Query Match 73.9%; Score 34; DB 1; Length 812;
Best Local Similarity 75.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/945,024
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 760-236
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 812 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-945-024-2

Query Match 73.9%; Score 34; DB 1; Length 812;
Best Local Similarity 75.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 VLRLRYFDV 9
DB 147 VKLQYFDV 154

RESULT 8
US-09-270-767-60383
Sequence 60383, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 60383
LENGTH: 127
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-270-767-60383

Query Match 71.7%; Score 33; DB 2; Length 127;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RLRYFD 8
DB 8 RLRYFD 13

RESULT 9
US-08-606-143-29
Sequence 29, Application US/08606143
Patent No. 5856155
GENERAL INFORMATION:
APPLICANT: Li, Min
TITLE OF INVENTION: COMPOUNDS AND RELATED METHODS FOR
MODULATING POTASSIUM ION CHANNELS AND ASSAYS FOR SUCH
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voigt & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/606,143
FILING DATE: 23-FEB-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kilyk Jr., John
REGISTRATION NUMBER: 30763
REFERENCE/DOCKET NUMBER: 71756
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
TELEFAX: (312) 616-5700
TELEX: 25-3533
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 150 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-606-143-29

Query Match 71.7%; Score 33; DB 1; Length 150;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RLRYFD 8
DB 34 RLRYFD 39

RESULT 10
US-09-134-000C-4110
Sequence 4110, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
SEQ ID NO 4110
LENGTH: 151
TYPE: PRT
ORGANISM: Enterococcus faecalis
US-09-134-000C-4110

Query Match 71.7%; Score 33; DB 2; Length 151;
Best Local Similarity 75.0%; Pred. No. 36;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EVRLRYFD 8
DB 121 EVTVRYFD 128

RESULT 11
US-08-606-143-21
Sequence 21, Application US/08606143
Patent No. 5856155
GENERAL INFORMATION:
APPLICANT: Li, Min
TITLE OF INVENTION: COMPOUNDS AND RELATED METHODS FOR
MODULATING POTASSIUM ION CHANNELS AND ASSAYS FOR SUCH
TITLE OF INVENTION:

TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/606,143
FILING DATE: 23-FEB-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kilyk Jr., John
REGISTRATION NUMBER: 30763
REFERENCE/DOCKET NUMBER: 71756
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5700
TELEFAX: (312) 616-5600
TELEX: 25-3533
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 152 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-606-143-21

Query Match 71.7%; Score 33; DB 1; Length 152;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RLRYFD 8
Db 34 RLRYFD 39

RESULT 12
US-09-252-991A-28792
Sequence 28792, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 28792
LENGTH: 311
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28792

Query Match 71.7%; Score 33; DB 2; Length 311;
Best Local Similarity 66.7%; Pred. No. 79;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EVRLRYFDV 9
Db 120 EVRLRYFDV 128

RESULT 13
US-09-270-767-44912
Sequence 44912, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 44912
LENGTH: 403
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-270-767-44912

Query Match 71.7%; Score 33; DB 2; Length 403;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RLRYFD 8
Db 281 RLRYFD 286

RESULT 14
US-09-270-957-6
Sequence 6, Application US/09270957
Patent No. 6641996
GENERAL INFORMATION:
APPLICANT: Richard A. Jefferson and Jorge E. Mayer
TITLE OF INVENTION: MICROBIAL-GLUCURONIDASE GENES, GENE
FILE REFERENCE: 190106.405C1
CURRENT APPLICATION NUMBER: US/09/270,957
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 112
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 563
TYPE: PRT
ORGANISM: Thermotoga maritima
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(563)
OTHER INFORMATION: Xaa = Any Amino Acid
US-09-270-957-6

Query Match 71.7%; Score 33; DB 2; Length 563;
Best Local Similarity 55.6%; Pred. No. 1.5e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EVRLRYFDV 9
Db 426 DVRLRYFDI 434

RESULT 15
US-09-270-957-21
Sequence 21, Application US/09270957
Patent No. 6641996
GENERAL INFORMATION:
APPLICANT: Richard A. Jefferson and Jorge E. Mayer
TITLE OF INVENTION: MICROBIAL-GLUCURONIDASE GENES, GENE
FILE REFERENCE: 190106.405C1
CURRENT APPLICATION NUMBER: US/09/270,957
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 112

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SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 563
; TYPE: PRT
; ORGANISM: Thermotoga maritima
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(563)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-270-957-21

Query Match
Best Local Similarity 71.7%; Score 33; DB 2; Length 563;
Best Local Similarity 55.6%; Pred. No. 1.5e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EVRLRYFDV 9
Db 426 DVALKYFDI 434

RESULT 16
US-09-275-252A-4
; Sequence 4, Application US/09275252A
; Patent No. 6641997
; GENERAL INFORMATION:
; APPLICANT: Macrimon, Roderick
; TITLE OF INVENTION: Assays for Screening Compounds Which Interact With
; TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation
; FILE REFERENCE: 018512-002901US
; CURRENT APPLICATION NUMBER: US/09/275,252A
; CURRENT FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: US 09/045,529
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/054,347
; PRIOR FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: WO PCT/US99/06307
; PRIOR FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 616
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-275-252A-4

Query Match
Best Local Similarity 71.7%; Score 33; DB 2; Length 616;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RLRYFD 8
Db 129 RLRYFD 134

RESULT 17
US-09-248-796A-24375
; Sequence 24375, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 24375
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```
; LENGTH: 62
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-24375

Query Match
Best Local Similarity 69.6%; Score 32; DB 2; Length 62;
Best Local Similarity 62.5%; Pred. No. 22;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EVRLRYFD 8
Db 41 EAKLRYD 48

RESULT 18
US-09-865-483-8
; Sequence 8, Application US/09865483
; Patent No. 6680053
; GENERAL INFORMATION:
; APPLICANT: LEE, Jong Wook et al.
; TITLE OF INVENTION: A VARIABLE REGION OF THE MONOCLONAL ANTIBODY AGAINST THE HBV S-SUR
; FILE REFERENCE: 1599-0197P
; CURRENT APPLICATION NUMBER: US/09/865,483
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-865-483-8

Query Match
Best Local Similarity 69.6%; Score 32; DB 2; Length 114;
Best Local Similarity 85.7%; Pred. No. 42;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 RLRYFDV 9
Db 97 RARYFDV 103

RESULT 19
US-10-726-555-8
; Sequence 8, Application US/10726555
; Patent No. 6924368
; GENERAL INFORMATION:
; APPLICANT: LEE, Jong Wook et al.
; TITLE OF INVENTION: A VARIABLE REGION OF THE MONOCLONAL ANTIBODY AGAINST THE HBV S-SUR
; TITLE OF INVENTION: ANTIGEN AND A GENE ENCODING THE SAME
; FILE REFERENCE: 1599-0197P
; CURRENT APPLICATION NUMBER: US/10/726,555
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: US/09/865,483
; PRIOR FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-726-555-8

Query Match
Best Local Similarity 69.6%; Score 32; DB 2; Length 114;
Best Local Similarity 85.7%; Pred. No. 42;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 RLRYFDV 9
Db 97 RARYFDV 103

RESULT 20
```

US-08-466-151-7
; Sequence 7, Application US/08466151
; Patent No. 6037453
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,151
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466163
; FILING DATE: 06-Jun-1995
; APPLICATION NUMBER: 08/405617
; FILING DATE: 15-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/185899
; FILING DATE: 26-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/879495
; FILING DATE: 07-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P2C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 137 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-466-151-7

Query Match 69.6%; Score 32; DB 2; Length 137;
Best Local Similarity 85.7%; Pred. No. 51;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 RLRYFDV 9
| | | | |
Db 107 RYRYFDV 113

RESULT 21
US-08-466-163B-7
; Sequence 7, Application US/08466163B
; Patent No. 6329509
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; FILE REFERENCE: P0718P2C1D1
; CURRENT APPLICATION NUMBER: US/08/466,163B
; CURRENT FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617

; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 7
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Mus musculus
US-08-466-163B-7

Query Match 69.6%; Score 32; DB 2; Length 137;
Best Local Similarity 85.7%; Pred. No. 51;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 RLRYFDV 9
| | | | |
Db 107 RYRYFDV 113

RESULT 22
US-09-802-096-7
; Sequence 7, Application US/09802096
; Patent No. 6685939
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C3US
; CURRENT APPLICATION NUMBER: US/09/802,096
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 7
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-802-096-7

Query Match 69.6%; Score 32; DB 2; Length 137;
Best Local Similarity 85.7%; Pred. No. 51;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 RLRYFDV 9
| | | | |
Db 107 RYRYFDV 113

RESULT 23
US-09-802-077-7
; Sequence 7, Application US/09802077
; Patent No. 6699472
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C3US
; CURRENT APPLICATION NUMBER: US/09/802,077
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15

; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 7
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-802-077-7

Query Match 69.6%; Score 32; DB 2; Length 137;
Best Local Similarity 85.7%; Pred. No. 51;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 RLRYFDV 9
Db 107 RYRYFDV 113

RESULT 24
US-09-925-179-7
; Sequence 7, Application US/09925179
; Patent No. 6914129

; GENERAL INFORMATION:
; APPLICANT: Jardiou, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Anti-15E Antibodies (as amended)
; FILE REFERENCE: P07182CIDICUS
; CURRENT APPLICATION NUMBER: US/09/925,179
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 08/466,163
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 7
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-925-179-7

Query Match 69.6%; Score 32; DB 2; Length 137;
Best Local Similarity 85.7%; Pred. No. 51;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 RLRYFDV 9
Db 107 RYRYFDV 113

RESULT 25
US-09-134-000C-5159
; Sequence 5159, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 03796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C

; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5159
; LENGTH: 385
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-5159

Query Match 69.6%; Score 32; DB 2; Length 385;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LRYFDV 9
Db 280 LRYFDV 285

RESULT 26
US-08-765-907A-13
; Sequence 13, Application US/08765907A
; Patent No. 6352839

; GENERAL INFORMATION:
; APPLICANT: BLANC, Veronique
; APPLICANT: BAWAS-JACQUES, Nathalie
; APPLICANT: BLANCHE, Francis
; APPLICANT: COUZET, Joel
; APPLICANT: BARRIERE, Jean-Claude
; APPLICANT: DEBUSSCHE, Laurent
; APPLICANT: FAMECHON, Alain
; APPLICANT: PARIS, Jean-Marc
; APPLICANT: DUTRUC-ROSSET, Gilles
; TITLE OF INVENTION: Streptogramins And Method For Preparing Same By
; FILE REFERENCE: Streptogramin genes
; CURRENT APPLICATION NUMBER: US/08/765,907A
; CURRENT FILING DATE: 1997-03-20
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Streptomyces pristinaespiralis
US-08-765-907A-13

Query Match 69.6%; Score 32; DB 2; Length 412;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVRLRYF 7
Db 336 EVQLRYF 342

RESULT 27
US-09-987-614A-13
; Sequence 13, Application US/09987614A
; Patent No. 6833382
; GENERAL INFORMATION:
; APPLICANT: BLANC, Veronique
; APPLICANT: THIBAUT, Denis
; APPLICANT: BAWAS-JACQUES, Nathalie
; APPLICANT: BLANCHE, Francis
; APPLICANT: COUZET, Joel
; APPLICANT: BARRIERE, Jean-Claude
; APPLICANT: DEBUSSCHE, Laurent
; APPLICANT: FAMECHON, Alain
; APPLICANT: PARIS, Jean-Marc
; APPLICANT: DUTRUC-ROSSET, Gilles
; TITLE OF INVENTION: Streptogramins And Method For Preparing Same By

TITLE OF INVENTION: Mataasynthesis
FILE REFERENCE: Streptogramin genes
CURRENT APPLICATION NUMBER: US/09/987,614A
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US/08/765,907
PRIOR FILING DATE: 1997-03-20
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 13
LENGTH: 412
TYPE: PRT
ORGANISM: Streptomyces pristinaespiralis
US-09-987-614A-13

Query Match 69.6%; Score 32; DB 2; Length 412;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVRLRYF 7
||:||||
Db 336 EVQLRYF 342

RESULT 28
US-08-984-171-3
Sequence 3, Application US/08984171
Patent No. 5952177

GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
APPLICANT: Au-Young, Janice
TITLE OF INVENTION: HUMAN CYTOSOLIC ISOCITRATE
TITLE OF INVENTION: DEHYDROGENASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PasteSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/984,171
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0434 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 452 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 872121
US-08-984-171-3

Query Match 69.6%; Score 32; DB 1; Length 452;

Best Local Similarity 44.4%; Pred. No. 1.9e+02;
Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EVRLRYFDV 9
:::||||:
Db 76 DIQLRYFDL 84

RESULT 29
US-09-270-767-31984
Sequence 31984, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 31984
LENGTH: 94
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-270-767-31984

Query Match 67.4%; Score 31; DB 2; Length 94;
Best Local Similarity 71.4%; Pred. No. 54;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RLRYFDV 9
:||||:
Db 73 KLRYFDV 79

RESULT 30
US-09-270-767-47201
Sequence 47201, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 47201
LENGTH: 94
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-270-767-47201

Query Match 67.4%; Score 31; DB 2; Length 94;
Best Local Similarity 71.4%; Pred. No. 54;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RLRYFDV 9
:||||:
Db 73 KLRYFDV 79

RESULT 31
US-08-606-143-5
Sequence 5, Application US/08606143
Patent No. 5856155
GENERAL INFORMATION:
APPLICANT: Li, Min
TITLE OF INVENTION: COMPOUNDS AND RELATED METHODS FOR
MODULATING POTASSIUM ION CHANNELS AND ASSAYS FOR SUCH
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:

ADDRESSEE: Leydig, Volt & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/606,143
FILING DATE: 23-FEB-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kilyk Jr., John
REGISTRATION NUMBER: 30763
REFERENCE/DOCKET NUMBER: 71756
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
TELEFAX: (312) 616-5700
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 152 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-606-143-5

Query Match 67.4%; Score 31; DB 1; Length 152;
Best Local Similarity 83.3%; Pred. No. 91;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RURYD 8
|:||||
Db 34 RURYD 39

RESULT 32
US-08-606-143-6
Sequence 6, Application US/08606143
Patent No. 5856155
GENERAL INFORMATION:
APPLICANT: Li, Min
TITLE OF INVENTION: COMPOUNDS AND RELATED METHODS FOR
TITLE OF INVENTION: MODULATING POTASSIUM ION CHANNELS AND ASSAYS FOR SUCH
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Volt & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/606,143
FILING DATE: 23-FEB-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kilyk Jr., John
REGISTRATION NUMBER: 30763
REFERENCE/DOCKET NUMBER: 71756
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600

TELEFAX: (312) 616-5700
TELEX: 25-3533
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 152 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-606-143-6

Query Match 67.4%; Score 31; DB 1; Length 152;
Best Local Similarity 83.3%; Pred. No. 91;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RURYD 8
|:||||
Db 34 RURYD 39

RESULT 33
US-08-606-143-7
Sequence 7, Application US/08606143
Patent No. 5856155
GENERAL INFORMATION:
APPLICANT: Li, Min
TITLE OF INVENTION: COMPOUNDS AND RELATED METHODS FOR
TITLE OF INVENTION: MODULATING POTASSIUM ION CHANNELS AND ASSAYS FOR SUCH
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Volt & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/606,143
FILING DATE: 23-FEB-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kilyk Jr., John
REGISTRATION NUMBER: 30763
REFERENCE/DOCKET NUMBER: 71756
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
TELEFAX: (312) 616-5700
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 152 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-606-143-7

Query Match 67.4%; Score 31; DB 1; Length 152;
Best Local Similarity 83.3%; Pred. No. 91;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RURYD 8
|:||||
Db 34 RURYD 39

RESULT 34

US-08-606-143-9
; Sequence 9, Application US/08606143
; Patent No. 5856155
; GENERAL INFORMATION:
; APPLICANT: Li, Min
; TITLE OF INVENTION: COMPOUNDS AND RELATED METHODS FOR
; TITLE OF INVENTION: MODULATING POTASSIUM ION CHANNELS AND ASSAYS FOR SUCH
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/606,143
; FILING DATE: 23-FEB-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kilyk Jr., John
; REGISTRATION NUMBER: 30763
; REFERENCE/DOCKET NUMBER: 71756
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 616-5700
; TELEFAX: (312) 616-5600
; TELEX: 25-3533
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 152 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-606-143-9

Query Match 67.4%; Score 31; DB 1; Length 152;
Best Local Similarity 83.3%; Pred. No. 91;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 3 RLRYFD 8
|:||||
Db 34 RMRYFD 39

RESULT 35
US-08-606-143-10
; Sequence 10, Application US/08606143
; Patent No. 5856155
; GENERAL INFORMATION:
; APPLICANT: Li, Min
; TITLE OF INVENTION: COMPOUNDS AND RELATED METHODS FOR
; TITLE OF INVENTION: MODULATING POTASSIUM ION CHANNELS AND ASSAYS FOR SUCH
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/606,143
; FILING DATE: 23-FEB-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kilyk Jr., John
; REGISTRATION NUMBER: 30763
; REFERENCE/DOCKET NUMBER: 71756
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 616-5600
; TELEFAX: (312) 616-5700
; TELEX: 25-3533
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 152 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-606-143-10

Query Match 67.4%; Score 31; DB 1; Length 152;
Best Local Similarity 83.3%; Pred. No. 91;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 3 RLRYFD 8
|:||||
Db 34 RMRYFD 39

RESULT 36
US-08-606-143-12
; Sequence 12, Application US/08606143
; Patent No. 5856155
; GENERAL INFORMATION:
; APPLICANT: Li, Min
; TITLE OF INVENTION: COMPOUNDS AND RELATED METHODS FOR
; TITLE OF INVENTION: MODULATING POTASSIUM ION CHANNELS AND ASSAYS FOR SUCH
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/606,143
; FILING DATE: 23-FEB-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kilyk Jr., John
; REGISTRATION NUMBER: 30763
; REFERENCE/DOCKET NUMBER: 71756
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 616-5600
; TELEFAX: (312) 616-5700
; TELEX: 25-3533
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 152 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-606-143-12

Query Match 67.4%; Score 31; DB 1; Length 152;
Best Local Similarity 83.3%; Pred. No. 91;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 RLRYPD 8
|:||||
Db 34 RMRYPD 39

RESULT 37
US-08-606-143-15
; Sequence 15, Application US/08606143
; Patent No. 5856155

GENERAL INFORMATION:
APPLICANT: Li, Min
TITLE OF INVENTION: COMPOUNDS AND RELATED METHODS FOR
MODULATING POTASSIUM ION CHANNELS AND ASSAYS FOR SUCH
TITLE OF INVENTION: MODULATING POTASSIUM ION CHANNELS AND ASSAYS FOR SUCH
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/606,143
FILING DATE: 23-FEB-1996
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: Kilyk Jr., John
REGISTRATION NUMBER: 30763
REFERENCE/DOCKET NUMBER: 71756
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
TELEFAX: (312) 616-5700
TELEX: 25-3533

INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 152 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-606-143-15

Query Match 67.4%; Score 31; DB 1; Length 152;
Best Local Similarity 83.3%; Pred. No. 91;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 RLRYPD 8
|:||||
Db 34 RMRYPD 39

RESULT 38
US-08-606-143-16
; Sequence 16, Application US/08606143
; Patent No. 5856155

GENERAL INFORMATION:
APPLICANT: Li, Min
TITLE OF INVENTION: COMPOUNDS AND RELATED METHODS FOR
MODULATING POTASSIUM ION CHANNELS AND ASSAYS FOR SUCH
TITLE OF INVENTION: MODULATING POTASSIUM ION CHANNELS AND ASSAYS FOR SUCH
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.

STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/606,143
FILING DATE: 23-FEB-1996
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: Kilyk Jr., John
REGISTRATION NUMBER: 30763
REFERENCE/DOCKET NUMBER: 71756
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
TELEFAX: (312) 616-5700
TELEX: 25-3533

INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 152 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-606-143-16

Query Match 67.4%; Score 31; DB 1; Length 152;
Best Local Similarity 83.3%; Pred. No. 91;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 RLRYPD 8
|:||||
Db 34 RMRYPD 39

RESULT 39
US-08-606-143-18
; Sequence 18, Application US/08606143
; Patent No. 5856155

GENERAL INFORMATION:
APPLICANT: Li, Min
TITLE OF INVENTION: COMPOUNDS AND RELATED METHODS FOR
MODULATING POTASSIUM ION CHANNELS AND ASSAYS FOR SUCH
TITLE OF INVENTION: MODULATING POTASSIUM ION CHANNELS AND ASSAYS FOR SUCH
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/606,143
FILING DATE: 23-FEB-1996
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: Kilyk Jr., John
REGISTRATION NUMBER: 30763
REFERENCE/DOCKET NUMBER: 71756
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
TELEFAX: (312) 616-5700

TELEX: 25-3533
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 152 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-606-143-18

Query Match 67.4%; Score 31; DB 1; Length 152;
Best Local Similarity 83.3%; Pred. No. 91;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 RURYD 8
|:||||
DB 34 RURYD 39

RESULT 40
US-08-606-143-20
Sequence 20, Application US/08606143
Patent No. 5856155

GENERAL INFORMATION:
APPLICANT: Li, Min
TITLE OF INVENTION: COMPOUNDS AND RELATED METHODS FOR
TITLE OF INVENTION: MODULATING POTASSIUM ION CHANNELS AND ASSAYS FOR SUCH
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/606,143
FILING DATE: 23-FEB-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kilyk Jr., John
REGISTRATION NUMBER: 30763
REFERENCE/DOCKET NUMBER: 71756
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
TELEFAX: (312) 616-5700
TELEX: 25-3533
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 152 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-606-143-20

Query Match 67.4%; Score 31; DB 1; Length 152;
Best Local Similarity 83.3%; Pred. No. 91;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 RURYD 8
|:||||
DB 34 RURYD 39

RESULT 41
US-08-606-143-25

Sequence 25, Application US/08606143
Patent No. 5856155
GENERAL INFORMATION:
APPLICANT: Li, Min
TITLE OF INVENTION: COMPOUNDS AND RELATED METHODS FOR
TITLE OF INVENTION: MODULATING POTASSIUM ION CHANNELS AND ASSAYS FOR SUCH
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/606,143
FILING DATE: 23-FEB-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kilyk Jr., John
REGISTRATION NUMBER: 30763
REFERENCE/DOCKET NUMBER: 71756
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
TELEFAX: (312) 616-5700
TELEX: 25-3533

INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 152 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-606-143-25

Query Match 67.4%; Score 31; DB 1; Length 152;
Best Local Similarity 83.3%; Pred. No. 91;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 RURYD 8
|:||||
DB 34 RURYD 39

RESULT 42
US-08-606-143-28
Sequence 28, Application US/08606143
Patent No. 5856155

GENERAL INFORMATION:
APPLICANT: Li, Min
TITLE OF INVENTION: COMPOUNDS AND RELATED METHODS FOR
TITLE OF INVENTION: MODULATING POTASSIUM ION CHANNELS AND ASSAYS FOR SUCH
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/606,143
FILING DATE: 23-FEB-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kilyk Jr., John
REGISTRATION NUMBER: 30763
REFERENCE/DOCKET NUMBER: 71756
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
TELEFAX: (312) 616-5700
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 28:
LENGTH: 152 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-606-143-28

Query Match 67.4%; Score 31; DB 1; Length 152;
Best Local Similarity 83.3%; Pred. No. 91;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 3 RLYRFD 8
|:||||
Db 34 RMYRFD 39

RESULT 43

US-08-606-143-30
Sequence 30, Application US/08606143

PATENT NO. 5856155
GENERAL INFORMATION:
APPLICANT: Li, Min
TITLE OF INVENTION: COMPOUNDS AND RELATED METHODS FOR
MODULATING POTASSIUM ION CHANNELS AND ASSAYS FOR SUCH
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/606,143
FILING DATE: 23-FEB-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kilyk Jr., John
REGISTRATION NUMBER: 30763
REFERENCE/DOCKET NUMBER: 71756
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
TELEFAX: (312) 616-5700
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 30:
LENGTH: 152 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-606-143-30

Query Match 67.4%; Score 31; DB 1; Length 152;

Best Local Similarity 83.3%; Pred. No. 91;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 3 RLYRFD 8
|:||||
Db 34 RMYRFD 39

RESULT 44

US-08-606-143-32
Sequence 32, Application US/08606143

PATENT NO. 5856155
GENERAL INFORMATION:
APPLICANT: Li, Min
TITLE OF INVENTION: COMPOUNDS AND RELATED METHODS FOR
MODULATING POTASSIUM ION CHANNELS AND ASSAYS FOR SUCH
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/606,143
FILING DATE: 23-FEB-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kilyk Jr., John
REGISTRATION NUMBER: 30763
REFERENCE/DOCKET NUMBER: 71756
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
TELEFAX: (312) 616-5700
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 32:
LENGTH: 152 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-606-143-32

Query Match 67.4%; Score 31; DB 1; Length 152;
Best Local Similarity 83.3%; Pred. No. 91;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 3 RLYRFD 8
|:||||
Db 34 RMYRFD 39

RESULT 45

US-09-902-540-16140
Sequence 16140, Application US/09902540

PATENT NO. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10

; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 16140
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-16140

Query Match 67.4%; Score 31; DB 2; Length 166;
Best Local Similarity 66.7%; Pred. No. 1e+02; 1; Indels 0; Gaps 0;
Matches 6; Conservative 2; Mismatches 1;

Qy 1 EVRLRYFDV 9
|:|:|:|:
Db 62 ELRLRVFEV 70

RESULT 46
US-09-248-796A-16052
; Sequence 16052, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 16052
; LENGTH: 207
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-16052

Query Match 67.4%; Score 31; DB 2; Length 207;
Best Local Similarity 55.6%; Pred. No. 1.3e+02; 3; Indels 0; Gaps 0;
Matches 5; Conservative 3; Mismatches 1;

Qy 1 EVRLRYFDV 9
|:|:|:|:
Db 102 KVRLLNYDL 110

RESULT 47
US-09-328-352-5849
; Sequence 5849, Application US/09328352
; Patent No. 6562358
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5849
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5849

Query Match 67.4%; Score 31; DB 2; Length 269;
Best Local Similarity 55.6%; Pred. No. 1.7e+02; 2; Indels 0; Gaps 0;
Matches 5; Conservative 2; Mismatches 2;

Qy 1 EVRLRYFDV 9
|:|:|:|:

Db 118 EIELKRYFSV 126

RESULT 48
US-09-134-001C-4707
; Sequence 4707, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4707
; LENGTH: 279
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4707

Query Match 67.4%; Score 31; DB 2; Length 279;
Best Local Similarity 62.5%; Pred. No. 1.8e+02; 1; Indels 0; Gaps 0;
Matches 5; Conservative 2; Mismatches 1;

Qy 1 EVRLRYFD 8
|:|:|:|:
Db 249 EIKRKYFD 256

RESULT 49
US-09-489-039A-12135
; Sequence 12135, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 12135
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12135

Query Match 67.4%; Score 31; DB 2; Length 290;
Best Local Similarity 50.0%; Pred. No. 1.8e+02; 4; Indels 0; Gaps 0;
Matches 4; Conservative 4; Mismatches 0;

Qy 2 VRLRYFDV 9
|:|:|:|:
Db 231 IRMRFDL 238

RESULT 50
US-09-252-991A-18599
; Sequence 18599, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18599
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18599

Query Match 67.4%; Score 31; DB 2; Length 314;
Best Local Similarity 55.6%; Pred. NO. 2e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EVRLRYFDV 9
||:|:|:
Db 119 EVEIRFEV 127

Search completed: May 4, 2006, 13:12:49
Job time : 31.2857 secs

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OM protein - protein search, using sw model

Run on: May 4, 2006, 13:43:49 ; Search time 65.2857 Seconds
(without alignments)
57.600 Million cell updates/sec

Title: US-10-700-632-3
Perfect score: 46
Sequence: 1 EVRLRYFDPV 9

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Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published Applications_AA_Main:*

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- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBSCOMB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBSCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBSCOMB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBSCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	46	100.0	20	US-10-700-632-53	Sequence 53, Appli
3	46	100.0	117	US-10-700-632-73	Sequence 73, Appli
4	46	100.0	118	US-10-700-632-7	Sequence 7, Appli
5	46	100.0	118	US-10-700-632-9	Sequence 9, Appli
6	38	82.6	252	US-10-424-599-167634	Sequence 167634, Appli
7	38	82.6	816	US-10-264-237-2159	Sequence 2159, Ap
8	38	82.6	1152	US-09-374-046A-46	Sequence 46, Appli
9	38	82.6	1217	US-10-616-263-46	Sequence 46, Appli
10	38	82.6	1217	US-10-764-425-101	Sequence 101, App
11	38	82.6	1217	US-10-756-149-5390	Sequence 5390, Ap
12	38	82.6	1217	US-10-287-436A-633	Sequence 633, App
13	35	76.1	59	US-10-469-013-45	Sequence 45, Appli
14	35	76.1	206	US-10-469-013-25	Sequence 162, Appli
15	35	76.1	228	US-09-881-752A-162	Sequence 3, Appli
16	35	76.1	356	US-09-791-961-3	Sequence 3, Appli
17	35	76.1	356	US-10-637-280-3	Sequence 52343, A
18	35	76.1	491	US-10-425-114-52343	Sequence 23767, A
19	35	76.1	547	US-10-425-115-237671	Sequence 2, Appli
20	35	76.1	868	US-10-469-013-2	Sequence 144903, A
21	35	76.1	888	US-10-437-963-144903	Sequence 237629, A
22	35	76.1	1169	US-11-097-143-33063	Sequence 33063, A
23	34	73.9	61	US-10-424-599-237629	Sequence 237348, A
24	34	73.9	127	US-10-424-599-233348	Sequence 53889, A
25	34	73.9	177	US-10-767-701-53889	Sequence 296096, A
26	34	73.9	194	US-10-425-115-296096	Sequence 206875, A
27	34	73.9	205	US-10-424-599-206875	Sequence 206875, A

28	34	73.9	233	US-10-369-493-3892	Sequence 3892, Ap
29	34	73.9	377	US-10-767-701-43782	Sequence 43782, A
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32	34	73.9	780	US-10-425-114-47224	Sequence 47224, A
33	34	73.9	808	US-10-424-599-171300	Sequence 171300, A
34	34	73.9	809	US-10-078-770-124	Sequence 124, App
35	34	73.9	809	US-10-424-599-206877	Sequence 206877, A
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37	34	73.9	812	US-10-425-115-29607	Sequence 29607, A
38	34	73.9	812	US-10-425-115-296104	Sequence 296104, A
39	34	73.9	812	US-10-425-115-296107	Sequence 296107, A
40	34	73.9	813	US-10-425-114-70103	Sequence 70103, A
41	34	73.9	815	US-10-425-115-296103	Sequence 296103, A
42	34	73.9	817	US-10-425-114-47222	Sequence 47222, A
43	34	73.9	820	US-10-425-114-53704	Sequence 53704, A
44	34	73.9	820	US-10-425-114-70197	Sequence 70197, A
45	34	73.9	821	US-10-425-114-57839	Sequence 57839, A
46	34	73.9	840	US-10-425-115-296105	Sequence 296105, A
47	34	73.9	849	US-10-425-114-47222	Sequence 47222, A
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50	33	71.7	174	US-10-425-115-339287	Sequence 339287, A
51	33	71.7	202	US-11-097-143-17169	Sequence 17169, A
52	33	71.7	256	US-10-424-599-192562	Sequence 192562, A
53	33	71.7	304	US-11-013-314-50	Sequence 50, Appli
54	33	71.7	345	US-11-097-143-32407	Sequence 32407, A
55	33	71.7	359	US-10-739-930-6131	Sequence 6131, Ap
56	33	71.7	419	US-11-013-314-51	Sequence 51, Appli
57	33	71.7	423	US-10-424-599-273945	Sequence 273945, A
58	33	71.7	464	US-10-437-963-109962	Sequence 109962, A
59	33	71.7	536	US-10-320-797-12247	Sequence 12247, Ap
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61	33	71.7	563	US-10-364-649-21	Sequence 21, Appli
62	33	71.7	563	US-10-369-493-2995	Sequence 2995, Ap
63	33	71.7	563	US-10-757-093-30	Sequence 20, Appli
64	33	71.7	571	US-11-013-314-49	Sequence 49, Appli
65	33	71.7	641	US-11-097-143-894	Sequence 894, App
66	33	71.7	643	US-11-013-314-48	Sequence 48, Appli
67	33	71.7	655	US-11-013-314-52	Sequence 52, Appli
68	33	71.7	656	US-10-377-139-4	Sequence 139, Appli
69	33	71.7	89	US-10-437-963-113495	Sequence 113495, A
70	32	69.6	114	US-10-425-115-220943	Sequence 220943, A
71	32	69.6	114	US-09-865-483-8	Sequence 8, Appli
72	32	69.6	137	US-10-802-077-7	Sequence 7, Appli
73	32	69.6	137	US-09-802-096-7	Sequence 7, Appli
74	32	69.6	137	US-09-925-179-7	Sequence 7, Appli
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76	32	69.6	170	US-10-767-701-53963	Sequence 53963, A
77	32	69.6	170	US-10-437-963-143056	Sequence 143056, A
78	32	69.6	230	US-10-282-122A-76757	Sequence 76757, A
79	32	69.6	279	US-10-282-122A-78561	Sequence 78561, A
80	32	69.6	309	US-10-425-114-36577	Sequence 36577, A
81	32	69.6	348	US-10-310-154-544	Sequence 544, App
82	32	69.6	348	US-10-424-599-201198	Sequence 201198, A
83	32	69.6	348	US-10-732-923-564	Sequence 564, App
84	32	69.6	399	US-10-425-115-323043	Sequence 323043, A
85	32	69.6	429	US-10-437-963-143058	Sequence 143058, A
86	32	69.6	430	US-10-425-114-16967	Sequence 46967, A
87	32	69.6	452	US-10-618-143-4	Sequence 4, Appli
88	32	69.6	452	US-10-408-765A-2467	Sequence 2467, Ap
89	32	69.6	452	US-10-408-765A-3014	Sequence 3014, Ap
90	32	69.6	468	US-10-732-923-6168	Sequence 6168, Ap
91	32	69.6	484	US-09-925-179-1422	Sequence 1422, Ap
92	32	69.6	494	US-10-156-761-11379	Sequence 11379, A
93	32	69.6	628	US-10-369-493-133988	Sequence 133988, A
94	32	69.6	72	US-10-424-599-155856	Sequence 155856, A
95	31	67.4	72	US-10-029-386-29199	Sequence 29199, A
96	31	67.4	98	US-10-424-599-224503	Sequence 224503, A
97	31	67.4	98	US-10-767-701-52852	Sequence 52852, A
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251	30	65.2	241	5	US-10-861-920-10	Sequence 10, Appli
252	30	65.2	241	5	US-10-617-320-4815	Sequence 4815, Ap
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254	30	65.2	257	3	US-09-880-748-1256	Sequence 1256, Ap
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260	30	65.2	266	3	US-10-282-122A-74110	Sequence 74110, A
261	30	65.2	266	5	US-10-472-928-3416	Sequence 3416, Ap
262	30	65.2	275	4	US-10-291-172-215	Sequence 215, App
263	30	65.2	275	4	US-10-221-278-215	Sequence 215, App
264	30	65.2	280	4	US-10-369-493-981	Sequence 981, Appli
265	30	65.2	290	4	US-10-398-663-2	Sequence 253335, A
266	30	65.2	291	4	US-10-424-599-253335	Sequence 253335, A
267	30	65.2	291	5	US-10-739-930-9046	Sequence 9046, Ap
268	30	65.2	298	6	US-11-097-143-42915	Sequence 42915, A
269	30	65.2	302	4	US-10-437-963-152285	Sequence 152285, A
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271	30	65.2	307	4	US-10-369-493-11137	Sequence 11137, A
272	30	65.2	308	4	US-10-282-122A-69373	Sequence 69373, A
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275	30	65.2	315	4	US-10-746-545-23	Sequence 23, Appli
276	30	65.2	315	6	US-11-021-951-163	Sequence 163, App
277	30	65.2	319	4	US-10-116-722A-6	Sequence 6, Appli
278	30	65.2	319	4	US-10-116-722A-8	Sequence 8, Appli
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280	30	65.2	325	5	US-10-733-9692A-99	Sequence 99, Appli
281	30	65.2	325	5	US-10-490-064-40	Sequence 40, Appli
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284	30	65.2	329	5	US-10-861-920-4	Sequence 24, Appli
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288	30	65.2	336	4	US-10-217-555-21	Sequence 38, Appli
289	30	65.2	341	5	US-10-491-183-38	Sequence 6, Appli
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295	30	65.2	380	4	US-10-335-977-7100	Sequence 9479, Ap
296	30	65.2	383	5	US-10-739-930-5758	Sequence 111246, A
297	30	65.2	387	4	US-10-156-761-9479	Sequence 3720, Ap
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309	30	65.2	445	6	US-11-097-143-36663	Sequence 11, Appli
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313	30	65.2	480	4	US-10-425-114-37865	Sequence 17891, A
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319	30	65.2	498	4	US-10-369-493-17891	


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977 28 60.9 619 4 US-10-369-493-7428 Sequence 7428, Ap
978 28 60.9 620 3 US-09-815-242-10068 Sequence 10068, A
979 28 60.9 620 3 US-09-815-242-14083 Sequence 14083, A
980 28 60.9 620 3 US-09-934-903-2 Sequence 2, Appl1
981 28 60.9 620 3 US-09-934-868-62 Sequence 62, Appl1
982 28 60.9 620 3 US-09-941-947A-6 Sequence 31, Appl1
983 28 60.9 620 4 US-10-381-779-31 Sequence 731, App
984 28 60.9 620 4 US-10-369-493-731 Sequence 56450, A
985 28 60.9 620 4 US-10-282-122A-56450 Sequence 75419, A
986 28 60.9 620 4 US-10-282-122A-75419 Sequence 2, Appl1
987 28 60.9 620 4 US-10-700-003-2 Sequence 2, Appl1
988 28 60.9 620 4 US-10-363-567-6 Sequence 6, Appl1
989 28 60.9 620 4 US-10-701-200-62 Sequence 6, Appl1
990 28 60.9 620 5 US-10-735-442-14 Sequence 14, Appl1
991 28 60.9 620 5 US-10-938-613-1 Sequence 1, Appl1
992 28 60.9 622 5 US-10-450-763-48065 Sequence 48065, A
993 28 60.9 623 4 US-10-369-493-15911 Sequence 15911, A
994 28 60.9 623 4 US-10-369-493-16259 Sequence 16259, A
995 28 60.9 623 4 US-10-369-493-16281 Sequence 16281, A
996 28 60.9 627 4 US-10-381-779-15 Sequence 15, Appl1
997 28 60.9 630 4 US-10-369-493-15888 Sequence 15888, A
998 28 60.9 632 4 US-10-369-493-15431 Sequence 15431, A
999 28 60.9 632 4 US-10-369-493-15800 Sequence 15800, A
1000 28 60.9 637 4 US-10-381-779-32 Sequence 32, Appl1
```

ALIGNMENTS

```
RESULT 1
US-10-700-632-3
; Sequence 3, Application US/10700632
; Publication No. US20050118183A1
; GENERAL INFORMATION:
; APPLICANT: Immunogen, Inc.
; TITLE OF INVENTION: ANTI-CD33 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID
; FILE REFERENCE: A8427
; CURRENT APPLICATION NUMBER: US/10/700,632
; CURRENT FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: US 60/424,332
; PRIOR FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-700-632-3
```

```
Query Match 100.0%; Score 46; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;
```

```
Oy 1 EVRLRYFDV 9
Db 1 EVRLRYFDV 9
```

```
RESULT 2
US-10-700-632-53
; Sequence 53, Application US/10700632
; Publication No. US20050118183A1
; GENERAL INFORMATION:
; APPLICANT: Immunogen, Inc.
; TITLE OF INVENTION: ANTI-CD33 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID
; FILE REFERENCE: A8427
; CURRENT APPLICATION NUMBER: US/10/700,632
; CURRENT FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: US 60/424,332
; PRIOR FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 94
```

```
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 53
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-700-632-53
```

```
Query Match 100.0%; Score 46; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.044; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;
```

```
Oy 1 EVRLRYFDV 9
Db 1 EVRLRYFDV 9
```

```
RESULT 3
US-10-700-632-73
; Sequence 73, Application US/10700632
; Publication No. US20050118183A1
; GENERAL INFORMATION:
; APPLICANT: Immunogen, Inc.
; TITLE OF INVENTION: ANTI-CD33 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID
; FILE REFERENCE: A8427
; CURRENT APPLICATION NUMBER: US/10/700,632
; CURRENT FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: US 60/424,332
; PRIOR FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 73
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-700-632-73
```

```
Query Match 100.0%; Score 46; DB 5; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.29; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;
```

```
Oy 1 EVRLRYFDV 9
Db 99 EVRLRYFDV 107
```

```
RESULT 4
US-10-700-632-7
; Sequence 7, Application US/10700632
; Publication No. US20050118183A1
; GENERAL INFORMATION:
; APPLICANT: Immunogen, Inc.
; TITLE OF INVENTION: ANTI-CD33 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID
; FILE REFERENCE: A8427
; CURRENT APPLICATION NUMBER: US/10/700,632
; CURRENT FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: US 60/424,332
; PRIOR FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-700-632-7
```

```
Query Match 100.0%; Score 46; DB 5; Length 118;
Best Local Similarity 100.0%; Pred. No. 0.29; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;
```

```
Oy 1 EVRLRYFDV 9
Db 1 EVRLRYFDV 9
```


Db 99 EVRLRYFDV 107

RESULT 5

US-10-700-632-9
; Sequence 9, Application US/10700632
; Publication No. US20050118183A1
; GENERAL INFORMATION:
; APPLICANT: Immunogen, Inc.
; TITLE OF INVENTION: ANTI-CD3 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID
; FILE REFERENCE: A8427
; CURRENT APPLICATION NUMBER: US/10/700,632
; CURRENT FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: US 60/424,332
; PRIOR FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized My9-6 antibody heavy chain variable region
US-10-700-632-9

Query Match 100.0%; Score 46; DB 5; Length 118;

Best Local Similarity 100.0%; Pred. No. 0.29; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVRLRYFDV 9

Db 99 EVRLRYFDV 107

RESULT 6

US-10-424-599-167634
; Sequence 167634, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 167634
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(252)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MKT3847_122390C.1.pcp
US-10-424-599-167634

Query Match 82.6%; Score 38; DB 4; Length 252;

Best Local Similarity 75.0%; Pred. No. 25; Indels 0; Gaps 0;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVRLRYFD 8

Db 199 EIRLRYFD 206

RESULT 7

US-10-264-237-2159

; Sequence 2159, Application US/10264237
; Publication No. US20040009491A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 2159
; LENGTH: 816
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (62)-
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (82)-
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (804)-
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (807)-
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (813)-
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-237-2159

Query Match 82.6%; Score 38; DB 4; Length 816;

Best Local Similarity 75.0%; Pred. No. 90; Indels 0; Gaps 0;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVRLRYFD 8

Db 40 EIRLRYFD 47

RESULT 8

US-09-374-046A-46
; Sequence 46, Application US/09374046A
; Publication No. US20030096951A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: Lavallee, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Werberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steinginger II, Robert J.
; APPLICANT: Spaulding, Vikki
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fechtel, Kim
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYPEPTIDES ENCODING THEM
; FILE REFERENCE: GI 6075-83A
; CURRENT APPLICATION NUMBER: US/09/374,046A
; CURRENT FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 240

```
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 1152
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-374-046A-46
```

```
Query Match      82.6%; Score 38; DB 3; Length 1152;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 EVRLRYFD 8
         |::|::|
Db      259 EIRLKYFD 266
```

RESULT 9

```
US-10-616-263-46
; Sequence 46, Application US/10616263
; Publication No. US20040038276A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: Lavallee, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steinger II, Robert J.
; APPLICANT: Spaulding, Vikki
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fectel, Kim
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYPEPTIDES ENCODING THEM
; FILE REFERENCE: 0076,000103.5
; CURRENT APPLICATION NUMBER: US/10/616,263
; CURRENT FILING DATE: 2003-07-08
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 1152
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-616-263-46
```

```
Query Match      82.6%; Score 38; DB 4; Length 1152;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 EVRLRYFD 8
         |::|::|
Db      259 EIRLKYFD 266
```

RESULT 10

```
US-10-764-425-101
; Sequence 101, Application US/10764425
; Publication No. US20040146921A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Pharmaceuticals Corporation
; APPLICANT: Eveleigh, Deepa
; APPLICANT: Bigwood, Douglas
; APPLICANT: Taylor, Ian
; TITLE OF INVENTION: EXPRESSION PROFILES FOR COLON CANCER AND METHODS OF USE
; FILE REFERENCE: 5151
; CURRENT APPLICATION NUMBER: US/10/764,425
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: 60/442,582
; PRIOR FILING DATE: 2003-01-24
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: PatentIn version 3.2
```

```
; SEQ ID NO 101
; LENGTH: 1217
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-764-425-101
```

```
Query Match      82.6%; Score 38; DB 4; Length 1217;
Best Local Similarity 75.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 EVRLRYFD 8
         |::|::|
Db      324 EIRLKYFD 331
```

RESULT 11

```
US-10-756-149-5390
; Sequence 5390, Application US/10756149
; Publication No. US20050181375A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/756,149
; CURRENT FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 5818
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5390
; LENGTH: 1217
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-756-149-5390
```

```
Query Match      82.6%; Score 38; DB 5; Length 1217;
Best Local Similarity 75.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 EVRLRYFD 8
         |::|::|
Db      324 EIRLKYFD 331
```

RESULT 12

```
US-10-287-436A-633
; Sequence 633, Application US/10287436A
; Publication No. US20050202421A1
; GENERAL INFORMATION:
; APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
; TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: RHEMATOID ARTHRITIS
; FILE REFERENCE: 10872,514696
; CURRENT APPLICATION NUMBER: US/10/287,436A
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/336,220
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 1446
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 633
; LENGTH: 1217
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-436A-633
```

```
Query Match      82.6%; Score 38; DB 5; Length 1217;
Best Local Similarity 75.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 EVRLRYFD 8
         |::|::|
Db      324 EIRLKYFD 331
```

```
RESULT 13
US-10-469-013-45
; Sequence 45, Application US/10469013
; Publication No. US20040096861A1
; GENERAL INFORMATION:
; APPLICANT: Syngenta Participations AG
; TITLE OF INVENTION: Oryza Sativa Nuclear Cap Binding Protein 80
; FILE REFERENCE: S-60023A
; CURRENT APPLICATION NUMBER: US/10/469,013
; PRIOR FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: US 60/282,370
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-469-013-45
```

```
Query Match          76.1%; Score 35; DB 4; Length 59;
Best Local Similarity 75.0%; Pred. No. 21;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 EVRLRYFD 8
   ||:|||||
Db 27 EIRLSYFD 34
```

```
RESULT 14
US-10-469-013-25
; Sequence 25, Application US/10469013
; Publication No. US20040096861A1
; GENERAL INFORMATION:
; APPLICANT: Syngenta Participations AG
; TITLE OF INVENTION: Oryza Sativa Nuclear Cap Binding Protein 80
; FILE REFERENCE: S-60023A
; CURRENT APPLICATION NUMBER: US/10/469,013
; PRIOR FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: US 60/282,370
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-469-013-25
```

```
Query Match          76.1%; Score 35; DB 4; Length 206;
Best Local Similarity 75.0%; Pred. No. 81;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 EVRLRYFD 8
   ||:|||||
Db 186 EIRLSYFD 193
```

```
RESULT 15
US-09-881-752A-162
; Sequence 162, Application US/09881752A
; Patent No. US20020115078A1
; GENERAL INFORMATION:
; APPLICANT: Kleantous, Harold
; APPLICANT: Al-Garawi, Amal
; APPLICANT: Miller, Charles
; APPLICANT: Tomb, Jean-Francois
; APPLICANT: Oomen, Raymond P.
; TITLE OF INVENTION: Identification of Polynucleotides
; TITLE OF INVENTION: Encoding No. US20020115078A1 Helicobacter Polypeptides in the
; FILE REFERENCE: 06132/041002
```

```
; CURRENT APPLICATION NUMBER: US/09/881,752A
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 08/833,457
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 370
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 162
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-881-752A-162
```

```
Query Match          76.1%; Score 35; DB 3; Length 228;
Best Local Similarity 66.7%; Pred. No. 90;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 EVRLRYFDV 9
   ||:|||||
Db 170 EVLKYFDI 178
```

```
RESULT 16
US-09-791-961-3
; Sequence 3, Application US/09791961
; Patent No. US20010047029A1
; GENERAL INFORMATION:
; APPLICANT: Brady, Sean
; APPLICANT: Bettermann, Alan
; APPLICANT: Gillespie, Doreen
; APPLICANT: Goodman, Robert
; APPLICANT: Handlesman, Jo
; APPLICANT: Clardy, Jon
; TITLE OF INVENTION: Triaryl Cation Antibiotics from Environmental DNA
; FILE REFERENCE: 09820.144
; CURRENT APPLICATION NUMBER: US/09/791,961
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Vibrio vulnificus
US-09-791-961-3
```

```
Query Match          76.1%; Score 35; DB 3; Length 356;
Best Local Similarity 62.5%; Pred. No. 1.4e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 2 VRLRYFDV 9
   ||:|||||
Db 188 VKIRYFDI 195
```

```
RESULT 17
US-10-637-280-3
; Sequence 3, Application US/10637280
; Publication No. US20040034088A1
; GENERAL INFORMATION:
; APPLICANT: Brady, Sean
; APPLICANT: Bettermann, Alan
; APPLICANT: Gillespie, Doreen
; APPLICANT: Goodman, Robert
; APPLICANT: Handlesman, Jo
; APPLICANT: Clardy, Jon
; TITLE OF INVENTION: Triaryl Cation Antibiotics from Environmental DNA
; FILE REFERENCE: 09820.144
; CURRENT APPLICATION NUMBER: US/10/637,280
; PRIOR FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: US/09/791,961
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
```

LENGTH: 356
TYPE: PRT
ORGANISM: Vibrio vulnificus
US-10-637-280-3

Query Match 76.1%; Score 35; DB 4; Length 356;
Best Local Similarity 62.5%; Pred. No. 1.4e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 2 EVRLRYFDV 9
DB 188 VKIRYFDI 195

RESULT 18
US-10-425-114-52343
Sequence 52343, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:

APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 52343
LENGTH: 491
TYPE: PRT
ORGANISM: Zea mays
FEATURE:

OTHER INFORMATION: Clone ID: 700351289_FLI.pep
US-10-425-114-52343

Query Match 76.1%; Score 35; DB 4; Length 491;
Best Local Similarity 66.7%; Pred. No. 2e+02;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 EVRLRYFDV 9
DB 303 KVRMRWFDV 311

RESULT 19
US-10-425-115-237671
Sequence 237671, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 237671
LENGTH: 547
TYPE: PRT
ORGANISM: Zea mays
FEATURE:

OTHER INFORMATION: Clone ID: MRT4577_148341C.1.pep
US-10-425-115-237671

Query Match 76.1%; Score 35; DB 4; Length 547;
Best Local Similarity 66.7%; Pred. No. 2.3e+02;

Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 EVRLRYFDV 9
DB 359 KVRMRWFDV 367

RESULT 20
US-10-469-013-2
Sequence 2, Application US/10469013
Publication No. US20040096861A1
GENERAL INFORMATION:

APPLICANT: Syngenta Participations AG
TITLE OF INVENTION: Oryza Sativa Nuclear Cap Binding Protein 80
FILE REFERENCE: S-60023A
CURRENT APPLICATION NUMBER: US/10/469,013
CURRENT FILING DATE: 2003-08-26
PRIOR APPLICATION NUMBER: US 60/282,370
PRIOR FILING DATE: 2001-04-06
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 868
TYPE: PRT
ORGANISM: Oryza sativa
US-10-469-013-2

Query Match 76.1%; Score 35; DB 4; Length 868;
Best Local Similarity 75.0%; Pred. No. 3.8e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 EVRLRYFD 8
DB 452 EIRLRYFD 459

RESULT 21
US-10-437-963-144903
Sequence 144903, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 144903
LENGTH: 888
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:

NAME/KEY: unsure
LOCATION: (1)..(888)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530145674C.1.pep
US-10-437-963-144903

Query Match 76.1%; Score 35; DB 4; Length 888;
Best Local Similarity 75.0%; Pred. No. 3.9e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 EVRLRYFD 8
DB 452 EIRLRYFD 459

Db 432 EIRLSYFD 439

RESULT 22

US-11-097-143-33063
; Sequence 33063, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: C1000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33063
; LENGTH: 1169
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-33063

Query Match 76.1%; Score 35; DB 6; Length 1169;
Best Local Similarity 62.5%; Pred. No. 5.2e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy 1 EVRLRYFD 8
|:|:|:|
Db 324 EIRLSYFD 331

RESULT 23

US-10-424-599-237629
; Sequence 237629, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 237629
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(61)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT3847_56604C.1.pep
US-10-424-599-237629

Query Match 73.9%; Score 34; DB 4; Length 61;
Best Local Similarity 66.7%; Pred. No. 35;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 EVRLRYFDV 9
|:|:|:|:|
Db 11 EVRLRHSFI 19

RESULT 24

US-10-424-599-233348
; Sequence 233348, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 233348
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(127)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_52739C.1.pep
US-10-424-599-233348

Query Match 73.9%; Score 34; DB 4; Length 127;
Best Local Similarity 85.7%; Pred. No. 76;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 EVRLRYF 7
|:|:|:|
Db 22 EVRLRYF 28

RESULT 25

US-10-767-701-53889
; Sequence 53889, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 53889
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(177)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: 13784478.pep
US-10-767-701-53889

Query Match 73.9%; Score 34; DB 4; Length 177;
Best Local Similarity 62.5%; Pred. No. 1.1e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVRLRYFD 8
|:|:|:|
Db 134 ELRIKYFD 141

RESULT 26
US-10-425-115-296096

; Sequence 296096, Application US/10425115
; Publication No. US20040214272A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants

; FILE REFERENCE: 38-21(53222)B

; CURRENT APPLICATION NUMBER: US/10/425,115

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 369326

; SEQ ID NO 296096

; LENGTH: 194

; TYPE: PRT

; ORGANISM: Zea mays

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1)..(194)

; OTHER INFORMATION: unsure at all Xaa locations

; FEATURE:

; OTHER INFORMATION: Clone ID: MFT4577_33116C.1.pcp

US-10-425-115-296096

Query Match 73.9%; Score 34; DB 4; Length 194;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 VRLRYFDV 9
|:|:|:|
Db 147 VKLQYFDV 154

RESULT 27
US-10-424-599-206875

; Sequence 206875, Application US/10424599
; Publication No. US20040031072A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53223)B

; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684

; SEQ ID NO 206875

; LENGTH: 205

; TYPE: PRT

; ORGANISM: Glycine max

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1)..(205)

; OTHER INFORMATION: unsure at all Xaa locations

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MFT3847_28835C.1.pcp

US-10-424-599-206875

Query Match 73.9%; Score 34; DB 4; Length 205;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 VRLRYFDV 9
|:|:|:|
Db 144 VKLQYFDV 151

RESULT 28
US-10-369-493-3892

; Sequence 3892, Application US/10369493
; Publication No. US2003023675A1

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Goldman, Barry S.

; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493

; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039

; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 3892

; LENGTH: 233

; TYPE: PRT

; ORGANISM: Neurospora crassa

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1)..(233)

; OTHER INFORMATION: unsure at all Xaa locations

US-10-369-493-3892

Query Match 73.9%; Score 34; DB 4; Length 233;
Best Local Similarity 77.8%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EVRLRYFDV 9
|:|:|:|
Db 51 EDNLRVFDV 59

RESULT 29
US-10-767-701-43782

; Sequence 43782, Application US/10767701
; Publication No. US20040172684A1

; GENERAL INFORMATION:

; APPLICANT: Zhou, Yihua

; APPLICANT: Kovalic, David K.

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53535)B

; CURRENT APPLICATION NUMBER: US/10/767,701

; CURRENT FILING DATE: 2004-01-29

; NUMBER OF SEQ ID NOS: 63128

; SEQ ID NO 43782

; LENGTH: 377

; TYPE: PRT

; ORGANISM: Sorghum bicolor

; FEATURE:

; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C25502_1.pcp

US-10-767-701-43782

Query Match 73.9%; Score 34; DB 4; Length 377;
Best Local Similarity 75.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 VRLRYFDV 9

Db 147 VKLOQYFDV 154

RESULT 30

US-10-282-122A-48744
; Sequence 48744, Application US/10282122A
; Publication No. US20040029129A1

GENERAL INFORMATION:

APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyckind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Foreyth, R.

APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 78614

SOFTWARE: PatentIn version 3.1

SEQ ID NO 48744

LENGTH: 661

TYPE: PRT

ORGANISM: Bacteroides fragilis

US-10-282-122A-48744

Query Match 73.9%; Score 34; DB 4; Length 661;
Best Local Similarity 55.6%; Pred. No. 4.4e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EVRLRYFDV 9
Db 322 ETNIRYFDI 330

RESULT 31

US-10-425-114-40631
; Sequence 40631, Application US/10425114
; Publication No. US2004003488A1

GENERAL INFORMATION:

APPLICANT: Liu, Jindong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E

APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(5313)B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 40631

LENGTH: 705

TYPE: PRT

ORGANISM: Glycine max

FEATURE:

OTHER INFORMATION: Clone ID: 700849742_FLI.pep

Query Match 73.9%; Score 34; DB 4; Length 705;
Best Local Similarity 75.0%; Pred. No. 4.8e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 VRLRYFDV 9
Db 40 VKLOQYFDV 47

RESULT 32

US-10-425-114-47224

Sequence 47224, Application US/10425114

Publication No. US2004003488A1

GENERAL INFORMATION:

APPLICANT: Liu, Jindong

APPLICANT: Zhou, Yihua

APPLICANT: Kovalic, David K.

APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(5313)B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 47224

LENGTH: 780

TYPE: PRT

ORGANISM: Zea mays

FEATURE:

OTHER INFORMATION: Clone ID: LIB143-064-F2_FLI.pep

Query Match 73.9%; Score 34; DB 4; Length 780;
Best Local Similarity 75.0%; Pred. No. 5.3e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 VRLRYFDV 9
Db 115 VKLOQYFDV 122

RESULT 33

US-10-424-599-171300

Sequence 171300, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J

APPLICANT: Kovalic, David K

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(5323)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

```
; SEQ ID NO 171300
; LENGTH: 808
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(808)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_12569C.1.pep
US-10-424-599-171300
```

```
Query Match          73.9%; Score 34; DB 4; Length 808;
Best Local Similarity 75.0%; Pred. No. 5.5e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 VRLRYFDV 9
      ||:|||||
Db      142 VKLQYFDV 149
```

```
RESULT 34
US-10-078-770-124
; Sequence 124, Application US/10078770
; Publication No. US20030003471A1
; GENERAL INFORMATION:
; APPLICANT: Farnodu, Omolayo O.
; APPLICANT: Forje, Charlie
; APPLICANT: Miao, Guo-Hua
; TITLE OF INVENTION: CDNAS Encoding Polypeptides
; FILE REFERENCE: BB-1365 US NA
; CURRENT APPLICATION NUMBER: US/10/078,770
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 09/614,188
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: 60/143,400
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/153,534
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: 60/161,223
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/159,878
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: 60/157,401
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/143,419
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/143,409
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 124
; LENGTH: 809
; TYPE: PRT
; ORGANISM: Glycine max
US-10-078-770-124
```

```
Query Match          73.9%; Score 34; DB 4; Length 809;
Best Local Similarity 75.0%; Pred. No. 5.5e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 VRLRYFDV 9
      ||:|||||
Db      144 VKLQYFDV 151
```

```
RESULT 35
US-10-424-599-206877
; Sequence 206877, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
```

```
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 206877
; LENGTH: 809
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_28837C.1.pep
US-10-424-599-206877
```

```
Query Match          73.9%; Score 34; DB 4; Length 809;
Best Local Similarity 75.0%; Pred. No. 5.5e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 VRLRYFDV 9
      ||:|||||
Db      144 VKLQYFDV 151
```

```
RESULT 36
US-10-437-963-162597
; Sequence 162597, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Bouharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 162597
; LENGTH: 812
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_61673C.1.pep
US-10-437-963-162597
```

```
Query Match          73.9%; Score 34; DB 4; Length 812;
Best Local Similarity 75.0%; Pred. No. 5.5e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 VRLRYFDV 9
      ||:|||||
Db      147 VKLQYFDV 154
```

```
RESULT 37
US-10-425-115-296097
; Sequence 296097, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
```



```
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 296097
; LENGTH: 812
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_33117C.1.pep
US-10-425-115-296097

Query Match
Best Local Similarity 73.9%; Score 34; DB 4; Length 812;
Pred. No. 5.5e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 VRLRYFDV 9
Db 147 VKLQYFDV 154

RESULT 38
US-10-425-115-296104
; Sequence 296104, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 296104
; LENGTH: 812
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_33123C.1.pep
US-10-425-115-296104

Query Match
Best Local Similarity 73.9%; Score 34; DB 4; Length 812;
Pred. No. 5.5e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 VRLRYFDV 9
Db 147 VKLQYFDV 154

RESULT 39
US-10-425-115-296107
; Sequence 296107, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 296107
; LENGTH: 812
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_33126C.1.pep
```

```
US-10-425-115-296107

Query Match
Best Local Similarity 73.9%; Score 34; DB 4; Length 812;
Pred. No. 5.5e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 VRLRYFDV 9
Db 147 VKLQYFDV 154

RESULT 40
US-10-425-114-70103
; Sequence 70103, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 70103
; LENGTH: 813
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-GMRON0IR042H06_FLI.pep
US-10-425-114-70103

Query Match
Best Local Similarity 73.9%; Score 34; DB 4; Length 813;
Pred. No. 5.5e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 VRLRYFDV 9
Db 148 VKLQYFDV 155

RESULT 41
US-10-425-115-296103
; Sequence 296103, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 296103
; LENGTH: 815
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(815)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_33122C.1.pep
US-10-425-115-296103

Query Match
Best Local Similarity 73.9%; Score 34; DB 4; Length 815;
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Best Local Similarity 75.0%; Pred. No. 5.6e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 VRLRYFDV 9
|:|:|:|

Db 148 VKLQYFDV 155

RESULT 42

US-10-425-114-47265
; Sequence 47265, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Yihua
; APPLICANT: Liu, Jindong
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 47265
; LENGTH: 817
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700849627_FLI.pep
US-10-425-114-47265

Query Match 73.9%; Score 34; DB 4; Length 817;
Best Local Similarity 75.0%; Pred. No. 5.6e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 VRLRYFDV 9
|:|:|:|

Db 152 VKLQYFDV 159

RESULT 43

US-10-425-114-53704
; Sequence 53704, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 53704
; LENGTH: 820
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLMO17321C01_FLI.pep
US-10-425-114-53704

Query Match 73.9%; Score 34; DB 4; Length 820;
Best Local Similarity 75.0%; Pred. No. 5.6e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 VRLRYFDV 9
|:|:|:|

Db 155 VKLQYFDV 162

RESULT 44

US-10-425-114-70197
; Sequence 70197, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Yihua
; APPLICANT: Liu, Jindong
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 70197
; LENGTH: 820
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLMO17153E02_FLI.pep
US-10-425-114-70197

Query Match 73.9%; Score 34; DB 4; Length 820;
Best Local Similarity 75.0%; Pred. No. 5.6e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 VRLRYFDV 9
|:|:|:|

Db 155 VKLQYFDV 162

RESULT 45

US-10-425-114-57839
; Sequence 57839, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 57839
; LENGTH: 821
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73225B12_FLI.pep
US-10-425-114-57839

Query Match 73.9%; Score 34; DB 4; Length 821;
Best Local Similarity 75.0%; Pred. No. 5.6e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 VRLRYFDV 9
|:|:|:|

Db 156 VKLQYFDV 163

RESULT 46

US-10-425-115-296105

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; Sequence 296105, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 296105
; LENGTH: 840
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(840)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_33124C.1.pep
US-10-425-115-296105

Query Match          73.9%; Score 34; DB 4; Length 840;
Best Local Similarity 75.0%; Pred. No. 5.7e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      2 VRLRYFDV 9
Db      175 VKLQYFDV 182

RESULT 47
US-10-425-114-47222
; Sequence 47222, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 47222
; LENGTH: 849
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700095546_FLI.pep
US-10-425-114-47222

Query Match          73.9%; Score 34; DB 4; Length 849;
Best Local Similarity 75.0%; Pred. No. 5.8e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      2 VRLRYFDV 9
Db      184 VKLQYFDV 191

RESULT 48
US-10-437-963-137236
; Sequence 137236, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
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; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 137236
; LENGTH: 1234
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_38738C.1.pep
US-10-437-963-137236

Query Match          73.9%; Score 34; DB 4; Length 1234;
Best Local Similarity 62.5%; Pred. No. 8.7e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EVRLRYFD 8
Db      336 ELRLRYFD 343

RESULT 49
US-10-424-599-205188
; Sequence 205188, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 205188
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(86)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_27313C.1.pep
US-10-424-599-205188

Query Match          71.7%; Score 33; DB 4; Length 86;
Best Local Similarity 75.0%; Pred. No. 79;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 EVRLRYFD 8
Db      29 ELRLRYFD 36

RESULT 50
US-10-425-115-339287
; Sequence 339287, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
```

; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 339287
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_72599C.1.pep
; US-10-425-115-339287

Query Match 71.7%; Score 33; DB 4; Length 174;
Best Local Similarity 66.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 EVRLRYFDV 9
: : : : :
Db 128 DVRLHFYDV 136

Search completed: May 4, 2006, 13:52:55
Job time : 80.4524 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 4, 2006, 13:46:13 ; Search time 10.4286 Seconds
(without alignments)
39.944 Million cell updates/sec

Title: US-10-700-632-3
Perfect score: 46
Sequence: 1 EVRLRYFDV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 235405 seqs, 46284737 residues

Total number of hits satisfying chosen parameters: 235405

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :

Published Applications_AA_New:*
1: /SIDS5/ptodata/2/pubpaa/US08_NEW_PUB.pep1.*
2: /SIDS5/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
3: /SIDS5/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
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5: /SIDS5/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
6: /SIDS5/ptodata/2/pubpaa/US09_NEW_PUB.pep1.*
7: /SIDS5/ptodata/2/pubpaa/US10_NEW_PUB.pep1.*
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9: /SIDS5/ptodata/2/pubpaa/US10_NEW_PUB.pep1.*
10: /SIDS5/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
11: /SIDS5/ptodata/2/pubpaa/US11_NEW_PUB.pep1.*
12: /SIDS5/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	38	82.6	1217	US-11-232-440-15	Sequence 15, Appl1
2	37	80.4	953	US-11-079-463-8639	Sequence 8639, Ap
3	34	73.9	584	US-11-079-463-6688	Sequence 6688, Ap
4	34	73.9	809	US-11-120-308-124	Sequence 124, App
5	33	71.7	321	US-11-188-298-5426	Sequence 5426, Ap
6	33	71.7	369	US-11-087-099-2749	Sequence 2749, Ap
7	33	71.7	616	US-10-613-744-4	Sequence 4, Appl1
8	33	71.7	671	US-11-188-298-9026	Sequence 9026, Ap
9	33	71.7	901	US-11-087-099-2095	Sequence 2095, Ap
10	33	71.7	901	US-11-188-298-2049	Sequence 8, Appl1
11	32	69.6	114	US-10-726-554-8	Sequence 35, Appl1
12	32	69.6	114	US-11-100-553B-35	Sequence 20125, A
13	32	69.6	274	US-11-096-568A-20125	Sequence 20124, A
14	32	69.6	346	US-11-096-568A-20124	Sequence 1773, A
15	32	69.6	439	US-11-188-298-1773	Sequence 127, App
16	32	69.6	452	US-10-878-556A-127	Sequence 7, Appl1
17	31	67.4	351	US-10-733-816-7	Sequence 3, Appl1
18	31	67.4	361	US-10-733-816-3	Sequence 6, Appl1
19	31	67.4	387	US-10-733-816-6	Sequence 2, Appl1
20	31	67.4	394	US-10-733-816-2	Sequence 788, App
21	31	67.4	402	US-10-506-454-768	

22	31	67.4	420	US-10-733-816-1	Sequence 1, Appl1
23	31	67.4	420	US-11-288-493-72	Sequence 72, Appl1
24	31	67.4	433	US-10-770-746-65	Sequence 65, Appl1
25	31	67.4	447	US-10-733-816-5	Sequence 5, Appl1
26	31	67.4	483	US-10-733-816-4	Sequence 4, Appl1
27	31	67.4	483	US-10-451-375-12	Sequence 12, Appl1
28	31	67.4	484	US-11-147-725-2	Sequence 2, Appl1
29	31	67.4	495	US-10-613-744-5	Sequence 52, Appl1
30	31	67.4	514	US-10-878-556A-32	Sequence 32, Appl1
31	31	67.4	515	US-10-510-093-18	Sequence 18, Appl1
32	31	67.4	523	US-11-288-493-10	Sequence 10, Appl1
33	30	65.2	9	US-11-193-512-48	Sequence 48, Appl1
34	30	65.2	19	US-11-054-515-2820	Sequence 2820, Ap
35	30	65.2	19	US-11-266-444-2820	Sequence 2820, Ap
36	30	65.2	109	US-11-087-099-978	Sequence 978, App
37	30	65.2	118	US-11-096-568A-20193	Sequence 20193, A
38	30	65.2	135	US-11-143-980-60	Sequence 60, Appl1
39	30	65.2	137	US-11-193-512-31	Sequence 31, Appl1
40	30	65.2	194	US-11-096-568A-20191	Sequence 20191, A
41	30	65.2	225	US-11-087-099-8824	Sequence 8824, Ap
42	30	65.2	244	US-11-045-004-1262	Sequence 1262, Ap
43	30	65.2	257	US-11-054-515-1256	Sequence 1256, Ap
44	30	65.2	257	US-11-266-444-1256	Sequence 1256, Ap
45	30	65.2	319	US-11-087-099-11767	Sequence 11767, A
46	30	65.2	321	US-11-087-099-9863	Sequence 9863, Ap
47	30	65.2	325	US-10-821-234-1261	Sequence 1261, Ap
48	30	65.2	326	US-11-087-099-2330	Sequence 2330, Ap
49	30	65.2	326	US-11-087-099-3028	Sequence 3028, Ap
50	30	65.2	326	US-11-087-099-8258	Sequence 8258, Ap
51	30	65.2	327	US-11-087-099-10008	Sequence 10008, A
52	30	65.2	327	US-11-087-099-10124	Sequence 10124, A
53	30	65.2	327	US-11-045-004-2672	Sequence 2672, Ap
54	30	65.2	328	US-11-087-099-4727	Sequence 4727, Ap
55	30	65.2	329	US-11-087-099-1058	Sequence 1058, Ap
56	30	65.2	329	US-11-087-099-9295	Sequence 9295, Ap
57	30	65.2	329	US-11-087-099-10332	Sequence 10332, A
58	30	65.2	330	US-11-087-099-7447	Sequence 7447, A
59	30	65.2	330	US-11-087-099-10448	Sequence 10448, A
60	30	65.2	331	US-11-087-099-3050	Sequence 3050, Ap
61	30	65.2	331	US-11-087-099-9511	Sequence 9511, Ap
62	30	65.2	331	US-11-087-099-9629	Sequence 9629, Ap
63	30	65.2	332	US-11-087-099-7358	Sequence 7358, Ap
64	30	65.2	334	US-11-087-099-2836	Sequence 2836, Ap
65	30	65.2	334	US-11-087-099-9497	Sequence 9497, Ap
66	30	65.2	337	US-11-087-099-7965	Sequence 7906, Ap
67	30	65.2	340	US-11-087-099-9253	Sequence 9253, Ap
68	30	65.2	341	US-11-087-099-6069	Sequence 6069, Ap
69	30	65.2	342	US-11-087-099-7901	Sequence 7901, Ap
70	30	65.2	343	US-11-087-099-2229	Sequence 2229, Ap
71	30	65.2	351	US-11-087-099-6216	Sequence 6216, Ap
72	30	65.2	354	US-11-087-099-931	Sequence 931, App
73	30	65.2	354	US-11-188-298-11907	Sequence 11907, A
74	30	65.2	360	US-11-087-099-6037	Sequence 6037, Ap
75	30	65.2	444	US-11-087-099-3419	Sequence 3419, Ap
76	30	65.2	565	US-11-098-686-17038	Sequence 10738, A
77	30	65.2	690	US-11-188-298-19708	Sequence 19708, A
78	30	65.2	743	US-11-188-298-11907	Sequence 11907, A
79	30	65.2	743	US-10-511-989-26	Sequence 26, Appl1
80	30	65.2	796	US-11-087-099-11950	Sequence 11950, A
81	30	65.2	797	US-11-188-298-7293	Sequence 7293, Ap
82	30	65.2	797	US-11-087-099-11959	Sequence 11959, A
83	30	65.2	833	US-11-188-298-22120	Sequence 22120, A
84	29	63.0	815	US-11-022-478-2	Sequence 2, Appl1
85	29	63.0	115	US-11-136-559-24	Sequence 24, Appl1
86	29	63.0	181	US-11-389-494-16	Sequence 16, Appl1
87	29	63.0	196	US-11-087-099-6085	Sequence 6085, Ap
88	29	63.0	232	US-11-025-712-10	Sequence 10, Appl1
89	29	63.0	264	US-11-173-564-2	Sequence 10, Appl1
90	29	63.0	291	US-11-096-568A-16485	Sequence 16485, A
91	29	63.0	330	US-10-506-454-1665	Sequence 1665, Ap
92	29	63.0	332	US-11-087-099-7121	Sequence 7121, Ap
93	29	63.0	333	US-11-087-099-8961	Sequence 8961, Ap
94	29	63.0	333	US-11-087-099-6265	Sequence 6265, Ap
	29	63.0	333	US-11-087-099-7614	Sequence 7614, Ap

95	63.0	333	11	US-11-087-099-11661	Sequence 11661, A	168	28	60.9	330	11	US-11-087-099-612	Sequence 612, App
29	63.0	335	11	US-11-188-298-9335	Sequence 9335, Ap	169	28	60.9	332	11	US-11-096-5688-4638	Sequence 4638, Ap
97	63.0	336	11	US-11-087-099-8846	Sequence 8846, Ap	170	28	60.9	330	11	US-11-087-099-4981	Sequence 4981, Ap
29	63.0	338	11	US-11-087-099-6636	Sequence 6636, Ap	171	28	60.9	332	11	US-11-087-099-7111	Sequence 7111, Ap
98	63.0	354	11	US-11-087-099-6791	Sequence 6791, Ap	172	28	60.9	336	11	US-11-087-099-1547	Sequence 1547, Ap
29	63.0	381	11	US-11-096-5688A-16484	Sequence 16484, A	173	28	60.9	337	11	US-11-087-099-4728	Sequence 4728, Ap
100	63.0	411	11	US-11-188-298-19357	Sequence 19357, A	174	28	60.9	337	11	US-11-087-099-6755	Sequence 6755, Ap
102	63.0	449	11	US-11-087-099-11175	Sequence 11175, A	175	28	60.9	338	11	US-11-087-099-2866	Sequence 2866, Ap
103	63.0	450	11	US-11-025-712-12	Sequence 12, Appl	176	28	60.9	340	9	US-10-506-454-19	Sequence 19, Appl
104	63.0	482	9	US-10-506-454-1092	Sequence 1092, Ap	177	28	60.9	340	11	US-11-087-099-2149	Sequence 2149, Ap
105	63.0	503	9	US-11-079-463-7133	Sequence 7133, Ap	178	28	60.9	341	11	US-11-087-099-3768	Sequence 3768, Ap
106	63.0	575	9	US-10-995-805-2	Sequence 2, Appl1	179	28	60.9	341	11	US-11-087-099-6142	Sequence 6142, Ap
107	63.0	612	11	US-11-218-020-9	Sequence 9, Appl1	180	28	60.9	342	11	US-11-087-099-9535	Sequence 9535, Ap
108	63.0	614	11	US-11-072-512-3276	Sequence 3276, Ap	181	28	60.9	342	11	US-11-096-5688A-4637	Sequence 4637, Ap
109	63.0	670	11	US-11-079-463-5950	Sequence 5950, Ap	182	28	60.9	344	11	US-11-087-099-4933	Sequence 4933, Ap
110	63.0	822	11	US-11-188-298-21553	Sequence 21553, A	183	28	60.9	344	11	US-11-087-099-7084	Sequence 7084, Ap
111	63.0	866	11	US-11-188-298-5746	Sequence 5746, Ap	184	28	60.9	344	11	US-11-087-099-9258	Sequence 9258, Ap
112	63.0	928	11	US-11-129-741-2921	Sequence 2921, Ap	185	28	60.9	345	11	US-11-087-099-7803	Sequence 7803, Ap
113	63.0	928	11	US-11-129-741-2923	Sequence 2923, Ap	186	28	60.9	345	11	US-11-087-099-8433	Sequence 8433, Ap
114	63.0	928	11	US-11-129-741-2925	Sequence 2925, Ap	187	28	60.9	346	11	US-11-087-099-9493	Sequence 9491, Ap
115	63.0	928	11	US-11-129-741-2927	Sequence 2927, Ap	188	28	60.9	348	11	US-11-087-099-9491	Sequence 1407, Ap
116	63.0	928	11	US-11-129-741-2929	Sequence 2929, Ap	189	28	60.9	348	11	US-11-087-099-6766	Sequence 6706, Ap
117	63.0	928	11	US-11-129-741-2931	Sequence 2931, Ap	190	28	60.9	351	11	US-11-096-5688-1664	Sequence 1866A, A
118	63.0	928	11	US-11-129-741-2933	Sequence 2933, Ap	191	28	60.9	352	11	US-11-188-298-6720	Sequence 6720, Ap
119	63.0	928	11	US-11-129-741-2935	Sequence 2935, Ap	192	28	60.9	356	11	US-11-188-298-2102	Sequence 2102, Ap
120	63.0	928	11	US-11-129-741-4243	Sequence 4243, Ap	193	28	60.9	360	11	US-11-096-5688A-25548	Sequence 2554A, A
121	63.0	1062	11	US-11-079-463-10432	Sequence 10432, A	194	28	60.9	363	11	US-11-096-5688-25547	Sequence 25547, A
122	63.0	2312	11	US-11-126-313-34	Sequence 34, Appl	195	28	60.9	378	11	US-11-096-5688-16663	Sequence 18663, A
123	63.0	2326	11	US-11-126-313-37	Sequence 37, Appl	196	28	60.9	393	9	US-10-793-626-162	Sequence 3162, Ap
124	63.0	2326	11	US-11-096-281-11	Sequence 11, Appl	197	28	60.9	398	11	US-11-096-5688-26114	Sequence 26114, A
125	63.0	2723	9	US-10-895-064-388	Sequence 388, App	198	28	60.9	419	9	US-10-873-588-157	Sequence 157, App
126	63.0	2723	11	US-11-129-741-388	Sequence 388, App	199	28	60.9	443	11	US-11-096-5688-9373	Sequence 9373, Ap
127	63.0	2723	11	US-11-129-741-3318	Sequence 3318, Ap	200	28	60.9	443	11	US-11-096-5688-9375	Sequence 9375, Ap
128	60.9	6	9	US-10-726-554-14	Sequence 14, Appl	201	28	60.9	451	9	US-10-793-626-210	Sequence 210, App
129	60.9	6	11	US-11-100-553B-40	Sequence 40, Appl	202	28	60.9	454	11	US-11-096-5688-26113	Sequence 26113, A
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131	60.9	18	11	US-11-054-515-2795	Sequence 2795, Ap	204	28	60.9	457	11	US-11-188-298-18336	Sequence 18336, A
132	60.9	18	11	US-11-266-444-2795	Sequence 2795, Ap	205	28	60.9	461	11	US-11-188-298-10270	Sequence 10270, A
133	60.9	20	11	US-11-054-515-3039	Sequence 3039, Ap	206	28	60.9	461	11	US-11-188-298-16566	Sequence 16566, A
134	60.9	20	11	US-11-266-444-3039	Sequence 3039, Ap	207	28	60.9	461	11	US-11-188-298-20911	Sequence 20911, A
135	60.9	83	11	US-11-096-5688A-16554	Sequence 16554, A	208	28	60.9	466	11	US-11-188-298-22936	Sequence 22496, A
136	60.9	106	11	US-11-096-5688A-16553	Sequence 16553, A	209	28	60.9	522	11	US-11-096-5688-16662	Sequence 18662, A
137	60.9	117	11	US-11-049-536-434	Sequence 434, App	210	28	60.9	536	11	US-11-087-099-5966	Sequence 5986, Ap
138	60.9	117	11	US-11-199-739-434	Sequence 434, App	211	28	60.9	559	11	US-11-079-463-6118	Sequence 6178, Ap
139	60.9	134	11	US-11-214-199-41	Sequence 41, Appl	212	28	60.9	609	11	US-11-058-655-2	Sequence 2, Appl1
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141	60.9	142	11	US-11-096-5688A-30868	Sequence 30868, A	214	28	60.9	637	9	US-10-467-657-1594	Sequence 1594, Ap
142	60.9	148	11	US-11-096-5688A-30867	Sequence 30867, A	215	28	60.9	677	11	US-11-079-463-9704	Sequence 9704, Ap
143	60.9	155	9	US-10-467-657-5596	Sequence 5596, Ap	216	28	60.9	690	11	US-11-188-298-4363	Sequence 4363, Ap
144	60.9	190	11	US-11-087-099-811	Sequence 811, App	217	28	60.9	737	9	US-10-467-657-9452	Sequence 9452, Ap
145	60.9	193	11	US-11-087-099-7976	Sequence 7976, Ap	218	28	60.9	779	11	US-11-079-463-9017	Sequence 9017, Ap
146	60.9	194	11	US-11-045-004-715	Sequence 715, App	219	28	60.9	833	11	US-11-079-463-7143	Sequence 7143, Ap
147	60.9	228	11	US-11-087-099-9428	Sequence 9428, Ap	220	28	60.9	853	11	US-11-087-099-4543	Sequence 4543, Ap
148	60.9	233	11	US-11-096-5688A-4639	Sequence 4639, Ap	221	28	60.9	853	11	US-11-188-298-15119	Sequence 15179, A
149	60.9	236	11	US-11-096-5688A-30866	Sequence 30866, A	222	28	60.9	861	11	US-11-079-463-9522	Sequence 9522, Ap
150	60.9	252	11	US-11-054-515-1731	Sequence 1731, Ap	223	28	60.9	868	11	US-11-264-096-2179	Sequence 2179, Ap
151	60.9	252	11	US-11-266-444-1731	Sequence 1731, Ap	224	28	60.9	903	9	US-10-500-941-7	Sequence 7, Appl1
152	60.9	253	11	US-11-054-515-1418	Sequence 1418, Ap	225	28	60.9	1017	11	US-11-087-099-6494	Sequence 6494, Ap
153	60.9	253	11	US-11-054-515-1672	Sequence 1672, Ap	226	28	60.9	1060	11	US-11-045-004-372	Sequence 10154, A
154	60.9	253	11	US-11-266-444-1418	Sequence 1418, Ap	227	28	60.9	1179	11	US-11-045-004-372	Sequence 372, App
155	60.9	253	11	US-11-266-444-1672	Sequence 1672, Ap	228	28	60.9	12505	11	US-11-126-513-33	Sequence 33, Appl
156	60.9	257	9	US-10-467-657-4170	Sequence 4170, Ap	229	27	58.7	53	11	US-10-834-387-211	Sequence 211, App
157	60.9	265	9	US-10-506-454-879	Sequence 879, App	230	27	58.7	17	9	US-11-096-5688-3988	Sequence 3988, Ap
158	60.9	266	7	US-09-995-493-6	Sequence 6, Appl1	231	27	58.7	90	11	US-11-096-5688-33362	Sequence 1022, Ap
159	60.9	273	11	US-11-214-199-57	Sequence 57, Appl	232	27	58.7	90	11	US-11-087-099-2149	Sequence 2149, Ap
160	60.9	283	11	US-11-079-463-8546	Sequence 8546, Ap	233	27	58.7	99	7	US-09-978-360A-492	Sequence 3768, Ap
161	60.9	297	11	US-11-096-5688A-25549	Sequence 25549, A	234	27	58.7	99	7	US-09-978-360A-618	Sequence 618, App
162	60.9	301	11	US-11-079-463-10179	Sequence 10179, A	235	27	58.7	118	9	US-10-886-383-1	Sequence 1, Appl1
163	60.9	302	11	US-11-096-5688A-26115	Sequence 26115, A	236	27	58.7	118	9	US-10-886-383-3	Sequence 3, Appl1
164	60.9	303	11	US-11-188-298-3385	Sequence 3385, Ap	237	27	58.7	149	11	US-11-188-298-1124	Sequence 1124, Ap
165	60.9	310	11	US-11-079-463-8539	Sequence 8539, Ap	238	27	58.7	151	11	US-11-096-5688-33361	Sequence 33361, A
166	60.9	326	11	US-11-087-099-2404	Sequence 2404, Ap	239	27	58.7	154	11	US-11-096-5688-1021	Sequence 1021, Ap
167	60.9	328	11	US-11-099-099-7207	Sequence 7207, Ap	240	27	58.7	157	11	US-11-096-5688-1020	Sequence 1020, Ap

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242	27	58.7	189	11	US-11-079-463-9072	Sequence 8072, Ap	315	27	58.7	370	11	US-11-096-568A-31923	Sequence 31923, A
243	27	58.7	194	11	US-11-074-176-118	Sequence 118, App	316	27	58.7	377	11	US-11-096-568A-28740	Sequence 28740, A
244	27	58.7	204	9	US-10-498-026-30	Sequence 30, Appl	317	27	58.7	378	11	US-11-087-099-8748	Sequence 8748, Ap
245	27	58.7	205	11	US-11-087-099-6712	Sequence 6712, Ap	318	27	58.7	379	11	US-11-067-003-9	Sequence 3, Appl1
246	27	58.7	209	11	US-11-108-172-1108	Sequence 1108, Ap	319	27	58.7	379	11	US-11-096-568A-29614	Sequence 29614, A
247	27	58.7	209	11	US-11-096-568A-19718	Sequence 19718, A	320	27	58.7	380	11	US-11-045-004-2011	Sequence 2011, Ap
248	27	58.7	223	11	US-11-096-568A-20180	Sequence 20180, A	321	27	58.7	391	11	US-11-096-568A-11965	Sequence 11965, A
249	27	58.7	230	11	US-11-096-568A-28778	Sequence 28778, A	322	27	58.7	391	11	US-11-096-568A-28776	Sequence 28776, A
250	27	58.7	232	11	US-11-096-568A-19717	Sequence 19717, A	323	27	58.7	391	11	US-11-096-568A-30577	Sequence 30577, A
251	27	58.7	236	11	US-11-087-099-12145	Sequence 12145, A	324	27	58.7	393	11	US-11-087-099-861	Sequence 861, App
252	27	58.7	251	11	US-11-054-515-1837	Sequence 1837, Ap	325	27	58.7	394	11	US-11-087-099-8713	Sequence 8713, Ap
253	27	58.7	251	11	US-11-266-444-1837	Sequence 1837, Ap	326	27	58.7	394	11	US-11-087-099-9018	Sequence 9018, Ap
254	27	58.7	252	11	US-11-054-515-1505	Sequence 1505, Ap	327	27	58.7	396	11	US-11-096-568A-10003	Sequence 10003, A
255	27	58.7	252	11	US-11-054-515-1506	Sequence 1506, Ap	328	27	58.7	399	11	US-11-096-568A-10002	Sequence 10002, A
256	27	58.7	252	11	US-11-266-444-1505	Sequence 1505, Ap	329	27	58.7	403	11	US-11-096-568A-31922	Sequence 31922, A
257	27	58.7	252	11	US-11-266-444-1506	Sequence 1506, Ap	330	27	58.7	412	11	US-11-096-568A-11964	Sequence 11964, A
258	27	58.7	260	11	US-11-098-686-10961	Sequence 10961, Ap	331	27	58.7	417	11	US-11-087-099-11336	Sequence 11336, A
259	27	58.7	263	11	US-11-096-568A-28777	Sequence 28777, A	332	27	58.7	419	11	US-11-096-568A-31921	Sequence 31921, A
260	27	58.7	263	11	US-11-096-568A-29616	Sequence 29616, A	333	27	58.7	422	11	US-11-096-568A-10001	Sequence 10001, A
261	27	58.7	263	11	US-11-096-568A-30578	Sequence 30578, A	334	27	58.7	425	9	US-10-467-657-8052	Sequence 8052, Ap
262	27	58.7	265	11	US-11-096-568A-19716	Sequence 19716, A	335	27	58.7	434	11	US-11-079-463-8226	Sequence 8226, Ap
263	27	58.7	270	9	US-10-506-454-276	Sequence 276, App	336	27	58.7	436	11	US-11-096-568A-30576	Sequence 30576, A
264	27	58.7	271	8	US-10-511-937-2592	Sequence 2592, Ap	337	27	58.7	441	11	US-11-087-099-8964	Sequence 8964, Ap
265	27	58.7	271	9	US-10-821-234-1419	Sequence 1419, Ap	338	27	58.7	442	9	US-10-793-626-1000	Sequence 1000, Ap
266	27	58.7	271	9	US-11-096-568A-28742	Sequence 28742, A	339	27	58.7	447	11	US-11-079-463-9897	Sequence 9897, Ap
267	27	58.7	274	9	US-10-467-657-706	Sequence 706, App	340	27	58.7	466	11	US-11-079-463-8506	Sequence 8506, Ap
268	27	58.7	274	11	US-11-096-568A-20179	Sequence 20179, A	341	27	58.7	467	11	US-11-188-298-17781	Sequence 17781, A
269	27	58.7	283	11	US-11-087-099-9363	Sequence 9363, Ap	342	27	58.7	477	11	US-11-188-298-19675	Sequence 19675, A
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271	27	58.7	293	9	US-10-467-657-1546	Sequence 1546, Ap	344	27	58.7	475	11	US-11-087-099-3359	Sequence 3359, Ap
272	27	58.7	294	11	US-11-087-099-6715	Sequence 6715, Ap	345	27	58.7	483	9	US-10-632-150-48	Sequence 48, Appl1
273	27	58.7	305	11	US-11-079-463-7579	Sequence 7579, Ap	346	27	58.7	483	10	US-11-106-014-48	Sequence 48, Appl1
274	27	58.7	308	9	US-10-793-626-578	Sequence 578, App	347	27	58.7	483	11	US-11-073-457-48	Sequence 48, Appl1
275	27	58.7	308	11	US-11-096-568A-28741	Sequence 28741, A	348	27	58.7	483	11	US-11-073-460-48	Sequence 48, Appl1
276	27	58.7	319	9	US-10-878-556A-159	Sequence 159, App	349	27	58.7	483	11	US-11-208-108-14	Sequence 14, Appl1
277	27	58.7	322	11	US-11-087-099-11973	Sequence 11973, A	350	27	58.7	491	11	US-11-087-099-3329	Sequence 3329, Ap
278	27	58.7	322	11	US-11-188-298-10184	Sequence 10184, A	351	27	58.7	497	11	US-11-087-099-9561	Sequence 9561, Ap
279	27	58.7	323	11	US-11-087-099-10262	Sequence 10262, A	352	27	58.7	516	11	US-11-096-568A-9826	Sequence 9826, Ap
280	27	58.7	326	11	US-11-024-959-325	Sequence 325, App	353	27	58.7	524	11	US-11-087-099-460	Sequence 460, App
281	27	58.7	326	11	US-11-024-959-446	Sequence 446, App	354	27	58.7	534	11	US-11-096-568A-9560	Sequence 9560, App
282	27	58.7	326	11	US-11-024-959-447	Sequence 447, App	355	27	58.7	537	11	US-11-098-686-10170	Sequence 10170, A
283	27	58.7	326	11	US-11-087-099-731	Sequence 731, App	356	27	58.7	538	11	US-11-094-917-6	Sequence 6, Appl1
284	27	58.7	326	11	US-11-087-099-9532	Sequence 9532, Ap	357	27	58.7	601	11	US-11-087-099-2496	Sequence 2496, Appl1
285	27	58.7	327	11	US-11-087-099-2947	Sequence 2947, Ap	358	27	58.7	609	11	US-11-096-568A-27554	Sequence 27554, A
286	27	58.7	327	11	US-11-045-004-1270	Sequence 1270, Ap	359	27	58.7	623	9	US-10-467-657-8260	Sequence 6260, App
287	27	58.7	328	11	US-11-087-099-1334	Sequence 1334, Ap	360	27	58.7	623	11	US-11-087-099-5188	Sequence 5188, Ap
288	27	58.7	328	11	US-11-087-099-1416	Sequence 1416, Ap	361	27	58.7	626	11	US-11-188-298-2725	Sequence 2725, Ap
289	27	58.7	328	11	US-11-087-099-7419	Sequence 7419, Ap	362	27	58.7	641	11	US-11-087-099-3276	Sequence 3276, Ap
290	27	58.7	328	11	US-11-087-099-7553	Sequence 7553, Ap	363	27	58.7	642	11	US-11-087-099-6026	Sequence 6026, Ap
291	27	58.7	328	11	US-11-087-099-9616	Sequence 9616, Ap	364	27	58.7	642	11	US-11-087-099-9818	Sequence 9818, Ap
292	27	58.7	329	11	US-11-087-099-3224	Sequence 3224, Ap	365	27	58.7	646	11	US-11-096-568A-27553	Sequence 27553, A
293	27	58.7	329	11	US-11-087-099-4422	Sequence 4422, Ap	366	27	58.7	648	11	US-11-087-099-11892	Sequence 11892, A
294	27	58.7	329	11	US-11-087-099-4660	Sequence 4660, Ap	367	27	58.7	667	11	US-11-098-686-11395	Sequence 11395, A
295	27	58.7	329	11	US-11-087-099-8392	Sequence 8392, Ap	368	27	58.7	693	11	US-11-079-463-6334	Sequence 6334, Ap
296	27	58.7	329	11	US-11-087-099-8594	Sequence 8594, Ap	369	27	58.7	712	11	US-11-096-568A-29777	Sequence 29777, A
297	27	58.7	329	11	US-11-087-099-11249	Sequence 11249, A	370	27	58.7	715	11	US-11-096-568A-27552	Sequence 27552, A
298	27	58.7	330	11	US-11-074-176-174	Sequence 174, App	371	27	58.7	715	11	US-11-096-568A-29776	Sequence 29776, A
299	27	58.7	330	11	US-11-087-099-1604	Sequence 1604, Ap	372	27	58.7	722	11	US-11-055-822-912	Sequence 912, App
300	27	58.7	330	11	US-11-087-099-2823	Sequence 2823, Ap	373	27	58.7	764	11	US-11-087-099-7846	Sequence 7846, App
301	27	58.7	333	11	US-11-087-099-10020	Sequence 10020, A	374	27	58.7	774	11	US-11-188-298-18278	Sequence 18278, A
302	27	58.7	337	11	US-11-087-099-783	Sequence 783, App	375	27	58.7	777	9	US-10-134-467-348	Sequence 348, App
303	27	58.7	337	11	US-11-087-099-8639	Sequence 8639, Ap	376	27	58.7	777	9	US-10-135-483-348	Sequence 348, App
304	27	58.7	344	11	US-11-087-099-7706	Sequence 7706, Ap	377	27	58.7	777	9	US-10-135-483-348	Sequence 348, App
305	27	58.7	351	11	US-11-087-099-6426	Sequence 6426, Ap	378	27	58.7	777	9	US-10-135-483-348	Sequence 348, App
306	27	58.7	352	11	US-11-087-099-1834	Sequence 1834, Ap	379	27	58.7	777	9	US-10-135-483-348	Sequence 348, App
307	27	58.7	352	11	US-11-087-099-2937	Sequence 2937, Ap	380	27	58.7	790	11	US-11-087-099-2459	Sequence 2459, Ap
308	27	58.7	353	11	US-11-087-099-7639	Sequence 7639, Ap	381	27	58.7	790	11	US-11-188-298-2358	Sequence 2358, Ap
309	27	58.7	354	11	US-11-087-099-2247	Sequence 2247, Ap	382	27	58.7	791	11	US-11-087-099-8040	Sequence 8040, Ap
310	27	58.7	356	11	US-11-087-099-1946	Sequence 1946, Ap	383	27	58.7	812	11	US-11-120-308-126	Sequence 126, App
311	27	58.7	359	9	US-10-888-962-5	Sequence 5, Appl1	384	27	58.7	821	11	US-11-096-568A-30590	Sequence 30590, A
312	27	58.7	363	11	US-11-096-568A-29615	Sequence 29615, A	385	27	58.7	840	11	US-11-188-298-10778	Sequence 10778, A
313	27	58.7	367	11	US-11-096-568A-11966	Sequence 11966, A	386	27	58.7	841	11	US-11-188-298-22093	Sequence 22093, A

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388	27	58.7	884	11	US-11-087-099-11219	Sequence 11219, A	461	26	56.5	336	11	US-11-188-298-10146	Sequence 10146, A
389	27	58.7	892	11	US-11-096-568A-30588	Sequence 30588, A	462	26	56.5	337	11	US-11-096-568A-33278	Sequence 33278, A
390	27	58.7	893	8	US-10-505-928-733	Sequence 733, App	463	26	56.5	339	11	US-11-087-099-11592	Sequence 11592, A
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393	27	58.7	1006	8	US-11-203-251A-90	Sequence 90, Appl	466	26	56.5	353	11	US-11-096-568A-33277	Sequence 33277, A
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396	27	58.7	1071	9	US-10-922-232B-59	Sequence 59, Appl	469	26	56.5	359	11	US-11-087-099-5310	Sequence 5310, Ap
397	27	58.7	1531	8	US-10-505-928-217	Sequence 217, App	470	26	56.5	361	11	US-11-045-004-2120	Sequence 2120, Ap
398	27	58.7	1531	11	US-11-087-227-24	Sequence 24, App	471	26	56.5	370	11	US-11-188-298-4882	Sequence 4882, Ap
399	27	58.7	1531	11	US-11-186-284-211	Sequence 211, App	472	26	56.5	377	11	US-11-096-568A-12191	Sequence 12191, A
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403	26.5	57.6	784	11	US-11-087-099-3348	Sequence 3348, Ap	476	26	56.5	381	11	US-11-087-099-8953	Sequence 8953, Ap
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409	26	56.5	101	11	US-11-096-568A-8401	Sequence 8401, Ap	482	26	56.5	400	11	US-11-096-568A-12190	Sequence 12190, A
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412	26	56.5	139	11	US-11-096-568A-899	Sequence 899, App	485	26	56.5	413	11	US-11-096-568A-33214	Sequence 33214, A
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414	26	56.5	146	11	US-11-096-568A-898	Sequence 898, App	487	26	56.5	422	11	US-11-079-463-6251	Sequence 6251, Ap
415	26	56.5	171	11	US-11-074-176-332	Sequence 332, App	488	26	56.5	422	11	US-11-096-568A-33213	Sequence 33213, A
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437	26	56.5	285	11	US-10-467-657-100	Sequence 100, App	510	26	56.5	491	11	US-11-188-298-18885	Sequence 18885, A
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443	26	56.5	303	11	US-11-096-568A-33215	Sequence 33215, A	516	26	56.5	511	11	US-11-087-099-10531	Sequence 10531, A
444	26	56.5	317	11	US-11-096-568A-28834	Sequence 28834, A	517	26	56.5	512	11	US-11-087-099-1062	Sequence 1062, Ap
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447	26	56.5	317	11	US-11-045-004-385	Sequence 385, App	520	26	56.5	515	9	US-10-915-002-240	Sequence 240, App
448	26	56.5	321	11	US-11-087-099-7288	Sequence 7288, Ap	521	26	56.5	524	11	US-11-096-568A-15787	Sequence 15787, A
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453	26	56.5	327	11	US-11-087-099-4124	Sequence 4124, Ap	526	26	56.5	533	9	US-10-195-883-44	Sequence 44, Appl1
454	26	56.5	328	11	US-11-087-099-2689	Sequence 2689, Ap	527	26	56.5	533	9	US-10-195-888-44	Sequence 44, Appl1
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457	26	56.5	330	11	US-11-087-099-1144	Sequence 1144, Ap	530	26	56.5	545	11	US-11-188-298-17504	Sequence 17504, A
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459	26	56.5	334	11	US-11-087-099-5342	Sequence 5342, Ap	532	26	56.5	546	11	US-11-087-099-4956	Sequence 4956, Ap

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535	26	56.5	601	11	US-11-045-004-900	Sequence 900, App	608	25	54.3	113	11	US-11-049-436-106	Sequence 106, App
536	26	56.5	637	11	US-11-087-039-7996	Sequence 7996, Ap	609	25	54.3	113	11	US-11-189-739-106	Sequence 106, App
537	26	56.5	649	11	US-11-079-463-10379	Sequence 10379, A	610	25	54.3	114	11	US-11-098-586-10855	Sequence 10855, A
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540	26	56.5	752	11	US-11-188-298-1988	Sequence 1988, Ap	613	25	54.3	117	11	US-11-049-536-222	Sequence 222, App
541	26	56.5	752	11	US-11-197-298-12440	Sequence 12440, A	614	25	54.3	117	11	US-11-049-536-226	Sequence 226, App
542	26	56.5	754	11	US-11-188-298-12440	Sequence 12440, A	615	25	54.3	117	11	US-11-096-568A-9935	Sequence 9935, Ap
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544	26	56.5	763	11	US-11-188-298-15673	Sequence 15673, A	617	25	54.3	117	11	US-11-199-739-222	Sequence 222, App
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549	26	56.5	837	11	US-11-188-298-5137	Sequence 5137, Ap	622	25	54.3	120	11	US-11-199-739-518	Sequence 518, App
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551	26	56.5	881	11	US-11-191-374-12	Sequence 12, Appl	624	25	54.3	122	9	US-10-771-257-57	Sequence 57, Appl
552	26	56.5	881	11	US-11-191-375-12	Sequence 12, Appl	625	25	54.3	122	11	US-11-127-577-55	Sequence 55, Appl
553	26	56.5	896	9	US-11-191-568-12	Sequence 12, Appl	626	25	54.3	122	11	US-11-045-004-1483	Sequence 1483, Ap
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558	26	56.5	1263	11	US-11-087-039-7209	Sequence 7209, Ap	631	25	54.3	136	11	US-11-144-947-385	Sequence 385, App
559	26	56.5	1442	9	US-10-793-626-2052	Sequence 2052, Ap	632	25	54.3	137	11	US-11-096-568A-10543	Sequence 10543, A
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562	26	56.5	1697	11	US-11-019-711-68	Sequence 68, Appl	635	25	54.3	148	11	US-11-188-298-953	Sequence 953, App
563	26	56.5	1717	11	US-11-192-967-2	Sequence 2, Appl1	636	25	54.3	149	11	US-11-096-568A-22421	Sequence 22421, A
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566	26	56.5	1728	11	US-11-019-711-72	Sequence 72, Appl	639	25	54.3	157	11	US-11-199-739-110	Sequence 110, App
567	26	56.5	1766	9	US-10-204-639-36	Sequence 36, Appl	640	25	54.3	162	9	US-10-506-454-158	Sequence 158, App
568	26	56.5	1857	9	US-10-055-877-252	Sequence 252, App	641	25	54.3	164	11	US-11-098-686-124	Sequence 124, App
569	26	56.5	2084	9	US-10-055-877-73	Sequence 73, Appl	642	25	54.3	168	11	US-11-096-568A-10541	Sequence 10541, A
570	26	56.5	2109	9	US-10-055-877-251	Sequence 251, App	643	25	54.3	169	11	US-11-045-004-487	Sequence 487, App
571	26	56.5	2333	11	US-11-096-281-13	Sequence 13, Appl	644	25	54.3	173	11	US-11-052-554-4302	Sequence 302, App
572	26	56.5	2491	9	US-10-995-561-769	Sequence 769, App	645	25	54.3	177	11	US-11-096-568A-311	Sequence 311, App
573	26	56.5	4443	11	US-11-129-741-1478	Sequence 3478, Ap	646	25	54.3	180	11	US-11-072-512-3220	Sequence 3220, App
574	26	56.5	4473	9	US-10-895-064-460	Sequence 460, App	647	25	54.3	180	11	US-11-096-568A-110886	Sequence 10886, A
575	26	56.5	4473	11	US-11-129-741-460	Sequence 460, App	648	25	54.3	180	11	US-11-096-568A-11708	Sequence 11708, A
576	26	54.3	9	11	US-11-054-515-3118	Sequence 3118, Ap	649	25	54.3	182	11	US-11-096-568A-310	Sequence 310, App
577	25	54.3	9	11	US-11-266-444-3118	Sequence 3118, Ap	650	25	54.3	185	11	US-11-096-568A-10885	Sequence 10885, A
578	25	54.3	10	9	US-10-902-546-7	Sequence 7, Appl1	651	25	54.3	186	11	US-11-188-298-9471	Sequence 9471, Ap
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580	25	54.3	10	11	US-11-130-206-40	Sequence 40, Appl	653	25	54.3	191	11	US-11-096-568A-11707	Sequence 11707, A
581	25	54.3	19	11	US-11-188-187A-14	Sequence 14, Appl	654	25	54.3	192	11	US-11-087-039-9855	Sequence 9855, App
582	25	54.3	20	11	US-11-188-187A-14	Sequence 14, Appl	655	25	54.3	194	11	US-11-079-463-8560	Sequence 8560, App
583	25	54.3	24	11	US-11-054-515-3045	Sequence 1345, Ap	656	25	54.3	194	11	US-11-045-004-2214	Sequence 2214, App
584	25	54.3	24	11	US-11-266-444-3045	Sequence 3045, Ap	657	25	54.3	197	11	US-11-106-270-10	Sequence 10, Appl
585	25	54.3	31	9	US-10-467-657-8794	Sequence 8794, Ap	658	25	54.3	198	11	US-11-079-463-7063	Sequence 7063, App
586	25	54.3	35	9	US-10-532-153-25	Sequence 25, Appl	659	25	54.3	201	11	US-11-188-298-16070	Sequence 16070, A
587	25	54.3	35	9	US-10-532-153-26	Sequence 26, Appl	660	25	54.3	202	11	US-11-096-568A-7687	Sequence 7687, Ap
588	25	54.3	35	9	US-10-532-153-27	Sequence 27, Appl	661	25	54.3	204	11	US-11-098-568A-10498	Sequence 10498, A
589	25	54.3	35	9	US-10-532-153-28	Sequence 28, Appl	662	25	54.3	206	11	US-11-096-568A-17406	Sequence 17406, A
590	25	54.3	35	9	US-10-532-153-29	Sequence 29, Appl	663	25	54.3	207	11	US-11-096-568A-24851	Sequence 24851, A
591	25	54.3	35	9	US-10-532-153-30	Sequence 30, Appl	664	25	54.3	208	11	US-11-045-004-417	Sequence 417, App
592	25	54.3	35	9	US-10-532-153-31	Sequence 31, Appl	665	25	54.3	213	11	US-11-082-889-184	Sequence 184, App
593	25	54.3	35	9	US-10-532-153-32	Sequence 32, Appl	666	25	54.3	214	11	US-11-072-512-3037	Sequence 3037, App
594	25	54.3	35	9	US-10-532-153-33	Sequence 33, Appl	667	25	54.3	215	9	US-10-506-454-429	Sequence 429, App
595	25	54.3	35	9	US-10-532-153-36	Sequence 36, Appl	668	25	54.3	218	11	US-11-087-039-4529	Sequence 4529, App
596	25	54.3	35	9	US-10-532-153-37	Sequence 37, Appl	669	25	54.3	218	11	US-11-096-568A-2526	Sequence 2526, A
597	25	54.3	36	9	US-10-532-153-34	Sequence 34, Appl	670	25	54.3	221	11	US-11-087-039-2693	Sequence 2693, App
598	25	54.3	66	11	US-11-145-861-601	Sequence 401, App	671	25	54.3	225	11	US-11-087-039-865	Sequence 865, App
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602	25	54.3	87	11	US-11-188-298-1305	Sequence 1305, Ap	675	25	54.3	228	11	US-11-156-084-100	Sequence 100, App
603	25	54.3	89	11	US-11-096-568A-9936	Sequence 9936, Ap	676	25	54.3	231	11	US-11-072-512-3585	Sequence 3585, App
604	25	54.3	91	11	US-11-096-568A-13276	Sequence 13276, A	677	25	54.3	232	11	US-11-096-568A-11405	Sequence 11405, A
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832	25	54.3	430	11	US-11-169-041-200	Sequence 200, App	905	25	54.3	546	9	US-10-195-889-412	Sequence 412, App
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834	25	54.3	434	9	US-10-821-234-1680	Sequence 1680, App	907	25	54.3	546	9	US-10-219-061-124	Sequence 124, App
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840	25	54.3	449	11	US-11-283-280-34	Sequence 34, App1	913	25	54.3	573	8	US-10-467-657-684	Sequence 684, App
841	25	54.3	454	11	US-11-059-867-18	Sequence 18, App1	914	25	54.3	580	8	US-10-506-928-181	Sequence 181, App
842	25	54.3	458	9	US-10-194-487-546	Sequence 546, App	915	25	54.3	598	11	US-11-090-878-10	Sequence 10, App1
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846	25	54.3	458	11	US-11-264-096-1150	Sequence 1150, App	919	25	54.3	613	9	US-10-137-873A-190	Sequence 190, App
847	25	54.3	460	11	US-11-079-463-8313	Sequence 8313, App	920	25	54.3	613	9	US-10-152-370-190	Sequence 190, App
848	25	54.3	466	11	US-11-188-298-20655	Sequence 20655, A	921	25	54.3	613	11	US-11-290-153-190	Sequence 190, App
849	25	54.3	466	11	US-11-188-298-15973	Sequence 15973, A	922	25	54.3	616	11	US-11-058-127-16	Sequence 16, App1
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856	25	54.3	483	11	US-11-045-004-507	Sequence 507, App	929	25	54.3	623	11	US-11-188-398-7869	Sequence 7869, App
857	25	54.3	487	9	US-10-454-437-420	Sequence 420, App	930	25	54.3	624	11	US-11-090-878-4	Sequence 4, App1
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861	25	54.3	491	9	US-10-506-454-338	Sequence 338, App	934	25	54.3	637	11	US-11-079-463-5747	Sequence 5747, App
862	25	54.3	491	11	US-11-188-298-1445	Sequence 1445, App	935	25	54.3	639	11	US-11-124-567A-379	Sequence 379, App
863	25	54.3	499	11	US-11-087-059-3242	Sequence 3242, App	936	25	54.3	659	11	US-11-079-463-1188	Sequence 6188, App
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865	25	54.3	499	11	US-11-283-280-31	Sequence 31, App1	938	25	54.3	669	11	US-11-088-127-12	Sequence 12, App1
866	25	54.3	501	11	US-11-188-298-1697	Sequence 1697, App	939	25	54.3	669	11	US-11-108-389-6	Sequence 6, App1
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872	25	54.3	506	11	US-11-188-298-8789	Sequence 8789, App	945	25	54.3	673	11	US-11-058-127-26	Sequence 26, App1
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880	25	54.3	510	11	US-11-188-298-5258	Sequence 5258, App	953	25	54.3	673	11	US-11-058-127-66	Sequence 66, App1
881	25	54.3	511	8	US-10-510-325-12	Sequence 12, App1	954	25	54.3	673	11	US-11-058-127-68	Sequence 68, App1
882	25	54.3	516	11	US-11-188-298-17942	Sequence 17942, A	955	25	54.3	673	11	US-11-058-127-70	Sequence 70, App1
883	25	54.3	517	11	US-11-188-298-2805	Sequence 2805, App	956	25	54.3	673	11	US-11-058-127-76	Sequence 76, App1
884	25	54.3	518	11	US-11-188-298-20809	Sequence 20809, A	957	25	54.3	673	11	US-11-058-127-86	Sequence 86, App1
885	25	54.3	520	11	US-11-087-059-11701	Sequence 11701, A	958	25	54.3	673	11	US-11-058-127-88	Sequence 88, App1
886	25	54.3	520	11	US-11-188-298-21871	Sequence 21871, A	959	25	54.3	673	11	US-11-058-127-90	Sequence 90, App1
887	25	54.3	522	11	US-11-079-463-7551	Sequence 7551, App	960	25	54.3	673	11	US-11-058-127-92	Sequence 92, App1
888	25	54.3	523	11	US-11-079-463-6629	Sequence 6629, App	961	25	54.3	673	11	US-11-058-127-94	Sequence 94, App1
889	25	54.3	525	11	US-11-188-298-3625	Sequence 3625, App	962	25	54.3	673	11	US-11-108-389-8	Sequence 8, App1
890	25	54.3	525	11	US-11-096-568A-26438	Sequence 26438, A	963	25	54.3	673	11	US-11-108-389-12	Sequence 12, App1
891	25	54.3	528	11	US-11-188-298-19384	Sequence 19384, A	964	25	54.3	673	11	US-11-108-389-26	Sequence 26, App1
892	25	54.3	529	9	US-10-194-487-472	Sequence 472, App	965	25	54.3	673	11	US-11-108-389-30	Sequence 30, App1
893	25	54.3	529	9	US-10-195-888-472	Sequence 472, App	966	25	54.3	673	11	US-11-108-389-34	Sequence 34, App1
894	25	54.3	529	9	US-10-195-888-472	Sequence 472, App	967	25	54.3	673	11	US-11-108-389-54	Sequence 54, App1
895	25	54.3	529	9	US-10-195-888-472	Sequence 472, App	968	25	54.3	673	11	US-11-108-389-56	Sequence 56, App1
896	25	54.3	529	11	US-11-124-368A-182	Sequence 182, App	969	25	54.3	673	11	US-11-108-389-58	Sequence 58, App1
897	25	54.3	529	11	US-11-283-290-28	Sequence 28, App1	970	25	54.3	673	11	US-11-108-389-60	Sequence 60, App1

971 25 54.3 673 11 US-11-108-389-62 Sequence 62, Appl
972 25 54.3 673 11 US-11-108-389-64 Sequence 64, Appl
973 25 54.3 673 11 US-11-108-389-66 Sequence 66, Appl
974 25 54.3 673 11 US-11-108-389-68 Sequence 68, Appl
975 25 54.3 673 11 US-11-108-389-70 Sequence 70, Appl
976 25 54.3 673 11 US-11-108-389-86 Sequence 86, Appl
977 25 54.3 673 11 US-11-108-389-88 Sequence 88, Appl
978 25 54.3 673 11 US-11-108-389-90 Sequence 90, Appl
979 25 54.3 673 11 US-11-108-389-92 Sequence 92, Appl
980 25 54.3 673 11 US-11-108-389-94 Sequence 94, Appl
981 25 54.3 673 11 US-11-224-624-8 Sequence 8, Appl
982 25 54.3 673 11 US-11-224-624-22 Sequence 22, Appl
983 25 54.3 673 11 US-11-224-624-26 Sequence 26, Appl
984 25 54.3 673 11 US-11-224-624-30 Sequence 30, Appl
985 25 54.3 673 11 US-11-224-624-34 Sequence 34, Appl
986 25 54.3 673 11 US-11-224-624-54 Sequence 54, Appl
987 25 54.3 673 11 US-11-224-624-56 Sequence 56, Appl
988 25 54.3 673 11 US-11-224-624-58 Sequence 58, Appl
989 25 54.3 673 11 US-11-224-624-60 Sequence 60, Appl
990 25 54.3 673 11 US-11-224-624-62 Sequence 62, Appl
991 25 54.3 673 11 US-11-224-624-64 Sequence 64, Appl
992 25 54.3 673 11 US-11-224-624-66 Sequence 66, Appl
993 25 54.3 673 11 US-11-224-624-68 Sequence 68, Appl
994 25 54.3 673 11 US-11-224-624-70 Sequence 70, Appl
995 25 54.3 673 11 US-11-224-624-86 Sequence 86, Appl
996 25 54.3 673 11 US-11-224-624-88 Sequence 88, Appl
997 25 54.3 673 11 US-11-224-624-80 Sequence 90, Appl
998 25 54.3 673 11 US-11-224-624-82 Sequence 92, Appl
999 25 54.3 673 11 US-11-224-624-94 Sequence 94, Appl
1000 25 54.3 673 11 US-11-079-463-9427 Sequence 9427, Ap

ALIGNMENTS

RESULT 1
US-11-232-440-15 Application US/11232440
Publication No. US20060068434A1
GENERAL INFORMATION:
APPLICANT: STOKER, JAY
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING CANCER USING
FILE REFERENCE: MTP-031
CURRENT APPLICATION NUMBER: US/11/232,440
CURRENT FILING DATE: 2005-09-21
PRIOR APPLICATION NUMBER: 60/612,310
PRIOR FILING DATE: 2004-09-21
NUMBER OF SEQ ID NOS: 88
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 15
LENGTH: 1217
TYPE: PRT
ORGANISM: Homo sapiens
US-11-232-440-15

Query Match 82.6%; Score 38; DB 11; Length 1217;
Best Local Similarity 75.0%; Pred. No. 20; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 2;

Qy 1 EVRLRYFD 8
Db 324 EIRLKYFD 331

RESULT 2
US-11-079-463-8639 Application US/11079463
Publication No. US20060073161A1
GENERAL INFORMATION:
APPLICANT: Gary L. Breton
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTERIOIDES FRA
FILE REFERENCE: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: PATH00-03DIV2
CURRENT APPLICATION NUMBER: US/11/079,463
CURRENT FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/128,705
PRIOR FILING DATE: 1999-04-09
PRIOR APPLICATION NUMBER: US 09/540,209
PRIOR FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 10444
SEQ ID NO 8639
LENGTH: 953
TYPE: PRT
ORGANISM: B.fragilis
US-11-079-463-8639

Query Match 80.4%; Score 37; DB 11; Length 953;
Best Local Similarity 87.5%; Pred. No. 25; Mismatches 1; Indels 0; Gaps 0;
Matches 7; Conservative 0;

Qy 1 EVRLRYFD 8
Db 412 EVRLRYFD 419

RESULT 3
US-11-079-463-6688 Application US/11079463
Publication No. US20060073161A1
GENERAL INFORMATION:
APPLICANT: Gary L. Breton
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTERIOIDES FRA
FILE REFERENCE: PATH00-03DIV2
CURRENT APPLICATION NUMBER: US/11/079,463
CURRENT FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/128,705
PRIOR FILING DATE: 1999-04-09
PRIOR APPLICATION NUMBER: US 09/540,209
PRIOR FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 10444
SEQ ID NO 6688
LENGTH: 584
TYPE: PRT
ORGANISM: B.fragilis
FEATURE:
NAME/KEY: UNSURE
LOCATION: (1),(584)
OTHER INFORMATION: Identity of amino acid sequences at the above locations are unkno
US-11-079-463-6688

Query Match 73.9%; Score 34; DB 11; Length 584;
Best Local Similarity 55.6%; Pred. No. 60; Mismatches 2; Indels 0; Gaps 0;
Matches 5; Conservative 2;

Qy 1 EVRLRYFDV 9
Db 343 ETNIRYFDI 351

RESULT 4
US-11-120-308-124 Application US/11120308
Publication No. US2006005277A1
GENERAL INFORMATION:
APPLICANT: Fomodu, Omolayo O.
APPLICANT: Forge, Charlie
APPLICANT: Miao, Guo-Hua
TITLE OF INVENTION: CDNAS Encoding Polypeptides
FILE REFERENCE: BB-1365 US NA
CURRENT APPLICATION NUMBER: US/11/120,308
CURRENT FILING DATE: 2005-05-02
PRIOR APPLICATION NUMBER: US/10/078,770
PRIOR FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: 09/614,188

;; PRIOR FILING DATE: 2000-07-12
;; PRIOR APPLICATION NUMBER: 60/143,400
;; PRIOR FILING DATE: 1999-07-12
;; PRIOR APPLICATION NUMBER: 60/153,534
;; PRIOR FILING DATE: 1999-09-13
;; PRIOR APPLICATION NUMBER: 60/161,223
;; PRIOR FILING DATE: 1999-10-22
;; PRIOR APPLICATION NUMBER: 60/159,878
;; PRIOR FILING DATE: 1999-10-15
;; PRIOR APPLICATION NUMBER: 60/157,401
;; PRIOR FILING DATE: 1999-10-01
;; PRIOR APPLICATION NUMBER: 60/143,419
;; PRIOR FILING DATE: 1999-07-12
;; PRIOR APPLICATION NUMBER: 60/143,409
;; PRIOR FILING DATE: 1999-07-12
;; NUMBER OF SEQ ID NOS: 196
;; SOFTWARE: Microsoft Office 97
;; SEQ ID NO: 124
;; LENGTH: 809
;; TYPE: PRT
;; ORGANISM: Glycine max
US-11-120-308-124

Query Match 73.9%; Score 34; DB 11; Length 809;
Best Local Similarity 75.0%; Pred. No. 82;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 VRLRYFDV 9
DB 144 VKLQYFDV 151

RESULT 5
US-11-188-298-5426
;; Sequence 5426, Application US/11188298
;; Publication No. US20060075522A1
;; GENERAL INFORMATION:
;; APPLICANT: Abad, Mark S. et al.
;; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
;; FILE REFERENCE: 38-21(53452)B
;; CURRENT APPLICATION NUMBER: US/11/188,298
;; PRIOR FILING DATE: 2005-07-22
;; PRIOR APPLICATION NUMBER: 60/592,978
;; PRIOR FILING DATE: 2004-07-31
;; NUMBER OF SEQ ID NOS: 22569
;; SEQ ID NO: 5426
;; LENGTH: 321
;; TYPE: PRT
;; ORGANISM: Listeria ivanovi
US-11-188-298-5426

Query Match 71.7%; Score 33; DB 11; Length 321;
Best Local Similarity 55.6%; Pred. No. 53;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EVRLRYFDV 9
DB 97 EARIRYIDI 105

RESULT 6
US-11-087-099-2749
;; Sequence 2749, Application US/11087099
;; Publication No. US20060041961A1
;; GENERAL INFORMATION:
;; APPLICANT: Abad, Mark S. et al.
;; TITLE OF INVENTION: Genes and Uses for Plant Improvement
;; FILE REFERENCE: 38-21(53450)B EP
;; CURRENT APPLICATION NUMBER: US/11/087,099
;; PRIOR FILING DATE: 2005-03-22
;; NUMBER OF SEQ ID NOS: 12464
;; SEQ ID NO: 2749
;; LENGTH: 369

;; TYPE: PRT
;; ORGANISM: Zea mays
US-11-087-099-2749

Query Match 71.7%; Score 33; DB 11; Length 369;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RLRYFD 8
DB 204 RLRYFD 209

RESULT 7
US-10-613-744-4
;; Sequence 4, Application US/10613744
;; Publication No. US20050272093A1
;; GENERAL INFORMATION:
;; APPLICANT: MacKinnon, Roderick
;; TITLE OF INVENTION: Assays for Screening Compounds Which Interact With
;; TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation
;; TITLE OF INVENTION: Channel Proteins, and Uses Thereof
;; FILE REFERENCE: 018512-002901US
;; CURRENT APPLICATION NUMBER: US/10/613,744
;; PRIOR FILING DATE: 2003-07-03
;; PRIOR APPLICATION NUMBER: US/09/275,252
;; PRIOR FILING DATE: 1999-03-24
;; PRIOR APPLICATION NUMBER: US 09/045,529
;; PRIOR FILING DATE: 1998-03-20
;; PRIOR APPLICATION NUMBER: US 09/054,347
;; PRIOR FILING DATE: 1998-04-02
;; PRIOR APPLICATION NUMBER: WO PCT/US99/06307
;; PRIOR FILING DATE: 1999-03-22
;; NUMBER OF SEQ ID NOS: 42
;; SOFTWARE: Patent Ver. 2.1
;; SEQ ID NO: 4
;; LENGTH: 616
;; TYPE: PRT
;; ORGANISM: Drosophila melanogaster
US-10-613-744-4

Query Match 71.7%; Score 33; DB 9; Length 616;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RLRYFD 8
DB 129 RLRYFD 134

RESULT 8
US-11-188-298-9026
;; Sequence 9026, Application US/11188298
;; Publication No. US20060075522A1
;; GENERAL INFORMATION:
;; APPLICANT: Abad, Mark S. et al.
;; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
;; FILE REFERENCE: 38-21(53452)B
;; CURRENT APPLICATION NUMBER: US/11/188,298
;; PRIOR FILING DATE: 2005-07-22
;; PRIOR APPLICATION NUMBER: 60/592,978
;; PRIOR FILING DATE: 2004-07-31
;; NUMBER OF SEQ ID NOS: 22569
;; SEQ ID NO: 9026
;; LENGTH: 671
;; TYPE: PRT
;; ORGANISM: GIBBERELLA ZEAE PH-1
US-11-188-298-9026

Query Match 71.7%; Score 33; DB 11; Length 671;
Best Local Similarity 62.5%; Pred. No. 1,1e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy 1 EVRLRYFD 8
|:|:|
Db 576 ELKLYFE 583

RESULT 9

US-11-087-099-2095
; Sequence 2095, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 2095
; LENGTH: 901
; TYPE: PRT
; ORGANISM: Xanthomonas axonopodis pv. citri str. 306
US-11-087-099-2095

Query Match 71.7%; Score 33; DB 11; Length 901;
Best Local Similarity 75.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 EVRLRYFD 8
|:|:|
Db 598 EVRLRYFE 605

RESULT 10

US-11-188-298-2049
; Sequence 2049, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 2049
; LENGTH: 901
; TYPE: PRT
; ORGANISM: Xanthomonas axonopodis pv. citri str. 306
US-11-188-298-2049

Query Match 71.7%; Score 33; DB 11; Length 901;
Best Local Similarity 75.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 EVRLRYFD 8
|:|:|
Db 598 EVRLRYFE 605

RESULT 11

US-10-726-554-8
; Sequence 8, Application US/10726554
; Publication No. US20050249753A1
; GENERAL INFORMATION:
; APPLICANT: LEE, Jong Wook et al.
; TITLE OF INVENTION: A VARIABLE REGION OF THE MONOCLONAL ANTIBODY AGAINST
; TITLE OF INVENTION: THE HBV S-SURFACE
; TITLE OF INVENTION: ANTIGEN AND A GENE ENCODING THE SAME
; FILE REFERENCE: 1599-0197P
; CURRENT APPLICATION NUMBER: US/10/726,554
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: US/09/865,483

; PRIOR FILING DATE: Prio Filing Date: 2001-03-29
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-726-554-8

Query Match 69.6%; Score 32; DB 9; Length 114;
Best Local Similarity 85.7%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 3 RLRYFDV 9
|:|:|
Db 97 RARYFDV 103

RESULT 12

US-11-100-553B-35
; Sequence 35, Application US/11100553B
; Publication No. US20060014937A1
; GENERAL INFORMATION:
; APPLICANT: Heu 11, KANG, et al.
; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST S-SURFACE ANTIGEN OF HEPATITIS B VIRUS
; FILE REFERENCE: 087350
; CURRENT APPLICATION NUMBER: US/11/100,553B
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: KR10-2004-25573
; PRIOR FILING DATE: 2004-04-14
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Kopatentin 1.71
; SEQ ID NO 35
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: variable region of humanized heavy chain HFW141
US-11-100-553B-35

Query Match 69.6%; Score 32; DB 11; Length 114;
Best Local Similarity 85.7%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 3 RLRYFDV 9
|:|:|
Db 97 RARYFDV 103

RESULT 13

US-11-096-568A-20125
; Sequence 20125, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 20125
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(274)
; OTHER INFORMATION: Ceres Seq. ID no. 12377690
US-11-096-568A-20125

Query Match 69.6%; Score 32; DB 11; Length 274;
Best Local Similarity 66.7%; Pred. No. 71;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EVRLRYFDV 9
| | | | |
Db 238 EARLAFDV 246

RESULT 14
US-11-096-568A-20124
; Sequence 20124, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; PRIORITY FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 20124
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(346)
; OTHER INFORMATION: Ceres Seq. ID no. 12377689
US-11-096-568A-20124

Query Match 69.6%; Score 32; DB 11; Length 346;
Best Local Similarity 66.7%; Pred. No. 89;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EVRLRYFDV 9
| | | | |
Db 310 EARLAFDV 318

RESULT 15
US-11-188-298-1773
; Sequence 1773, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; PRIORITY FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIORITY FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 1773
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Trifolium aestivum
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(439)
; OTHER INFORMATION: unsure at all Xaa locations
US-11-188-298-1773

Query Match 69.6%; Score 32; DB 11; Length 439;
Best Local Similarity 55.6%; Pred. No. 1,1e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EVRLRYFDV 9
| | | | |
Db 170 ELVRYFDL 178

RESULT 16
US-10-878-556A-127
; Sequence 127, Application US/10878556A

; Publication No. US20050266399A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann La-Roche Inc.
; TITLE OF INVENTION: HCV regulated protein expression
; FILE REFERENCE: 21762
; CURRENT APPLICATION NUMBER: US/10/878,556A
; PRIORITY FILING DATE: 2004-06-28
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 127
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: sw_hum/ldhp_human
; DATABASE ENTRY DATE: 1996-02-01
US-10-878-556A-127

Query Match 69.6%; Score 32; DB 9; Length 452;
Best Local Similarity 44.4%; Pred. No. 1,1e+02;
Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVRLRYFDV 9
| | | | |
Db 76 DIOLRYFDL 84

RESULT 17
US-10-733-816-7
; Sequence 7, Application US/10733816
; Publication No. US20060088932A1
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calderon-Cacia, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Colt, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: 59516-162/PP-15876.002/200130.524
; CURRENT APPLICATION NUMBER: US/10/733,816
; PRIORITY FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US/10/211,412
; PRIORITY FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US09/916,109
; PRIORITY FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-733-816-7

Query Match 67.4%; Score 31; DB 8; Length 351;
Best Local Similarity 100.0%; Pred. No. 1,1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VRLRYF 7
| | | | |
Db 77 VRLRYF 82

RESULT 18
US-10-733-816-3
; Sequence 3, Application US/10733816
; Publication No. US20060088932A1
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calderon-Cacia, Maria

```

; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Colt, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: 59516-162/PP-15876.002/200130.524
; CURRENT APPLICATION NUMBER: US/10/733,816
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US/10/211,412
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US09/916,109
; PRIOR FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-733-816-3
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Query Match          67.4%; Score 31; DB 8; Length 361;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 2 VRLRYF 7
Db 87 VRLRYF 92
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RESULT 19
US-10-733-816-6
; Sequence 6, Application US/10733816
; Publication No. US20060088932A1
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calderon-Cacia, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Colt, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: 59516-162/PP-15876.002/200130.524
; CURRENT APPLICATION NUMBER: US/10/733,816
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US/10/211,412
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US09/916,109
; PRIOR FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-733-816-6
```

```

Query Match          67.4%; Score 31; DB 8; Length 387;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 2 VRLRYF 7
Db 77 VRLRYF 82
```

```

RESULT 20
US-10-733-816-2
; Sequence 2, Application US/10733816
; Publication No. US20060088932A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calderon-Cacia, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Colt, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: 59516-162/PP-15876.002/200130.524
; CURRENT APPLICATION NUMBER: US/10/733,816
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US/10/211,412
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US09/916,109
; PRIOR FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-733-816-2
```

```

Query Match          67.4%; Score 31; DB 8; Length 394;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 2 VRLRYF 7
Db 120 VRLRYF 125
```

```

RESULT 21
US-10-506-454-788
; Sequence 788, Application US/10506454
; Publication No. US20060088386A1
; GENERAL INFORMATION:
; APPLICANT: Slesarev, Alexi I
; APPLICANT: Mezhevaeva, Katja V
; APPLICANT: Polushin, Nikolai N
; APPLICANT: Shcherbina, Olga V
; APPLICANT: Shakhova, Vera V
; APPLICANT: Mal'kh, Andrei G
; APPLICANT: Kozaykin, Sergei A
; TITLE OF INVENTION: The Complete Genome and Protein Sequences of the Hyperthermophile
; TITLE OF INVENTION: Methanopyrus kandleri AV19 and Monophyly of Archaeal Methanogens
; FILE REFERENCE: FID001
; CURRENT APPLICATION NUMBER: US/10/506,454
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/US03/06664
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: 60/361,742
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 1722
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 788
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Methanopyrus kandleri
US-10-506-454-788
```

```

Query Match          67.4%; Score 31; DB 9; Length 402;
Best Local Similarity 85.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 EVRLRYF 7
Db 343 EVRLRYF 349
```

```
RESULT 22
```



```
US-10-733-816-1
; Sequence 1, Application US/10733816
; Publication No. US20060088932A1
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calderon-Cacia, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Colt, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: 59516-162/PP-15876.002/200130.524
; CURRENT APPLICATION NUMBER: US/10/733,816
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US/10/211,412
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US09/916,109
; PRIOR FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-733-816-1
```

```
Query Match      67.4%; Score 31; DB 8; Length 420;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      2 VRLRYF 7
        |||||
Db      110 VRLRYF 115
```

```
RESULT 23
US-11-288-493-72
; Sequence 72, Application US/11288493
; Publication No. US20060078947A1
; GENERAL INFORMATION:
; APPLICANT: Kelly, Louise M.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Farlow, Deborah
; APPLICANT: Healy, Aileen
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 918, 990, 17662, 81982, 630,
; TITLE OF INVENTION: 21472, 17692, 19290, 21620, 21689, 28899, 53659, 64549,
; TITLE OF INVENTION: 9465, 23544, 7366, 27417, 57259, 21844, 943, 2061, 5891,
; TITLE OF INVENTION: 9137, 13908, 14310, 17600, 25584, 27824, 28469, 38947,
; TITLE OF INVENTION: 53003, 965, 56639, 9661, 16052, 1521, 6662, 13913, 12405 OR
; FILE REFERENCE: MP103-015P1NOMIM
; CURRENT APPLICATION NUMBER: US/11/288,493
; PRIOR FILING DATE: 2005-11-29
; PRIOR APPLICATION NUMBER: US/10/772,636
; PRIOR FILING DATE: 2004-02-05
; PRIOR APPLICATION NUMBER: US 60/445,241
; PRIOR FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US 60/448,389
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/456,320
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: US 60/460,279
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: US 60/465,924
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/470,052
; PRIOR FILING DATE: 2003-05-13
; PRIOR APPLICATION NUMBER: US 60/498,106
; PRIOR FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: US 60/500,179
```

```
; PRIOR FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: US 60/502,909
; PRIOR FILING DATE: 2003-09-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-288-493-72
```

```
Query Match      67.4%; Score 31; DB 11; Length 420;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      2 VRLRYF 7
        |||||
Db      110 VRLRYF 115
```

```
RESULT 24
US-10-770-726-65
; Sequence 65, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyleth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 65
; LENGTH: 433
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-770-726-65
```

```
Query Match      67.4%; Score 31; DB 9; Length 433;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      2 VRLRYF 7
        |||||
Db      110 VRLRYF 115
```

```
RESULT 25
US-10-733-816-5
; Sequence 5, Application US/10733816
; Publication No. US20060088932A1
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calderon-Cacia, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Colt, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: 59516-162/PP-15876.002/200130.524
; CURRENT APPLICATION NUMBER: US/10/733,816
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US/10/211,412
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US09/916,109
; PRIOR FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 11
```

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-733-816-5
```

```
Query Match          67.4%; Score 31; DB 8; Length 447;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      2 VRLRYF 7
        |||||
Db       173 VRLRYF 178
```

```
RESULT 26
US-10-733-816-4
; Sequence 4, Application US/10733816
; Publication No. US20060088932A1
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calderon-Cacela, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Colt, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: 59516-162/PP-15876.002/200130.524
; CURRENT APPLICATION NUMBER: US/10/733.816
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US/10/211.412
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US09/916.109
; PRIOR FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-733-816-4
```

```
Query Match          67.4%; Score 31; DB 8; Length 483;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      2 VRLRYF 7
        |||||
Db       173 VRLRYF 178
```

```
RESULT 27
US-10-451-375-12
; Sequence 12, Application US/10451375
; Publication No. US20050261482A1
; GENERAL INFORMATION:
; APPLICANT: Bayer AG
; TITLE OF INVENTION: REGULATION OF HUMAN SERINE-THREONINE PROTEIN KINASE
; FILE REFERENCE: L10264 Foreign Countries
; CURRENT APPLICATION NUMBER: US/10/451.375
; CURRENT FILING DATE: 2003-07-02
; PRIOR APPLICATION NUMBER: US 60/259.215
; PRIOR FILING DATE: 2001-01-03
; PRIOR APPLICATION NUMBER: US 60/306.468
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/308.098
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
```

```
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-451-375-12
```

```
Query Match          67.4%; Score 31; DB 9; Length 483;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      2 VRLRYF 7
        |||||
Db       173 VRLRYF 178
```

```
RESULT 28
US-11-147-725-2
; Sequence 2, Application US/11147725
; Publication No. US20050244878A1
; GENERAL INFORMATION:
; APPLICANT: Dunn-Coleman, Nigel
; APPLICANT: Goedegebuur, Frits
; APPLICANT: Ward, Michael
; APPLICANT: Yao, Jian
; TITLE OF INVENTION: BGL5 Beta-glucosidase and Nucleic Acids
; FILE REFERENCE: GC697
; CURRENT APPLICATION NUMBER: US/11/147.725
; CURRENT FILING DATE: 2005-06-07
; PRIOR APPLICATION NUMBER: US 10/026.140
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 484
; TYPE: PRT
; ORGANISM: Trichoderma reesei
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)-(484)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-11-147-725-2
```

```
Query Match          67.4%; Score 31; DB 11; Length 484;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      3 RLRYFD 8
        |||||
Db       405 RLRYFD 410
```

```
RESULT 29
US-10-613-744-5
; Sequence 5, Application US/10613744
; Publication No. US2005027093A1
; GENERAL INFORMATION:
; APPLICANT: MacKinnon, Roderick
; TITLE OF INVENTION: Assays for Screening Compounds Which Interact With
; TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation
; FILE REFERENCE: 018512-002901US
; CURRENT APPLICATION NUMBER: US/10/613.744
; CURRENT FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: US/09/275.252
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: US 09/045.529
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/054.347
; PRIOR FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: WO PCT/US99/06307
; PRIOR FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 42
```

```
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 5
/ LENGTH: 495
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-613-744-5
```

```
Query Match          67.4%; Score 31; DB 9; Length 495;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      3 RLRYPD 8
        |::|||
Db      69 RMRYPD 74
```

```
RESULT 30
US-10-878-556A-32
/ Sequence 32, Application US/10878556A
/ Publication No. US2005026399A1
/ GENERAL INFORMATION:
/ APPLICANT: Hoffmann La-Roche Inc.
/ TITLE OF INVENTION: HCV regulated protein expression
/ FILE REFERENCE: 21762
/ CURRENT APPLICATION NUMBER: US/10/878,556A
/ CURRENT FILING DATE: 2004-06-28
/ NUMBER OF SEQ ID NOS: 199
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 32
/ LENGTH: 514
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ PUBLICATION INFORMATION:
/ DATABASE ACCESSION NUMBER: sw hum/g6pdc_human
/ DATABASE ENTRY DATE: 1989-10-01
US-10-878-556A-32
```

```
Query Match          67.4%; Score 31; DB 9; Length 514;
Best Local Similarity 66.7%; Pred. No. 2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 EVRLRYFDV 9
        |||::||
Db     367 EVRLQFHDV 375
```

```
RESULT 31
US-10-510-903-18
/ Sequence 18, Application US/10510903
/ Publication No. US20060051755A1
/ GENERAL INFORMATION:
/ APPLICANT: Hitoshi, Yasumichi
/ APPLICANT: Jenkins, Yonchu
/ APPLICANT: Rigel Pharmaceuticals, Inc.
/ TITLE OF INVENTION: Methods of Assaying for Cell Cycle Modulators
/ FILE REFERENCE: 021044-00310PC
/ CURRENT APPLICATION NUMBER: US/10/510,903
/ CURRENT FILING DATE: 2004-10-08
/ PRIOR APPLICATION NUMBER: US 10/123,568
/ PRIOR FILING DATE: 2002-04-15
/ PRIOR APPLICATION NUMBER: US 10/123,731
/ PRIOR FILING DATE: 2002-04-15
/ PRIOR APPLICATION NUMBER: US 60/373,366
/ PRIOR FILING DATE: 2002-04-16
/ PRIOR APPLICATION NUMBER: WO PCT/US03/11867
/ PRIOR FILING DATE: 2003-04-15
/ NUMBER OF SEQ ID NOS: 60
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 18
/ LENGTH: 515
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
```

```
/ OTHER INFORMATION: glucose-6-phosphate dehydrogenase (G6PD)
US-10-510-903-18
```

```
Query Match          67.4%; Score 31; DB 9; Length 515;
Best Local Similarity 66.7%; Pred. No. 2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 EVRLRYFDV 9
        |||::||
Db     368 EVRLQFHDV 376
```

```
RESULT 32
US-11-288-493-10
/ Sequence 10, Application US/11288493
/ Publication No. US20060078947A1
/ GENERAL INFORMATION:
/ APPLICANT: Kelly, Louise M.
/ APPLICANT: Carroll, Joseph M.
/ APPLICANT: Farlow, Deborah
/ APPLICANT: Healy, Aileen
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
/ TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 9118, 990, 17662, 81982, 630,
/ TITLE OF INVENTION: 21472, 17692, 19290, 21620, 21689, 28899, 53659, 64549,
/ TITLE OF INVENTION: 9465, 23544, 7366, 27417, 57259, 21844, 943, 2061, 5891,
/ TITLE OF INVENTION: 9137, 13908, 14310, 17600, 25584, 27824, 28469, 38947,
/ TITLE OF INVENTION: 53003, 965, 56639, 9661, 16052, 1521, 6662, 13913, 12405 OR
/ TITLE OF INVENTION: 5014
/ FILE REFERENCE: MP103-015P1RNONNIM
/ CURRENT APPLICATION NUMBER: US/11/288,493
/ CURRENT FILING DATE: 2005-11-29
/ PRIOR APPLICATION NUMBER: US/10/772,636
/ PRIOR FILING DATE: 2004-02-05
/ PRIOR APPLICATION NUMBER: US 60/445,241
/ PRIOR FILING DATE: 2003-02-05
/ PRIOR APPLICATION NUMBER: US 60/448,389
/ PRIOR FILING DATE: 2003-02-18
/ PRIOR APPLICATION NUMBER: US 60/456,320
/ PRIOR FILING DATE: 2003-03-20
/ PRIOR APPLICATION NUMBER: US 60/460,279
/ PRIOR FILING DATE: 2003-04-03
/ PRIOR APPLICATION NUMBER: US 60/465,924
/ PRIOR FILING DATE: 2003-04-28
/ PRIOR APPLICATION NUMBER: US 60/470,052
/ PRIOR FILING DATE: 2003-05-13
/ PRIOR APPLICATION NUMBER: US 60/498,106
/ PRIOR FILING DATE: 2003-08-26
/ PRIOR APPLICATION NUMBER: US 60/500,179
/ PRIOR FILING DATE: 2003-09-04
/ PRIOR APPLICATION NUMBER: US 60/502,909
/ PRIOR FILING DATE: 2003-09-15
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 80
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 10
/ LENGTH: 523
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-288-493-10
```

```
Query Match          67.4%; Score 31; DB 11; Length 523;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      3 RLRYPD 8
        |::|||
Db      84 RMRYPD 89
```

```
RESULT 33
US-11-193-512-48
/ Sequence 48, Application US/11193512
/ Publication No. US20050272918A1
```

```

; GENERAL INFORMATION:
; APPLICANT: KOIKE, Masamichi
; FURUYA, Akiko
; NAKAMURA, Kazuyasu
; IIDA, Akihito
; ANAZAWA, Hideharu
; HANAI, Nobuo
; TAKATSU, Kiyoshi
; TITLE OF INVENTION: Antibody Against Human Interleukin-5
; RECEPTOR Alpha Chain
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/193,512
; FILING DATE: 01-Aug-2005
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/10/283,349
; FILING DATE: 29-Oct-2002
; APPLICATION NUMBER: US/08/836,561
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: JP 232384/95
; FILING DATE: 11-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lawrence, III, Stanton T
; REGISTRATION NUMBER: 25,736
; REFERENCE/DOCKET NUMBER: 7005-115-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-11-193-512-48

Query Match      65.2%; Score 30; DB 11; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.9e+05;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      2 VLRYFD 8
       : |||: ||
Db      2 LRLRFD 8

RESULT 34
US-11-054-515-2820
; Sequence 2820, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
```

```

; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2820
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2820

Query Match      65.2%; Score 30; DB 11; Length 19;
Best Local Similarity 83.3%; Pred. No. 14;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      3 RLRYFD 8
       : |||||
Db      4 KLRVFD 9

RESULT 35
US-11-266-444-2820
; Sequence 2820, Application US/11266444
; Publication No. US20060062789A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulato
; FILE REFERENCE: PF523P1D1
; CURRENT APPLICATION NUMBER: US/11/266,444
; CURRENT FILING DATE: 2005-11-04
; PRIOR APPLICATION NUMBER: 09/880,746
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2820
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-266-444-2820

Query Match      65.2%; Score 30; DB 11; Length 19;
Best Local Similarity 83.3%; Pred. No. 14;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      3 RLRYFD 8
       : |||||
Db      4 KLRVFD 9
```

```
RESULT 36
US-11-087-099-978
; Sequence 978, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 978
; TYPE: PRT
; ORGANISM: Enterococcus faecium
US-11-087-099-978

Query Match
Best Local Similarity 65.2%; Score 30; DB 11; Length 109;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 VALRYFDV 9
| | | | |
| | | | |
Db 77 VALRYFNV 84

RESULT 37
US-11-096-568A-20193
; Sequence 20193, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 20193
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)-(118)
; OTHER INFORMATION: Ceres Seq. ID no. 12379363
US-11-096-568A-20193

Query Match
Best Local Similarity 65.2%; Score 30; DB 11; Length 118;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EVRLRYFD 8
| | | | |
| | | | |
Db 9 EVRLRYFD 16

RESULT 38
US-11-143-980-60
; Sequence 60, Application US/11143980
; Publication No. US20050272133A1
; GENERAL INFORMATION:
; APPLICANT: He, Min
; APPLICANT: Hucul, John
; APPLICANT: Hucul, Bradley A.
; APPLICANT: Wagenaar, Melissa M.
; APPLICANT: Graziani, Edmund
; APPLICANT: Summers, Mia
; APPLICANT: Kulowski, Kerry
; APPLICANT: Pong, Kevin
; TITLE OF INVENTION: Biosynthetic Gene Cluster for the Production of a Complex
; POLYPEPTIDE
```

```
; FILE REFERENCE: AM-101426US
; CURRENT APPLICATION NUMBER: US/11/143,980
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 60/664,483
; PRIOR FILING DATE: 2005-03-23
; PRIOR APPLICATION NUMBER: US 60/576,895
; PRIOR FILING DATE: 2004-06-03
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 60
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Streptomyces sp.
US-11-143-980-60

Query Match
Best Local Similarity 65.2%; Score 30; DB 11; Length 135;
Matches 6; Conservative 100.0%; Pred. No. 89;
Mismatches 0; Indels 0; Gaps 0;

QY 1 EVRLRY 6
| | | | |
| | | | |
Db 95 EVRLRY 100

RESULT 39
US-11-193-512-31
; Sequence 31, Application US/11193512
; Publication No. US20050272918A1
; GENERAL INFORMATION:
; APPLICANT: KOIKE, Masamichi
; APPLICANT: FURUYA, Akiyo
; APPLICANT: NAKAMURA, Kazuyasu
; APPLICANT: IIDA, Akihiro
; APPLICANT: ANAZAWA, Hideharu
; APPLICANT: HANAI, Nobuo
; TITLE OF INVENTION: Antibody Against Human Interleukin-5
; RECEPTOR ALPHA CHAIN
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/193,512
; FILING DATE: 01-Aug-2005
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/10/283,349
; FILING DATE: 29-Oct-2002
; APPLICATION NUMBER: US/08/836,561
; FILING DATE: 09-May-1997
; APPLICATION NUMBER: JP 232384/95
; FILING DATE: 11-Sep-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lawrence, Iii, Stanton T
; REGISTRATION NUMBER: 25,736
; REFERENCE/DOCKET NUMBER: 7005-115-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELE: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 137 amino acids
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-11-193-512-31

Query Match 65.2%; Score 30; DB 11; Length 137;
Best Local Similarity 71.4%; Pred. No. 90;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 VRLRYFD 8
Db 119 LRLRFED 125

RESULT 40
US-11-096-568A-20191
; Sequence 20191, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 20191
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(194)
; OTHER INFORMATION: Ceres Seq. ID no. 12379361
US-11-096-568A-20191

Query Match 65.2%; Score 30; DB 11; Length 194;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EVRLRYFD 8
Db 85 EVRLRYFD 92

RESULT 41
US-11-087-099-8824
; Sequence 8824, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abadi, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 8824
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Lactobacillus sakei
US-11-087-099-8824

Query Match 65.2%; Score 30; DB 11; Length 225;
Best Local Similarity 75.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 VRLRYFD 9
Db 59 VALRYFNV 66

RESULT 42
US-11-045-004-1262
; Sequence 1262, Application US/11045004
; Publication No. US20060078901A1
; GENERAL INFORMATION:
; APPLICANT: BUCHRIESER, CARMEN
; APPLICANT: FRANGEUL, LIONEL
; APPLICANT: COUVE, ELISABETH
; APPLICANT: RUSNIOK, CHRISTOPHE
; APPLICANT: FSIHI, HAÏDA
; APPLICANT: DEHOUX, PIERRE
; APPLICANT: DUSSENET, OLIVIER
; APPLICANT: CHETOUNI, FARID
; APPLICANT: NEDJARI, HAFED
; APPLICANT: GLASER, PHILIPPE
; APPLICANT: KUNST, FRANCK
; APPLICANT: COSSART, PASCALE
; APPLICANT: DANIELS, JUSTIN
; APPLICANT: GOEBEL, WERNER
; APPLICANT: KREFT, JURGEN
; APPLICANT: KUHN, MICHAEL
; APPLICANT: NG, EVA
; APPLICANT: VAQUEZ-BOLAND, ANTONIO
; APPLICANT: DOMINGUEZ-BERNAL, GUSTAVO
; APPLICANT: GARRIDO-GARCIA, PATRICIA
; APPLICANT: TIERREZ-MARTINEZ, ALBERTO
; APPLICANT: AMEND, ALEXANDRA
; APPLICANT: CHAKRABORTY, TRINAD
; APPLICANT: DOMANN, EUGEN
; APPLICANT: HAIN, THORSTEN
; APPLICANT: BERCHE, PATRICK
; APPLICANT: CHARBIT, ALAIN
; APPLICANT: DURANT, LIONEL
; APPLICANT: PEREZ-DIAZ, JOSE-CLAUDIO
; APPLICANT: BAQUERO, FERNANDO
; APPLICANT: GARCIA DEL PORTILLO, FRANCISCO
; APPLICANT: GOMEZ-LOPEZ, NURIA
; APPLICANT: MADUENIO, ENCARN
; APPLICANT: PABLOS, BETRIZ DE
; APPLICANT: WEHLAND, JURGEN
; APPLICANT: KARTST, UWE
; APPLICANT: ENTIAN, KARL-DIETER
; APPLICANT: HAUF, JORG
; APPLICANT: ROSE, MATTHIAS
; APPLICANT: VOSS, HAMUT
; TITLE OF INVENTION: LISTERIA MONOCYTOGENES GENOME, POLYPEPTIDES AND USES
; FILE REFERENCE: 05394.0018-02
; CURRENT APPLICATION NUMBER: US/11/045,004
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: 10/637,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: 10/257,023
; PRIOR FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: PCT/FR01/01118
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: FR 00/04,629
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 2854
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1262
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Listeria monocytogenes
US-11-045-004-1262

Query Match 65.2%; Score 30; DB 11; Length 244;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 RLRYFD 8
Db 20 RLRYFD 25

```
RESULT 43
US-11-054-515-1256
; Sequence 1256, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF533P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO: 1256
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1256

Query Match          65.2%; Score 30; DB 11; Length 257;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      3 RLRYFDV 8
Db      102 KLRYFD 107

RESULT 44
US-11-266-444-1256
; Sequence 1256, Application US/11266444
; Publication No. US20060062789A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulatc
; FILE REFERENCE: PF533P1D1
; CURRENT APPLICATION NUMBER: US/11/266,444
; CURRENT FILING DATE: 2005-11-04
; PRIOR APPLICATION NUMBER: 09/880,746
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 1256
```

```
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-266-444-1256

Query Match          65.2%; Score 30; DB 11; Length 257;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      3 RLRYFDV 8
Db      102 KLRYFD 107

RESULT 45
US-11-087-099-11767
; Sequence 11767, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO: 11767
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis MA-4680
US-11-087-099-11767

Query Match          65.2%; Score 30; DB 11; Length 319;
Best Local Similarity 75.0%; Pred. No. 2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 VRLRYFDV 9
Db      162 VSLRYFNV 169

RESULT 46
US-11-087-099-9863
; Sequence 9863, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO: 9863
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Streptomyces coelicolor A3(2)
US-11-087-099-9863

Query Match          65.2%; Score 30; DB 11; Length 321;
Best Local Similarity 75.0%; Pred. No. 2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 VRLRYFDV 9
Db      162 VSLRYFNV 169

RESULT 47
US-10-821-234-1261
; Sequence 1261, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
```

```

; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc_seq_genes Version 1.0
; SEQ ID NO 1261
; LENGTH: 325
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1261

```

```

Query Match      65.2%; Score 30; DB 9; Length 325;
Best Local Similarity 71.4%; Pred. No. 2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      2 VRLRYFDV 8
        |||:|
Db      309 VALRYFNV 315

```

```

RESULT 48
US-11-087-099-2330
; Sequence 2330, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 2330
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Lactococcus lactis subsp. lactis
US-11-087-099-2330

```

```

Query Match      65.2%; Score 30; DB 11; Length 326;
Best Local Similarity 75.0%; Pred. No. 2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      2 VRLRYFDV 9
        |||:|
Db      164 VALRYFNV 171

```

```

RESULT 49
US-11-087-099-3028
; Sequence 3028, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 3028
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Lactococcus lactis
US-11-087-099-3028

```

```

Query Match      65.2%; Score 30; DB 11; Length 326;
Best Local Similarity 75.0%; Pred. No. 2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      2 VRLRYFDV 9

```

```

Db      164 VALRYFNV 171

```

```

RESULT 50
US-11-087-099-8258
; Sequence 8258, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 8258
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Lactococcus lactis
US-11-087-099-8258

```

```

Query Match      65.2%; Score 30; DB 11; Length 326;
Best Local Similarity 75.0%; Pred. No. 2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      2 VRLRYFDV 9
        |||:|
Db      164 VALRYFNV 171

```

```

Search completed: May 4, 2006, 13:54:05
Job time : 20.4286 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: May 4, 2006, 12:46:10 ; Search time 151.111 Seconds
(without alignments)
49.430 Million cell updates/sec

Title: US-10-700-632-4

Perfect score: 81

Sequence: 1 KSSQSVFSSSQNYIA 17

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 1000 summaries

Database :

A_Geneseq_21:*

1: geneseqp1980s:*
2: geneseqp1980s:*
3: geneseqp2000s:*
4: geneseqp2000s:*
5: geneseqp2002s:*
6: geneseqp2003s:*
7: geneseqp2003s:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	81	100.0	17	ADO32088	Mouse ant
2	81	100.0	17	ADO32132	Mouse ant
3	81	100.0	113	ADO32094	Humanised
4	81	100.0	113	ADO32092	Mouse ant
5	81	100.0	114	ADO32146	Mouse ant
6	72	88.9	272	ABG31024	Synthetic
7	72	88.9	272	ADD25453	Binding d
8	72	88.9	272	ADM42728	Synthetic
9	72	88.9	272	AEB95396	Mouse G28
10	72	88.9	272	AEB94430	Mouse ant
11	69	85.2	17	AEE29274	Anti-ClfA
12	69	85.2	17	ADY98289	Human ant
13	69	85.2	17	AEA38785	Murine 2G
14	69	85.2	99	ADO32144	Mouse ant
15	69	85.2	112	AAE54932	FC recept
16	69	85.2	112	AAE54933	MAB 022 V
17	69	85.2	112	AAE29270	S. aureus
18	69	85.2	112	AAE29264	S. aureus
19	69	85.2	112	ADU39970	Antibody
20	69	85.2	113	ADY98289	HEV relat
21	69	85.2	113	ADY98289	HEV relat
22	69	85.2	113	ADY98289	Murine SM
23	69	85.2	113	ADY98289	SM5-1 hum
24	69	85.2	113	ADY98289	Human ant

25	69	85.2	113	9	AEA86699	Humanized
26	69	85.2	113	9	AEA88701	Mouse ant
27	69	85.2	116	9	AEA38741	Murine ant
28	69	85.2	133	9	ADY92466	Mouse SM5
29	69	85.2	133	9	ADY98529	Novel chi
30	69	85.2	133	9	ADY98254	Human ant
31	69	85.2	135	9	ADY92474	SM5-1 hum
32	69	85.2	135	9	ADY98537	Novel chi
33	69	85.2	239	9	ADY92470	SM5-1 chi
34	69	85.2	239	9	ADY98533	Novel chi
35	69	85.2	241	9	ADY92478	SM5-1 hum
36	69	85.2	241	9	ADY98541	Novel chi
37	69	85.2	263	2	AAW90226	Anti-B7.2
38	69	85.2	268	2	AAW90222	Anti-B7.2
39	69	85.2	268	2	AAW90228	Anti-B7.1
40	69	85.2	273	2	AAW90224	Anti-B7.1
41	69	85.2	301	2	AAW11507	Single ch
42	69	85.2	301	2	AAW73217	Multiple ch
43	69	85.2	301	4	AAW61959	Single ch
44	69	85.2	301	4	AAW61959	Single ch
45	69	85.2	352	2	AAW06272	Anti-Fc g
46	69	85.2	553	2	AAW11508	Single ch
47	69	85.2	553	2	AAW73223	H22-anti-
48	69	85.2	553	4	AAW61960	Bispecifi
49	69	85.2	553	4	AAW61960	Bispecifi
50	69	85.2	556	2	AAW90218	Bispecifi
51	69	85.2	580	2	AAW90217	Bispecifi
52	69	85.2	661	9	ADY92484	FL/Fc/hus
53	69	85.2	661	9	ADY92490	FL/Fc/hus
54	69	85.2	661	9	ADY98553	Novel chi
55	69	85.2	661	9	ADY98553	Novel chi
56	69	85.2	667	9	ADY98547	Novel chi
57	69	85.2	702	9	AEA38768	Humanized
58	69	85.2	984	9	AEA54975	Novel valen
59	67	82.7	17	7	ABO33862	Anti-GPI-
60	67	82.7	17	7	ABO33865	Anti-GPI-
61	67	82.7	17	9	ADY98294	Human ant
62	67	82.7	17	9	ADY35808	Anti-glyc
63	67	82.7	109	7	ABO33830	Human ant
64	67	82.7	109	7	ABO33827	Human ant
65	67	82.7	109	7	ADY35773	Anti-glyc
66	67	82.7	109	9	ADY35776	Anti-glyc
67	67	82.7	113	9	ADY98400	Human ant
68	67	82.7	133	9	ADY98264	Human ant
69	67	82.7	133	2	AAW57963	MAB NPS2
70	66	81.5	17	2	AAW50316	MAB NPS2
71	66	81.5	17	2	ADY45514	Murine fa
72	66	81.5	17	9	ADY45514	Murine fa
73	66	81.5	17	9	ADY45514	Murine fa
74	66	81.5	110	2	AAW30012	Light cha
75	66	81.5	112	5	AAE29268	S. aureus
76	66	81.5	113	2	AAW50322	MAB NPS2
77	66	81.5	113	2	AAW50314	Humanised
78	66	81.5	113	2	AAW50313	Humanised
79	66	81.5	113	2	AAW50313	Humanised
80	66	81.5	113	3	AAW90819	260P9 hyb
81	66	81.5	113	9	ABE23170	Antibody
82	66	81.5	114	9	ADY86716	Anti-FlJ3
83	66	81.5	114	9	ADY86715	Anti-FlJ3
84	66	81.5	114	9	ADY86715	Anti-FlJ3
85	66	81.5	132	2	AAW21651	Murine fa
86	66	81.5	132	2	AAW21651	Humanised
87	66	81.5	134	4	AAW74792	H1A-DR sp
88	66	81.5	137	2	AAW21653	Anti-CA12
89	66	81.5	137	2	AAW21655	Mouse Mab
90	66	81.5	139	2	AAW21655	Chimeric
91	66	81.5	154	8	ADY99469	Monoclonal
92	66	81.5	220	2	ADY52342	Human ant
93	66	81.5	220	2	ADY52342	Anti-HGF
94	66	81.5	251	4	AAW74793	Murine/hu
95	66	81.5	258	4	AAW74794	Single ch
96	66	81.5	259	3	AAW09779	Single ch
97	66	81.5	259	3	AAW09779	Antiviral
98	66	81.5	259	3	AAW09779	Antiviral
99	66	81.5	259	3	AAW09779	Antiviral
100	66	81.5	259	3	AAW09779	Antiviral

98	66	81.5	259	8	ADV20698	scFv-3 m	171	64	79.0	115	8	ADL23042	AdL23042 Humanised
99	66	81.5	329	7	ADG32359	Precurser	172	64	79.0	115	8	ADS88801	ADS88801 Amino aci
100	65	80.2	117	9	ADM77438	Human pla	173	64	79.0	115	8	ADS88800	ADS88800 Amino aci
101	65	80.2	113	9	ADZ66386	MOP11 ant	174	64	79.0	115	8	ADS88802	ADS88802 Amino aci
102	65	80.2	220	2	AAy08601	JP112785	175	64	79.0	115	8	ADZ88799	ADZ88799 Amino aci
103	65	80.2	294	2	ADZ66387	MOP11 ant	176	64	79.0	115	8	ADZ88799	ADZ88799 Amino aci
104	64	79.0	17	3	AAy95232	Human mon	177	64	79.0	116	9	ADZ02149	ADZ02149 SARS coro
105	64	79.0	17	3	AAy70334	Human Kap	178	64	79.0	116	9	ADZ02201	ADZ02201 SARS coro
106	64	79.0	17	8	ADL23026	Myelin as	179	64	79.0	116	9	ADZ02177	ADZ02177 SARS coro
107	64	79.0	17	8	ADZ058064	S2 cell d	180	64	79.0	116	9	ADZ02185	ADZ02185 SARS coro
108	64	79.0	17	8	ADP47273	Human pho	181	64	79.0	116	9	ADZ02073	ADZ02073 SARS coro
109	64	79.0	17	8	ADP47249	Human pho	182	64	79.0	116	9	ADZ02089	ADZ02089 SARS coro
110	64	79.0	17	8	ADZ88786	Light cha	183	64	79.0	116	9	ADZ02133	ADZ02133 SARS coro
111	64	79.0	17	9	ADV21415	Human ant	184	64	79.0	116	9	ADZ02085	ADZ02085 SARS coro
112	64	79.0	17	9	ADW47129	Anti-CD20	185	64	79.0	116	9	ADZ02169	ADZ02169 SARS coro
113	64	79.0	17	9	ADY59129	Anti-Tag-	186	64	79.0	116	9	ADZ02137	ADZ02137 SARS coro
114	64	79.0	17	9	ADY59135	Human mon	187	64	79.0	116	9	ADZ02157	ADZ02157 SARS coro
115	64	79.0	17	9	AEA45512	Apoliopor	188	64	79.0	116	9	ADZ02161	ADZ02161 SARS coro
116	64	79.0	58	9	AEC20830	Human var	189	64	79.0	116	9	ADZ02153	ADZ02153 SARS coro
117	64	79.0	58	9	AEC20836	Human var	190	64	79.0	116	9	ADZ02193	ADZ02193 SARS coro
118	64	79.0	82	2	AAW62807	Amino aci	191	64	79.0	116	9	ADZ02145	ADZ02145 SARS coro
119	64	79.0	94	8	ADU04213	Human imm	192	64	79.0	116	9	ADZ02165	ADZ02165 SARS coro
120	64	79.0	94	8	ADU04221	Human imm	193	64	79.0	117	9	ADZ02109	ADZ02109 SARS coro
121	64	79.0	101	6	ABJ18656	Antibody	194	64	79.0	119	5	ABB07172	ebvHlgM M
122	64	79.0	101	6	ABO27156	Human ger	195	64	79.0	119	8	ADL26660	ADL26660 Human ant
123	64	79.0	101	7	ADC98826	Germ line	196	64	79.0	120	4	AAW65565	Amino aci
124	64	79.0	101	7	ADD05430	Anti-MUC1	197	64	79.0	122	8	ADL26708	ADL26708 Human ant
125	64	79.0	101	7	ADF10202	Antibody	198	64	79.0	124	2	AAV57181	Amino aci
126	64	79.0	101	7	ADF09998	Antibody	199	64	79.0	126	6	AAW55903	Human mab
127	64	79.0	101	7	ADF09998	Antibody	200	64	79.0	133	1	AAW80894	V region
128	64	79.0	101	7	ADF09998	Antibody	201	64	79.0	133	2	AAW48633	Sequence
129	64	79.0	101	7	ADF09998	Antibody	202	64	79.0	133	8	ADP12956	Protein e
130	64	79.0	101	8	ADU07345	Vkappa ge	203	64	79.0	134	2	AAW25158	V-region
131	64	79.0	101	8	ADU07345	Human ant	204	64	79.0	134	2	AAW38317	Sequence
132	64	79.0	101	9	ABE13654	Human ger	205	64	79.0	134	2	AAW50690	Human Hum
133	64	79.0	101	9	ABE13654	Human var	206	64	79.0	134	7	ADB17730	Human Hum
134	64	79.0	101	5	ABG70739	Variable	207	64	79.0	134	7	ADG46850	Human Hum
135	64	79.0	112	8	ADP03685	Amino aci	208	64	79.0	144	9	ADW47080	Light cha
136	64	79.0	113	3	AAW18865	Amino aci	209	64	79.0	149	8	ADK52322	Human ant
137	64	79.0	113	3	AAW18873	Amino aci	210	64	79.0	155	2	AAW32483	Kappa lig
138	64	79.0	113	3	AAW18857	Amino aci	211	64	79.0	155	2	AAW06912	Human var
139	64	79.0	113	3	AAW18867	Amino aci	212	64	79.0	159	8	ADK52410	Human ant
140	64	79.0	113	3	AAW18861	Amino aci	213	64	79.0	159	8	ADK52406	Human ant
141	64	79.0	113	3	AAW18869	Amino aci	214	64	79.0	161	7	ADG46871	Protein e
142	64	79.0	113	3	AAW18881	Amino aci	215	64	79.0	171	2	AAW38320	Sequence
143	64	79.0	113	3	AAW18883	Amino aci	216	64	79.0	171	2	AAW50693	Plasemid p
144	64	79.0	113	4	AAW62769	Human HTV	217	64	79.0	171	2	AAW57184	Amino aci
145	64	79.0	113	8	ADP94121	Human VKI	218	64	79.0	238	5	ABG70744	Mouse/hum
146	64	79.0	113	8	ADP94121	Human VKI	219	64	79.0	238	8	ADL23052	ADL23052 Humanised
147	64	79.0	113	9	ADV21413	Human ant	220	64	79.0	238	8	ADL23055	ADL23055 Humanised
148	64	79.0	113	9	ADW77056	LEN light	221	64	79.0	238	8	ADS88793	ADS88793 A mouse/h
149	64	79.0	113	9	AEA62459	Human ant	222	64	79.0	238	8	ADS88804	Humanised
150	64	79.0	114	5	ABW77333	Human Len	223	64	79.0	239	3	AAW03697	Immunoglo
151	64	79.0	114	5	ADL1976	Human TS-	224	64	79.0	239	7	ADW72862	Human AAA
152	64	79.0	114	8	ADZ02154	Mouse ant	225	64	79.0	240	9	ADW23408	Human L61
153	64	79.0	114	8	ADZ036406	Intreacell	226	64	79.0	240	9	ADZ51047	Amino aci
154	64	79.0	114	8	ADZ036363	Intreacell	227	64	79.0	240	9	ADZ56181	Protein s
155	64	79.0	114	8	ADP03699	Human ant	228	64	79.0	241	9	ADW23426	Human L55
156	64	79.0	114	8	ADP03705	Human ant	229	64	79.0	241	9	AEW45897	Human mon
157	64	79.0	114	8	ADP03709	Human ant	230	64	79.0	250	8	ADL161980	Human scF
158	64	79.0	114	8	ADP03711	Human ant	231	64	79.0	251	9	ADV21486	Mature fo
159	64	79.0	114	8	ADP03683	Human ant	232	64	79.0	252	8	ADZ058062	S2 cell d
160	64	79.0	114	8	ADP03687	Human ant	233	64	79.0	252	9	ADZ01974	SARS coro
161	64	79.0	114	8	ADP03685	Human ant	234	64	79.0	252	9	ADZ02024	SARS coro
162	64	79.0	114	8	ADP03701	Human ant	235	64	79.0	252	9	ADZ01968	SARS coro
163	64	79.0	114	8	ADP03713	Human ant	236	64	79.0	252	9	ADZ02010	SARS coro
164	64	79.0	114	9	AEA47268	Human Len	237	64	79.0	252	9	ADZ01998	SARS coro
165	64	79.0	114	9	AEA41082	Germ line	238	64	79.0	252	9	ADZ02000	SARS coro
166	64	79.0	114	9	AEA45971	Human mon	239	64	79.0	252	9	ADZ02004	SARS coro
167	64	79.0	115	7	ADL91336	VL chain	240	64	79.0	252	9	ADZ02006	SARS coro
168	64	79.0	115	8	ADL23043	Humanised	241	64	79.0	252	9	ADZ02014	SARS coro
169	64	79.0	115	8	ADL23040	Humanised	242	64	79.0	252	9	ADZ01976	SARS coro
170	64	79.0	115	8	ADL23041	Humanised	243	64	79.0	252	9	ADZ01972	SARS coro

244	64	79.0	252	9	ADx02008	Adx02008 SARS coro	317	62	76.5	113	6	ABU10147	Abu10147 Humanised
245	64	79.0	252	9	ADx02032	Adx02032 SARS coro	318	62	76.5	113	6	ADb17745	ADb17745 Humanised
246	64	79.0	252	9	ADx02012	Adx02012 SARS coro	319	62	76.5	113	6	ADb17743	ADb17743 Native CC
247	64	79.0	252	9	ADx02016	Adx02016 SARS coro	320	62	76.5	113	6	ABU62757	ABU62757 Murine mo
248	64	79.0	254	9	ADx02020	Adx02020 SARS coro	321	62	76.5	113	6	ABU62759	ABU62759 Humanised
249	64	79.0	254	9	ADx02028	Adx02028 SARS coro	322	62	76.5	113	6	ABU62763	ABU62763 Murine mo
250	64	79.0	255	9	ADx01986	Adx01986 SARS coro	323	62	76.5	113	7	ABU62764	ABU62764 Light cha
251	64	79.0	260	2	AAy50691	AAy50691 Human SCF	324	62	76.5	113	7	AAE39070	AAE39070 Humanised
252	64	79.0	260	2	AAy57182	AAy57182 Amino aci	325	62	76.5	113	7	AAE39069	AAE39069 Murine CC
253	64	79.0	260	6	ADb17736	ADb17736 SCFV. 11	326	62	76.5	113	7	AAE39063	AAE39063 Murine CC
254	64	79.0	260	6	ADG46856	ADG46856 SCFV1 fus	327	62	76.5	113	7	AAE39065	AAE39065 Humanised
255	64	79.0	264	5	ABP43142	ABP43142 Human ova	328	62	76.5	113	7	ADG46863	ADG46863 Murine CC
256	64	79.0	274	2	AAE38319	AAE38319 Sequence	329	62	76.5	113	7	ADG46865	ADG46865 Humanised
257	64	79.0	274	2	AAy50692	AAy50692 Human Hum	330	62	76.5	113	8	ADP71407	ADP71407 Humanised
258	64	79.0	274	2	AAy57183	AAy57183 Amino aci	331	62	76.5	113	8	ADP71406	ADP71406 Murine CC
259	64	79.0	274	6	ADb17738	ADb17738 Hum4 VL-C	332	62	76.5	113	9	ADW77055	ADW77055 Murine CC
260	64	79.0	274	6	ADG46858	ADG46858 Hum4 VL-1i	333	62	76.5	113	9	ADW77058	ADW77058 Human CC4
261	64	79.0	283	8	ADP03815	ADP03815 Human ant	334	62	76.5	113	9	ADW77057	ADW77057 Human CC4
262	64	79.0	284	2	AAE38321	AAE38321 Sequence	335	62	76.5	113	9	ADY59145	ADY59145 Anti-Tag-
263	64	79.0	284	2	AAy50694	AAy50694 Plasmid p	336	62	76.5	113	9	ADY59201	ADY59201 Anti-Tag-
264	64	79.0	284	2	AAy57185	AAy57185 Amino aci	337	62	76.5	113	9	ADZ48271	ADZ48271 Pharmaceu
265	64	79.0	284	6	ADb17742	ADb17742 PSQ49FLAG	338	62	76.5	116	5	AAU81281	AAU81281 Human trk
266	64	79.0	284	7	ADG46862	ADG46862 Hum4 VL-1i	339	62	76.5	116	8	ADG25822	ADG25822 Anti-CD30
267	64	79.0	286	8	ADP03811	ADP03811 Human ant	340	62	76.5	130	6	AAE34366	AAE34366 Escherich
268	64	79.0	342	2	AAW32482	AAW32482 Growth fa	341	62	76.5	133	3	AAy57051	AAy57051 Amino aci
269	64	79.0	342	2	AAy06909	AAy06909 TLH1 amin	342	62	76.5	133	3	AAy90719	AAy90719 CC49 VL r
270	64	79.0	495	2	AAW32480	AAW32480 Growth fa	343	62	76.5	133	4	AAU02138	AAU02138 Mouse par
271	64	79.0	495	2	AAy06908	AAy06908 CATAB-TEV	344	62	76.5	133	6	ADb17751	ADb17751 Humanised
272	64	79.0	504	9	ADY21525	ADY21525 Mature fo	345	62	76.5	133	7	ADG46872	ADG46872 Humanised
273	64	79.0	504	9	ADY21535	ADY21535 Mature fo	346	62	76.5	133	7	ADK66824	ADK66824 Mouse CC4
274	64	79.0	506	9	ADV21505	ADV21505 Mature fo	347	62	76.5	137	3	AAy95243	AAy95243 Humanised
275	64	79.0	506	9	ADV21515	ADV21515 Mature fo	348	62	76.5	120	9	ADW77054	ADW77054 Light cha
276	64	79.0	956	9	AEA36460	AEA36460 SCFV-GalV	349	62	76.5	220	9	ADW77046	ADW77046 Light cha
277	64	77.8	17	9	AEA38758	AEA38758 Humanized	350	62	76.5	220	9	ADW44589	ADW44589 Antibody
278	63	77.8	17	9	AEA38788	AEA38788 Humanized	351	62	76.5	240	5	AAE27927	AAE27927 Human CC4
279	63	77.8	98	7	ADG98627	ADG98627 Anti-huma	352	62	76.5	240	6	ABB82836	ABB82836 Antibody
280	63	77.8	98	7	ADP05431	ADP05431 Anti-MOC1	353	62	76.5	242	2	AAE55865	AAE55865 CC49 VL/
281	63	77.8	98	7	ADP09869	ADP09869 Anti-MOC1	354	62	76.5	242	2	AAW95439	AAW95439 Linked fu
282	63	77.8	112	2	AAE28807	AAE28807 5A8 VL. 3	355	62	76.5	242	2	AAW88101	AAW88101 Single ch
283	63	77.8	113	2	AAE25407	AAE25407 Light cha	356	62	76.5	242	3	AAE07937	AAE07937 A single-
284	63	77.8	113	2	AAE59513	AAE59513 Sequence	357	62	76.5	242	3	AAE57256	AAE57256 4-4-20 Vh
285	63	77.8	114	2	AAE28743	AAE28743 Light cha	358	62	76.5	242	3	AAE27681	AAE27681 Bivalent
286	63	77.8	114	9	ADW10844	ADW10844 Antibody	359	62	76.5	242	3	AAE80926	AAE80926 Single ch
287	63	77.8	116	9	AEA38743	AEA38743 Humanized	360	62	76.5	242	3	AAE54835	AAE54835 Antibody
288	63	77.8	133	2	AAE59509	AAE59509 Sequence	361	62	76.5	242	4	AAE31422	AAE31422 Protein u
289	63	77.8	133	2	AAE59511	AAE59511 Sequence	362	62	76.5	242	6	ABU61811	ABU61811 Antigen b
290	63	77.8	134	2	AAE30485	AAE30485 V kappa r	363	62	76.5	244	2	AAE88096	AAE88096 Single-ch
291	63	77.8	291	3	AAE96305	AAE96305 Human IGF	364	62	76.5	244	3	AAE07932	AAE07932 A heterob
292	63	77.8	244	3	AAE38766	AAE38766 Humanized	365	62	76.5	244	3	AAE57251	AAE57251 4-4-20 Vh
293	63	77.8	667	9	AEA38767	AEA38767 Humanized	366	62	76.5	244	3	AAE27676	AAE27676 Bivalent
294	63	77.8	667	9	AEA38769	AEA38769 Humanized	367	62	76.5	244	3	AAE80921	AAE80921 Single ch
295	63	77.8	667	9	AEA38764	AEA38764 Humanized	368	62	76.5	244	6	ABU61806	ABU61806 Antigen b
296	63	77.8	695	9	AEA38765	AEA38765 Humanized	369	62	76.5	246	6	AAE81523	AAE81523 Single ch
297	62	76.5	17	5	AAU81250	AAU81250 Human trk	370	62	76.5	248	2	AAE37646	AAE37646 Sequence
298	62	76.5	17	6	AAE34368	AAE34368 Escherich	371	62	76.5	248	2	AAE97382	AAE97382 CC49 VL-P
299	62	76.5	17	6	AAE59151	AAE59151 Anti-Tag-	372	62	76.5	249	2	AAE97888	AAE97888 CC49/218
300	62	76.5	17	5	ADZ48267	ADZ48267 Pharmaceu	373	62	76.5	257	5	AAW81524	AAW81524 Single ch
301	62	76.5	112	5	ABG76514	ABG76514 HCV EL an	374	62	76.5	257	5	AAU75157	AAU75157 CC49/218
302	62	76.5	113	2	AAE56964	AAE56964 CC49 V-1i	375	62	76.5	257	6	ABG73145	ABG73145 CC49/218
303	62	76.5	113	2	AAE42269	AAE42269 Humanised	376	62	76.5	257	6	ABG73865	ABG73865 CC49/218
304	62	76.5	113	2	AAE42267	AAE42267 Murine an	377	62	76.5	262	2	AAE97380	AAE97380 CC49/212
305	62	76.5	113	2	AAW97177	AAW97177 Monoclonal	378	62	76.5	262	4	AAE31421	AAE31421 Protein u
306	62	76.5	113	2	AAW05759	AAW05759 Anti-Tag-	379	62	76.5	264	2	AAE97381	AAE97381 PLAP CC49
307	62	76.5	113	5	AAU78327	AAU78327 Human CC4	380	62	76.5	265	9	ADZ48272	ADZ48272 Pharmaceu
308	62	76.5	113	5	AAU78320	AAU78320 Murine CC	381	62	76.5	269	5	AAU75158	AAU75158 CC49/218
309	62	76.5	113	5	AAU78322	AAU78322 Humanised	382	62	76.5	269	6	ABG73146	ABG73146 CC49/218
310	62	76.5	113	6	ABU09367	ABU09367 Light cha	383	62	76.5	269	6	ABG73866	ABG73866 CC49/218
311	62	76.5	113	6	ABU09371	ABU09371 Light cha	384	62	76.5	271	4	AAE31423	AAE31423 Protein u
312	62	76.5	113	6	ABU09372	ABU09372 Murine mo	385	62	76.5	272	4	AAE31424	AAE31424 Protein u
313	62	76.5	113	6	ABU09365	ABU09365 Murine mo	386	62	76.5	275	2	AAE49137	AAE49137 Sequence
314	62	76.5	113	6	ABU10146	ABU10146 Murine TA	387	62	76.5	275	2	AAE49139	AAE49139 Sequence
315	62	76.5	113	6	ABU10142	ABU10142 Humanised	388	62	76.5	280	2	AAE49138	AAE49138 Sequence
316	62	76.5	113	6	ABU10140	ABU10140 Murine TA	389	62	76.5	282	2	AAE4636	AAE4636 Sequence

390	62	75.5	282	2	AAR48635	Aar48635	Sequence	463	61	75.3	240	2	AAV50156	AAV50156	Chimeric
391	62	75.5	444	6	ABJ39018	Abj39018	CC49 sing	464	61	75.3	240	2	AAV50161	AAV50161	Human res
392	62	76.5	483	3	AAW8099	Aaw8099	A protein	465	61	75.3	242	6	ADA91406	ADA91406	Anti-Abet
393	62	76.5	483	3	AAW07935	Aaw07935	A divalen	466	61	75.3	244	8	ADG17481	ADG17481	Anti-CD22
394	62	76.5	483	3	AAV57254	Aay57254	Divalent	467	61	75.3	244	8	ADG17479	ADG17479	Anti-CD22
395	62	76.5	483	3	AAW27679	Aab27679	Bivalent	468	61	75.3	244	8	ADG17485	ADG17485	Anti-CD22
396	62	76.5	483	3	AAW80924	Aay80924	Bivalent	469	61	75.3	244	8	ADG17476	ADG17476	Anti-CD22
397	62	76.5	483	3	ABU61809	Abu61809	Divalent	470	61	75.3	244	8	ADG17486	ADG17486	Anti-CD22
398	62	76.5	486	2	AAW37649	Aar37649	Sequence	471	61	75.3	244	8	ADG17478	ADG17478	Anti-CD22
399	62	76.5	515	9	ADZ48330	Adz48330	Pharmaceu	472	61	75.3	252	9	ADX01996	ADX01996	SARS coro
400	62	76.5	515	9	ADZ48331	Adz48331	Pharmaceu	473	61	75.3	254	9	ADX01962	ADX01962	SARS coro
401	62	76.5	553	2	AAR56966	Aar56966	CC49 VL-L	474	61	75.3	260	8	ADT02521	ADT02521	Anti-CD22
402	62	76.5	553	2	AAR56967	Aar56967	CC49 VL-L	475	61	75.3	432	5	AAO17498	AAO17498	Anti-CD22
403	62	76.5	553	2	AAW97181	Aaw97181	A multiiva	476	61	75.3	480	5	AAO17495	AAO17495	Anti-CD22
404	62	76.5	553	2	AAW97180	Aaw97180	A multiiva	477	61	75.3	601	5	AAO17494	AAO17494	Anti-CD22
405	62	76.5	553	2	AAW05762	Aay05762	CC49 sing	478	61	75.3	614	5	AAO17494	AAO17494	Anti-CD22
406	62	76.5	553	2	AAW05763	Aay05763	CC49 sing	479	61	75.3	658	5	AAO17495	AAO17495	Anti-CD22
407	62	76.5	603	2	ADW44587	Adw44587	Antibody	480	60	74.1	17	8	ADP47240	ADP47240	Human pho
408	62	76.5	621	9	ADW44588	Adw44588	Antibody	481	60	74.1	17	8	ADP47240	ADP47240	Human pho
409	62	76.5	643	9	ADW44592	Adw44592	Antibody	482	60	74.1	17	8	ADP47240	ADP47240	Human pho
410	62	76.5	661	9	ADW44593	Adw44593	Antibody	483	60	74.1	113	2	AAR35031	AAR35031	Humanised
411	61	75.3	17	6	AAE38108	Aae38108	Human COU	484	60	74.1	113	2	AAR35031	AAR35031	Humanised
412	61	75.3	17	7	ADC97708	Adc97708	Mouse mon	485	60	74.1	113	7	ADO51595	ADO51595	Human TRG
413	61	75.3	18	6	ABJ18708	Abj18708	Antibody	486	60	74.1	113	9	AEI1697	AEI1697	Anti-Pseu
414	61	75.3	18	6	ABJ18714	Abj18714	Antibody	487	60	74.1	115	8	ADO32147	ADO32147	Mouse ant
415	61	75.3	18	6	ABJ18706	Abj18706	Antibody	488	60	74.1	116	9	ADX02057	ADX02057	SARS coro
416	61	75.3	18	6	ABJ18736	Abj18736	Antibody	489	60	74.1	120	2	AAR61240	AAR61240	Monoclonal
417	61	75.3	94	6	AAV56669	Aay56669	Partial p	490	60	74.1	122	2	AAV27075	AAV27075	Monoclonal
418	61	75.3	108	6	AAE38116	Aae38116	Human can	491	60	74.1	131	2	AAR55553	AAR55553	DRBG-200
419	61	75.3	112	8	ADT02527	Adt02527	Anti-CD22	492	60	74.1	133	2	AAR55555	AAR55555	DRBG-200
420	61	75.3	113	2	AAR92215	Aar92215	IL2 Mab V	493	60	74.1	149	8	ADK52402	ADK52402	Human ant
421	61	75.3	113	2	AAR92217	Aar92217	Humanised	494	60	74.1	154	3	AAW53686	AAW53686	Human col
422	61	75.3	113	2	AAW27695	Aaw27695	Variable	495	60	74.1	159	8	ADK52302	ADK52302	Human ant
423	61	75.3	113	2	AAV50143	Aay50143	Antibody	496	60	74.1	163	8	ADK52374	ADK52374	Human ant
424	61	75.3	113	2	AAV50145	Aay50145	Antibody	497	60	74.1	163	8	ADK52306	ADK52306	Human ant
425	61	75.3	113	2	AAV50144	Aay50144	Antibody	498	60	74.1	220	8	ADK52298	ADK52298	Human ant
426	61	75.3	113	2	AAV21818	Aay21818	IL210 ant	499	60	74.1	220	8	ADK52386	ADK52386	Human ant
427	61	75.3	113	6	ABB98748	Abb98748	Human res	500	60	74.1	220	8	ADK52334	ADK52334	Human ant
428	61	75.3	113	6	ABB98749	Abb98749	Human res	501	60	74.1	220	8	ADK52334	ADK52334	Human ant
429	61	75.3	113	6	ABB98747	Abb98747	Human res	502	60	74.1	240	4	AAU00815	AAU00815	Human Imm
430	61	75.3	113	6	ABR54914	Abx54914	Light Cna	503	60	74.1	240	4	AEA41033	AEA41033	Human ant
431	61	75.3	113	6	ABJ18724	Abj18724	Antibody	504	60	74.1	248	2	AAV17965	AAV17965	Mouse scf
432	61	75.3	113	7	ADC97685	Adc97685	Mouse mon	505	60	74.1	254	9	ADX01960	ADX01960	SARS coro
433	61	75.3	113	7	ADC97689	Adc97689	Human mon	506	60	74.1	259	7	ADG32324	ADG32324	Mouse scf
434	61	75.3	113	4	ABE19280	Aeb19280	IGG kappa	507	60	74.1	259	7	ADG32325	ADG32325	Mouse scf
435	61	75.3	113	4	ABE19280	Aeb19280	IGG kappa	508	60	74.1	329	7	ADG32361	ADG32361	Precursor
436	61	75.3	114	6	ABJ18682	Abj18682	Human HTV	509	60	74.1	371	7	ADG32362	ADG32362	Precursor
437	61	75.3	114	8	ADQ75236	Adq75236	Immunoglo	510	60	74.1	626	7	ADG32340	ADG32340	Fusion pr
438	61	75.3	115	2	AAW27546	Aaw27546	Human Ab	511	59	72.8	112	5	ABG76548	ABG76548	HCV EI an
439	61	75.3	115	2	AAW27697	Aaw27697	Variable	512	59	72.8	112	5	ADG99793	ADG99793	Anti-huma
440	61	75.3	115	6	ADA89107	Ada89107	MS-Pro-21	513	59	72.8	113	7	ADDO5397	ADDO5397	Anti-WC1
441	61	75.3	115	6	ADA90113	Ada90113	Anti-Abet	514	59	72.8	113	7	ADPO9835	ADPO9835	Human ant
442	61	75.3	115	7	AAO31078	Aao31078	Human ant	515	59	72.8	113	7	ADPO9835	ADPO9835	Human ant
443	61	75.3	115	7	ADG74358	Adg74358	MSPRO 11g	516	59	72.8	114	2	AAK45605	AAK45605	Monoclonal
444	61	75.3	115	9	ADW38833	Adw38833	T-cell me	517	59	72.8	116	9	ADX02077	ADX02077	SARS coro
445	61	75.3	115	9	ADY96985	Ady96985	Human imm	518	59	72.8	116	9	ADX02141	ADX02141	SARS coro
446	61	75.3	115	9	ADY96984	Ady96984	Human imm	519	59	72.8	116	9	ADX02173	ADX02173	SARS coro
447	61	75.3	115	9	ADY96986	Ady96986	Human imm	520	59	72.8	145	8	ADR10316	ADR10316	Human pro
448	61	75.3	115	9	ADY96984	Ady96984	Human imm	521	59	72.8	179	8	ADK52434	ADK52434	SARS coro
449	61	75.3	115	9	ADY96986	Ady96986	Human imm	522	59	72.8	252	9	ADX01970	ADX01970	SARS coro
450	61	75.3	115	9	ADY96977	Ady96977	Human imm	523	59	72.8	252	9	ADX02002	ADX02002	SARS coro
451	61	75.3	116	9	ADX02129	Adx02129	SARS coro	524	59	72.8	254	9	ADX02018	ADX02018	SARS coro
452	61	75.3	116	9	ADX02061	Adx02061	SARS coro	525	59	72.8	285	2	AAK48638	AAK48638	Sequence
453	61	75.3	128	3	AAV56774	Aay56774	Amino act	526	58	71.6	94	2	AAW62808	AAW62808	Amino act
454	61	75.3	133	2	AAV50154	Aay50154	Murine mo	527	58	71.6	105	5	ABB07184	ABB07184	MS119E5.1
455	61	75.3	133	3	AAV50154	Aay50154	Murine mo	528	58	71.6	105	5	ABB07184	ABB07184	MS119E5.1
456	61	75.3	135	6	ADA47343	Ada47343	Human ant	529	58	71.6	105	8	ADJ26684	ADJ26684	Human ant
457	61	75.3	135	7	ADT872875	Adt872875	Human AAA	530	58	71.6	113	3	AAI18877	AAI18877	Human ant
458	61	75.3	135	8	ADP88458	Adp88458	Human ant	531	58	71.6	113	3	AAI18855	AAI18855	Human ant
459	61	75.3	135	8	ADP87927	Adp87927	Human Hst	532	58	71.6	113	3	AAI18871	AAI18871	Amino aci
460	61	75.3	141	2	AAV24374	Aay24374	Human mon	533	58	71.6	113	3	AAI18859	AAI18859	Amino aci
461	61	75.3	220	2	AAV50172	Aay50172	Antibody	534	58	71.6	113	3	AAI18875	AAI18875	Amino aci
462	61	75.3	238	7	ADBE4203	Ade4203	IL2LC pro	535	58	71.6	147	2	AAV34314	AAV34314	IGM antiib

536	58	71.6	149	2	AAV34311	Aay34311 IGM antib	609	57	70.4	638	8	ADL27333	Adl27333 Amino aci
537	58	71.6	149	9	ADY21959	Ady21959 Antibody	610	56	69.1	17	2	AAR54107	Aar54107 Humanised
538	58	71.6	158	8	ADK52366	Adk52366 Human ant	611	56	69.1	17	2	AAR98484	Aar98484 Anti-IL-5
539	58	71.6	166	7	ADD28248	Add28248 Human bet	612	56	69.1	17	2	AAW42460	Aaw42460 Mouse ant
540	58	71.6	166	9	ADV86835	Adv86835 Bacillus	613	56	69.1	17	4	ABE28265	AbE28265 Anti-SAF-
541	58	71.6	171	8	ADK52422	Adk52422 Human ant	614	56	69.1	17	7	ADD94135	Add94135 Mouse HUI
542	58	71.6	174	7	ADB65048	Adb65048 Human pro	615	56	69.1	105	2	AAR98495	Aar98495 MAb 2F2 1
543	58	71.6	241	9	AEB45859	Aeb45859 Human mon	616	56	69.1	105	2	AAR98497	Aar98497 MAb 2E3 1
544	58	71.6	244	8	ADG17477	Adg17477 Anti-CD22	617	56	69.1	105	2	AAW42454	Aaw42454 Mouse ant
545	58	71.6	244	8	ADG17487	Adg17487 Anti-CD22	618	56	69.1	105	2	AAW42456	Aaw42456 Mouse ant
546	58	71.6	244	8	ADG17482	Adg17482 Anti-CD22	619	56	69.1	113	2	AAR54102	Aar54102 Humanised
547	58	71.6	244	8	ADG17483	Adg17483 Anti-CD22	620	56	69.1	113	2	AAR98489	Aar98489 Humanised
548	58	71.6	244	8	ADG17480	Adg17480 Anti-CD22	621	56	69.1	113	2	AAR98493	Aar98493 REI human
549	58	71.6	244	8	ADG17484	Adg17484 Anti-CD22	622	56	69.1	113	2	AAW42472	Aaw42472 Interleuk
550	58	71.6	270	9	ADY21963	Ady21963 Single ch	623	56	69.1	113	2	AAW42472	Aaw42472 Interleuk
551	58	71.6	270	9	ADY21967	Ady21967 Antibody	624	56	69.1	113	2	AAW42466	Aaw42466 Interleuk
552	58	71.6	293	2	AAMS9928	Aaw59928 Human AaA	625	56	69.1	113	2	AAW42468	Aaw42468 Fab15 11g
553	58	71.6	293	3	AAE03671	Adb03671 Recombina	626	56	69.1	113	2	AAW42452	AAW42452 Mouse ant
554	58	71.6	293	7	ADB72835	Adb72835 Human AaA	627	56	69.1	113	2	AAW42467	AAW42467 Fab2 11gh
555	58	71.6	328	3	AAE03696	Human aor	628	56	69.1	113	6	ABO10744	ABO10744 Variable
556	58	71.6	328	7	ADB72861	Adb72861 Human AaA	629	56	69.1	113	6	ABR44700	ABR44700 Variable
557	58	71.6	502	9	ADY21971	Ady21971 Antibody	630	56	69.1	113	6	ABR44688	ABR44688 Murine Mu
558	58	71.6	502	9	ADY21969	Ady21969 Antibody	631	56	69.1	113	6	ADD94117	Add94117 Mouse HUI
559	57	70.4	17	2	AAV08712	Aay08712 Human m11	632	56	69.1	113	7	ADQ90822	Adq90822 Kabat sub
560	57	70.4	17	3	AAV95231	Aay95231 Humanised	633	56	69.1	113	8	ADQ90842	Adq90842 Kabat sub
561	57	70.4	17	6	ABG71652	Abg71652 CDR1 of H	634	56	69.1	113	8	ADU67950	Adu67950 Mouse Kab
562	57	70.4	17	7	ADG94182	Adg94182 Mouse HUI	635	56	69.1	113	8	ADU67970	Adu67970 Mouse Kab
563	57	70.4	17	8	ADJ25672	Adj25672 Mouse aPC	636	56	69.1	113	8	ADV66167	Adv66167 Human EPC
564	57	70.4	17	9	ADY58493	Ady58493 Peptide u	637	56	69.1	113	9	ADV66167	Adv66167 Human EPC
565	57	70.4	104	8	ADJ65022	Adj65022 Rat anti-	638	56	69.1	113	9	ADZ83525	Adz83525 AntiIePCam
566	57	70.4	110	2	AAW56520	AAW56520 Anti-DNA	639	56	69.1	114	2	AAW54111	Aaw54111 Humanised
567	57	70.4	112	5	ABG76524	Abg76524 HCV EI an	640	56	69.1	114	4	AAW62864	AAW62864 Anti-SAF-
568	57	70.4	113	8	ADJ25652	Adj25652 Mouse act	641	56	69.1	114	8	ADP03697	Adp03697 Human ant
569	57	70.4	114	2	AAZ22419	Aaz22419 Murine ka	642	56	69.1	114	9	ADZ70849	Adz70849 Human Ig
570	57	70.4	114	2	AAZ22422	Aaz22422 Antibody	643	56	69.1	114	9	ABE28921	AbE28921 Human ant
571	57	70.4	114	2	AAE63804	Aae63804 Humanised	644	56	69.1	115	3	AAAB28395	AAAB28395 Anti-VGCF
572	57	70.4	114	2	AAE63803	Aae63803 Mouse HMF	645	56	69.1	115	5	AAU77947	Aau77947 Variable
573	57	70.4	133	3	AAV83647	Aay83647 Consensus	646	56	69.1	137	5	ABP62187	ABP62187 Human imm
574	57	70.4	133	6	ABG71660	Abg71660 HMFg-1 1i	647	56	69.1	163	8	ADK52394	Adk52394 Human ant
575	57	70.4	153	6	ABU11788	Abu11788 Human MDD	648	56	69.1	173	8	ADK52438	Adk52438 Human ant
576	57	70.4	163	8	ADK52338	Adk52338 Human ant	649	56	69.1	241	2	AAZ28809	Aaz28809 Vector pM
577	57	70.4	173	8	ADK52430	Adk52430 Human ant	650	56	69.1	248	2	AAV17960	Aay17960 Mouse scF
578	57	70.4	178	8	ADK52418	Adk52418 Human ant	651	56	69.1	255	5	AAU72870	Aau72870 P5-23 sin
579	57	70.4	211	5	ADP43134	Adp43134 Human ova	652	56	69.1	497	9	ADZ83445	Adz83445 CD3 speci
580	57	70.4	240	4	ADJ65029	Adj65029 Plasmid p	653	56	69.1	500	9	ADV66137	Adv66137 Anti-CD3-
581	57	70.4	242	4	AAU80338	Aau80338 Human m11	654	56	69.1	503	9	ADV66133	Adv66133 Anti-CD3-
582	57	70.4	242	4	AAU97949	Aau97949 HMFg1 Fab	655	56	69.1	503	9	ADV66135	Adv66135 Anti-CD3-
583	57	70.4	242	4	AAU80039	Aau80039 HMFg1 Fab	656	56	69.1	515	9	ADZ83436	Adz83436 Deimmuniz
584	57	70.4	246	8	ADQ27057	Adq27057 Single-ch	657	56	69.1	521	9	ADV66116	Adv66116 Anti-CD3-
585	57	70.4	246	8	ADQ27057	Adq27057 Human ant	658	56	69.1	12	8	ADQ32133	Ado32133 Mouse ant
586	57	70.4	247	9	ADZ76001	Adz76001 huHMFg1 (659	56	69.1	17	6	AAV30156	Aav30156 MAb GAH v
587	57	70.4	248	9	AAE17635	Aae17635 Single ch	660	56	69.1	17	6	ABP98688	ABP98688 Human GAH
588	57	70.4	249	2	AAW60770	Aaw60770 Single ch	661	56	69.1	17	6	ABP98680	ABP98680 Human GAH
589	57	70.4	336	9	ADW38884	Adw38884 Novel pla	662	56	69.1	17	6	ADD94189	Add94189 Mouse HUI
590	57	70.4	380	9	ADW38880	Adw38880 Novel pla	663	56	69.1	17	7	ADG43188	Adg43188 Mouse HUI
591	57	70.4	518	9	AAE17596	Aae17596 Apolipoppr	664	55	67.9	113	6	ABE19288	ABE19288 IGG kappa
592	57	70.4	519	9	AAE17600	Aae17600 Apolipoppr	665	55	67.9	114	2	AAAR30144	AAAR30144 MAb GAH v
593	57	70.4	522	9	AAE17604	Aae17604 Apolipoppr	666	55	67.9	17	8	ADQ28263	Adq28263 Method of
594	57	70.4	523	9	AAE17609	Aae17609 Apolipoppr	667	55	67.9	17	8	ADT50350	Adt50350 Human mon
595	57	70.4	524	9	AAE17598	Aae17598 Apolipoppr	668	55	67.9	17	9	ADW77471	Adw77471 Human pla
596	57	70.4	526	9	AAE17602	Aae17602 Apolipoppr	669	55	67.9	109	9	AE440152	Ae440152 Mouse Ig
597	57	70.4	528	9	AAE17607	Aae17607 Apolipoppr	670	55	67.9	113	6	ABE54912	ABE54912 Light cha
598	57	70.4	530	9	AAE17611	Aae17611 Apolipoppr	671	55	67.9	113	6	ABE19288	ABE19288 IGG kappa
599	57	70.4	556	9	AAE17613	Aae17613 Apolipoppr	672	55	67.9	114	2	AAAR30144	AAAR30144 MAb GAH v
600	57	70.4	557	9	AAE17618	Aae17618 Apolipoppr	673	55	67.9	114	6	ABP98692	ABP98692 Human GAH
601	57	70.4	560	9	AAE17622	Aae17622 Apolipoppr	674	55	67.9	114	6	ABP98684	ABP98684 Human GAH
602	57	70.4	561	9	AAE17626	Aae17626 Apolipoppr	675	55	67.9	114	7	ADG43870	Adg43870 Human pro
603	57	70.4	562	9	AAE17616	Aae17616 Apolipoppr	676	55	67.9	114	8	ADQ36408	Adq36408 Intracell
604	57	70.4	564	9	AAE17620	Aae17620 Apolipoppr	677	55	67.9	114	8	ADQ28267	Adq28267 Method of
605	57	70.4	566	9	AAE17624	Aae17624 Apolipoppr	678	55	67.9	114	8	ADT50354	Adt50354 Human mon
606	57	70.4	568	9	AAE17628	Aae17628 Apolipoppr	679	55	67.9	115	9	ADX02113	Adx02113 SARS coro
607	57	70.4	637	9	ABE95915	Abe95915 Phaeoelin	680	55	67.9	116	3	AAAB15673	Aab15673 Murine 5B
608	57	70.4	638	8	ADL27332	Adl27332 Amino aci	681	55	67.9	116	9	ADX02053	Adx02053 SARS coro

682	55	67.9	134	2	AAW06206	AAW06206	Xenografit	755	52	64.2	119	2	AA848564	AA848564	Sequence
683	55	67.9	151	6	AB004853	AB004853	Human epi	756	52	64.2	133	2	AA85909	AA85909	Monoclonal
684	55	67.9	151	9	AEa17765	AEa17765	Hybridoma	757	169	64.2	2	AA853806	AA853806	IMCP V-mi	
685	55	67.9	153	9	AEa17763	AEa17763	Hybridoma	758	220	64.2	2	AA853802	AA853802	FAB light	
686	55	67.9	154	6	AB004851	AB004851	Human epi	759	242	64.2	2	AA894962	AA894962	Single ch	
687	55	67.9	154	6	AEa17778	AEa17778	Hybridoma	760	248	64.2	2	AA894964	AA894964	Mouse scf	
688	55	67.9	157	6	AB004855	AB004855	Human epi	761	251	64.2	2	AA848632	AA848632	Sequence	
689	55	67.9	157	9	AEa17779	AEa17779	Hybridoma	762	254	64.2	2	ADX01984	ADX01984	SARS coro	
690	55	67.9	159	9	AEa17767	AEa17767	Hybridoma	763	258	64.2	5	AAU72865	AAU72865	p5-2. sing	
691	55	67.9	163	8	ADK52346	ADK52346	Human ant	764	259	64.2	5	AAU72871	AAU72871	3B10xp4-3	
692	55	67.9	163	8	ADK52326	ADK52326	Human ant	765	260	64.2	5	AAU72862	AAU72862	p4-3. sing	
693	55	67.9	220	8	ADK52362	ADK52362	Human ant	766	263	64.2	7	AA838318	AA838318	Sequence	
694	55	67.9	253	9	ADX01988	ADX01988	SARS coro	767	277	64.2	2	AA839336	AA839336	scfV frag	
695	55	67.9	254	9	ADX01958	ADX01958	SARS coro	768	284	64.2	2	AA844225	AA844225	Chimeric	
696	54	66.7	17	7	AAW70908	AAW70908	CDRI of t	769	295	64.2	5	ABG68848	ABG68848	C219scfV	
697	54	66.7	17	7	ADDP94190	ADDP94190	Mouse HUI	770	354	64.2	3	AA882515	AA882515	Anti-HA p	
698	54	66.7	17	8	ADDP94187	ADDP94187	Mouse HUI	771	378	64.2	3	AEa36900	AEa36900	Anti-CD3x	
699	54	66.7	17	8	ADU66954	ADU66954	Human 3B1	772	380	64.2	5	ABG68852	ABG68852	Interfero	
700	54	66.7	17	9	AEa40131	AEa40131	TNF resis	773	482	64.2	2	AA806915	AA806915	Amino aci	
701	54	66.7	100	2	AAW70948	AAW70948	TNF cha	774	482	64.2	2	ADV21531	ADV21531	Mature fo	
702	54	66.7	109	9	AEa40129	AEa40129	TNF resis	775	494	64.2	9	ADV21521	ADV21521	Mature fo	
703	54	66.7	112	8	ADU66952	ADU66952	Human 3B1	776	495	64.2	9	ADV21517	ADV21517	Mature fo	
704	54	66.7	113	8	AD032153	AD032153	Mouse ant	777	495	64.2	9	ADV21527	ADV21527	Mature fo	
705	54	66.7	137	2	AAW10544	AAW10544	Humanised	778	495	64.2	9	ADV21523	ADV21523	Mature fo	
706	54	66.7	137	2	AAW10545	AAW10545	Humanised	779	496	64.2	9	ADV21533	ADV21533	Mature fo	
707	54	66.7	137	2	AAW10547	AAW10547	Wild type	780	496	64.2	9	ADV21533	ADV21533	Mature fo	
708	54	66.7	158	8	ADK52378	ADK52378	Human ant	781	496	64.2	9	ADZ83619	ADZ83619	CD3 speci	
709	54	66.7	175	5	ABG60106	ABG60106	Human DIT	782	496	64.2	9	ADZ83625	ADZ83625	CD3 speci	
710	53	65.4	111	6	ABR42303	ABR42303	Mouse mon	783	496	64.2	9	ADZ83641	ADZ83641	CD3 speci	
711	53	65.4	111	6	ABR42302	ABR42302	Mouse mon	784	496	64.2	9	ADZ83615	ADZ83615	CD3 speci	
712	53	65.4	113	7	AA890834	AA890834	17P6.1ligh	785	496	64.2	9	ADZ83653	ADZ83653	CD3 speci	
713	53	65.4	113	7	AD003128	AD003128	Colo spe	786	496	64.2	9	ADZ83637	ADZ83637	CD3 speci	
714	53	65.4	159	8	ADK52382	ADK52382	Human ant	787	496	64.2	9	ADZ83629	ADZ83629	CD3 speci	
715	53	65.4	219	2	AAK44495	AAK44495	Sequence	788	496	64.2	9	ADZ83645	ADZ83645	CD3 speci	
716	53	65.4	247	7	AD003132	AD003132	Colo spe	789	496	64.2	9	ADZ83649	ADZ83649	CD3 speci	
717	53	65.4	267	6	ABR42292	ABR42292	Bispecifi	790	496	64.2	9	ADZ83633	ADZ83633	CD3 speci	
718	53	65.4	267	6	ABR42299	ABR42299	Bispecifi	791	496	64.2	9	ADZ83657	ADZ83657	CD3 speci	
719	53	65.4	267	6	ABR42296	ABR42296	Bispecifi	792	497	64.2	9	ADZ83621	ADZ83621	CD3 speci	
720	53	65.4	267	6	ABR42294	ABR42294	Bispecifi	793	497	64.2	9	ADZ83659	ADZ83659	CD3 speci	
721	53	65.4	268	6	ABR42288	ABR42288	Diabody 6	794	497	64.2	9	ADZ83415	ADZ83415	C-termina	
722	53	65.4	268	6	ABR42287	ABR42287	Diabody 6	795	497	64.2	9	ADZ83417	ADZ83417	C-termina	
723	53	65.4	268	6	ABR42286	ABR42286	Diabody 6	796	497	64.2	9	ADZ83635	ADZ83635	CD3 speci	
724	53	65.4	268	6	ABR42297	ABR42297	Diabody h	797	497	64.2	9	ADZ83627	ADZ83627	CD3 speci	
725	53	65.4	268	6	ABR83644	ABR83644	h679-scFv	798	497	64.2	9	ADZ83639	ADZ83639	CD3 speci	
726	53	65.4	268	6	ABR83643	ABR83643	h679-scFv	799	497	64.2	9	ADZ83647	ADZ83647	CD3 speci	
727	53	65.4	358	8	ADU26571	ADU26571	Chimeric	800	497	64.2	9	ADZ83655	ADZ83655	CD3 speci	
728	53	65.4	358	8	ADU26561	ADU26561	Chimeric	801	497	64.2	9	ADZ83651	ADZ83651	CD3 speci	
729	53	65.4	391	6	ABR83649	ABR83649	TSI VL ch	802	497	64.2	9	ADZ83623	ADZ83623	CD3 speci	
730	52	64.2	16	5	AAU70346	AAU70346	Mouse Kap	803	497	64.2	9	ADZ83631	ADZ83631	CD3 speci	
731	52	64.2	17	5	AAV32226	AAV32226	G-CSF ago	804	497	64.2	9	ADZ83617	ADZ83617	CD3 speci	
732	52	64.2	17	5	ABG68853	ABG68853	CDRI VL p	805	497	64.2	9	ADZ83617	ADZ83617	CD3 speci	
733	52	64.2	17	7	ADDP94180	ADDP94180	Mouse HUI	806	500	64.2	9	ADV66095	ADV66095	Anti-CD3-	
734	52	64.2	17	7	ADDP94191	ADDP94191	Mouse HUI	807	500	64.2	9	ADV66097	ADV66097	Anti-CD3-	
735	52	64.2	17	8	ADP47267	ADP47267	Human pho	808	501	64.2	9	ADV21519	ADV21519	Mature fo	
736	52	64.2	111	2	AAW71242	AAW71242	Light cha	809	501	64.2	9	ADV21529	ADV21529	Mature fo	
737	52	64.2	113	2	AA838603	AA838603	MCPC ligh	810	503	64.2	9	ADV66087	ADV66087	Anti-CD3-	
738	52	64.2	113	2	AA868742	AA868742	Mab MCPc6	811	503	64.2	5	AAU72875	AAU72875	Human NKG	
739	52	64.2	113	2	AA858483	AA858483	Murine MC	812	505	64.2	5	ADZ83441	ADZ83441	Deimmuniz	
740	52	64.2	113	8	AD101145	AD101145	Murine MC	813	515	64.2	9	ADV66121	ADV66121	Anti-CD3-	
741	52	64.2	113	8	AD032155	AD032155	Mouse ant	814	515	64.2	2	AA863780	AA863780	Chain C	
742	52	64.2	113	9	ADV66175	ADV66175	Human BPC	815	517	64.2	2	AA863780	AA863780	Chain C	
743	52	64.2	113	9	ADV21427	ADV21427	Human ant	816	517	64.2	7	AA876082	AA876082	MAB 55.1	
744	52	64.2	113	9	ADX37190	ADX37190	Human SMS	817	517	64.2	7	ADDP94185	ADDP94185	Mouse HUI	
745	52	64.2	113	9	ADZ83553	ADZ83553	AntiEPCam	818	517	64.2	7	ADDP94186	ADDP94186	Mouse HUI	
746	52	64.2	113	9	AEa88707	AEa88707	Human ant	819	517	64.2	7	ADDP94181	ADDP94181	Mouse HUI	
747	52	64.2	113	8	AEa88703	AEa88703	Human ant	820	517	64.2	7	AA863770	AA863770	Humanised	
748	52	64.2	114	8	AEa11692	AEa11692	Anti-Pseu	821	517	64.2	2	AA863769	AA863769	Murine L	
749	52	64.2	115	2	AA852036	AA852036	Light cha	822	517	64.2	2	AA890839	AA890839	14G1.1ligh	
750	52	64.2	115	8	AD032148	AD032148	Mouse ant	823	517	64.2	8	ADP03707	ADP03707	Human ant	
751	52	64.2	115	8	AD032149	AD032149	Mouse ant	824	517	64.2	8	ADP032150	ADP032150	Human ant	
752	52	64.2	115	8	AD032152	AD032152	Mouse ant	825	517	64.2	8	ADK52310	ADK52310	Human ant	
753	52	64.2	116	1	AA80460	AA80460	Sequence	826	517	64.2	7	ADDP05274	ADDP05274	Female mo	
754	52	64.2	116	9	ADX02105	ADX02105	SARS coro	827	517	63.0	218	8	ADM80365	ADM80365	Murine ho

828	51	63.0	219	2	AAR76086	Aar76086 MAB 55.1	901	40	49.4	113	6	ABR54918	Ab-54918 Light cha
829	51	63.0	239	2	AAR76087	Aar76087 MAB 55.1	902	40	49.4	113	8	ABE19294	Aeb19294 Igg kappa
830	51	63.0	244	8	ADR59117	Ad559117 Anti-K88/	903	40	49.4	207	9	ADT87228	Adt87228 Yeast Str
831	51	63.0	288	2	AAM82743	Aam82743 Fusion pr	904	40	49.4	339	3	AB141313	Ab141313 Human sec
832	51	63.0	673	2	AAM82742	Aam82742 Plasmid p	905	40	49.4	339	4	ABR85235	Abbr85235 Human sec
833	50	61.7	17	7	ADD94183	Add94183 Mouse HUI	906	40	49.4	564	4	ABG07079	Abg07079 Novel hum
834	50	61.7	114	2	AAW15537	Aaw15537 Anti-TGF	907	40	49.4	566	4	ABG12959	Abg12959 Novel hum
835	50	61.7	163	8	ADK52398	Adk52398 Human ant	908	40	49.4	565	4	ABG08640	Abg08640 Novel hum
836	50	61.7	265	2	AAR52864	Aar52864 Glycophor	909	40	49.4	698	8	ADS24123	Ads24123 Bacterial
837	49	60.5	14	5	ABP62326	Abp62326 Human imm	910	39.5	48.8	107	2	AAR38599	Aar38599 Human hea
838	49	60.5	17	7	ADD94274	Add94274 Mouse HUI	911	38.5	48.8	107	2	AAW58499	Aaw58499 Human kap
839	49	60.5	17	7	ADD94184	Add94184 Mouse HUI	912	39.5	48.8	107	8	AD101161	Ad101161 Human kap
840	49	60.5	113	7	ADD94275	Add94275 Mouse HUI	913	39	48.1	42	9	ADY17071	Ady17071 PRO polyp
841	49	60.5	113	8	AAR90836	Aar90836 10B6 light	914	39	48.1	50	4	AAW88183	Aaw88183 Human imm
842	49	60.5	115	8	AD032151	Ad032151 Mouse ant	915	39	48.1	77	4	AAW84012	Aaw84012 Human imm
843	49	60.5	124	4	AAM24229	Aam24229 Human EST	916	39	48.1	66	3	AAW18522	Aaw18522 Zee may's
844	48.5	59.9	111	2	AAR52059	Aar52059 Light cha	917	39	48.1	114	2	AAW06831	Aaw06831 Mouse MAB
845	48	59.3	14	2	AAW95269	Aaw95269 Anti-piog	918	39	48.1	121	7	ABM89528	Abm89528 Rice adio
846	48	59.3	17	7	ADD94273	Add94273 Mouse HUI	919	39	48.1	124	3	AAW18521	Aaw18521 Zee may's
847	48	59.3	17	7	ADD94276	Add94276 Mouse HUI	920	39	48.1	132	4	AAW74266	Aaw74266 Human col
848	48	59.3	110	2	AAW56517	Aaw56517 H221 anti	921	39	48.1	136	6	ABU15097	Abu15097 Protein e
849	48	59.3	134	2	AAR81841	Aar81841 E-selecti	922	39	48.1	136	6	ADK13802	Adk13802 E. coli i
850	48	59.3	134	2	AAR81838	Aar81838 E-selecti	923	39	48.1	265	2	AAW20580	Aaw20580 H. pylori
851	47	58.0	14	2	AAW95267	Aaw95267 Anti-piog	924	39	48.1	343	8	AD145313	Ad145313 Rice leop
852	47	58.0	17	2	AAW70914	Aaw70914 Peptide p	925	39	48.1	367	6	ADA33716	Ada33716 Actinoba
853	47	58.0	17	7	ABM07951	Abm07951 CDRI sequ	926	39	48.1	430	3	AAW20784	Aaw20784 Arabidops
854	47	58.0	17	7	ADD94272	Add94272 Mouse HUI	927	39	48.1	468	3	AAW20783	Aaw20783 Arabidops
855	47	58.0	132	3	ABM07964	Abm07964 Amino aci	928	39	48.1	468	3	ADW72198	Adw72198 Arabidops
856	47	58.0	132	3	ABM07966	Abm07966 A light c	929	39	48.1	474	3	AAW22416	Aaw22416 Arabidops
857	47	58.0	133	5	ABP51942	Abp51942 Silenced	930	39	48.1	510	9	ADW72215	Adw72215 Rice prot
858	46	56.8	15	8	ADN08047	Adn08047 Human ant	931	39	48.1	553	6	ABU31136	Abu31136 Protein e
859	46	56.8	110	8	ADN08040	Adn08040 Human ant	932	39	48.1	566	2	AAW20945	Aaw20945 H. pylori
860	46	56.8	114	2	AAW06830	Aaw06830 Mouse MAB	933	39	48.1	752	8	ADP98846	Adp98846 C. albica
861	46	56.8	148	1	AAW93078	Aaw93078 Light cha	934	39	48.1	957	2	AAW20841	Aaw20841 H. pylori
862	46	56.8	151	6	AB004847	Ab004847 Human epi	935	39	48.1	1432	8	ADM67236	Adm67236 Human hom
863	46	56.8	151	9	AEAI7759	Aeai7759 Hybriidoma	936	38.5	47.5	304	5	ABW48913	Abw48913 Listeria
864	46	56.8	674	4	AAW95164	Aaw95164 Human pro	937	38	46.9	14	2	AAW95271	Aaw95271 Anti-test
865	45	55.6	12	9	ADV86676	Adv86676 Anti-FLJ3	938	38	46.9	15	7	ABR82269	AbR82269 Anti-gang
866	45	55.6	12	9	ABE08046	Abe08046 Chimeric	939	38	46.9	15	8	ADP84124	Adp84124 Anti-mono
867	44	54.3	114	8	ADO36402	Ado36402 Intracell	940	38	46.9	15	8	ADS31786	Ads31786 CDRI regi
868	44	54.3	497	8	ADN24292	Adn24292 Bacterial	941	38	46.9	90	4	AAW47414	Aaw47414 Propionib
869	44	54.3	674	4	AAW94461	Aaw94461 Human pro	942	38	46.9	90	6	ABW43933	Abw43933 Propionib
870	44	54.3	674	5	ABG66691	Abg66691 Human nov	943	38	46.9	93	4	AAW86579	Aaw86579 Novel hum
871	44	54.3	674	5	ADZ64035	Adz64035 Human can	944	38	46.9	93	7	ADBS5913	Adbs5913 Connectiv
872	44	54.3	674	9	ADZ64036	Adz64036 Human can	945	38	46.9	112	7	ABR82259	AbR82259 Anti-gang
873	44	54.3	692	4	ABG22381	Abg22381 Novel hum	946	38	46.9	112	7	ABR82263	AbR82263 Anti-gang
874	43	53.1	117	9	ADK02101	Adk02101 SARS coro	947	38	46.9	112	8	ADP84128	Adp84128 Armenian
875	43	53.1	147	7	AAW09817	Aaw09817 Female mo	948	38	46.9	112	8	ADP84132	Adp84132 Armenian
876	43	53.1	208	7	ADD05282	Add05282 Female mo	949	38	46.9	112	8	ADS31794	Ads31794 Light var
877	43	53.1	255	2	ADK01982	Adk01982 SARS coro	950	38	46.9	112	8	ADS31790	Ads31790 Light var
878	43	53.1	258	2	AAW09820	Aaw09820 VL3418-1i	951	38	46.9	131	4	AAW99116	Aaw99116 Human pro
879	43	53.1	282	2	AAW09818	Aaw09818 VH4715-1i	952	38	46.9	132	7	ABR82265	AbR82265 Anti-gang
880	43	53.1	282	2	AAW35564	Aaw35564 HindIII-E	953	38	46.9	132	8	ADP84134	Adp84134 Armenian
881	43	53.1	289	2	AAW35563	Aaw35563 HindIII-E	954	38	46.9	132	8	ADS31796	Ads31796 Light var
882	43	53.1	532	2	AAW35565	Aaw35565 HindIII-E	955	38	46.9	144	4	AAO01924	Aao01924 Human pol
883	42	51.9	56	5	ABP06907	Abp06907 Human ORF	956	38	46.9	152	5	ADK35333	Adk35333 Novel hum
884	42	51.9	115	6	ABO10757	Ab010757 Consensus	957	38	46.9	154	2	AAW01685	Aaw01685 T cell re
885	42	51.9	115	6	ABR44701	AbR44701 Murine B9	958	38	46.9	218	7	ABR82261	AbR82261 Chimeric
886	42	51.9	115	6	ADU67971	Adu67971 Mouse ant	959	38	46.9	218	8	ADP84136	Adp84136 Anti-mono
887	42	51.9	116	2	AAW04386	Aaw04386 Colon Can	960	38	46.9	218	8	ADP84130	Adp84130 Anti-mono
888	42	51.9	116	8	ADQ090843	Adq090843 Kabat sub	961	38	46.9	218	8	ADS31792	Ads31792 Chimeric
889	42	51.9	419	8	ADY09590	Ady09590 Plant ful	962	38	46.9	249	6	ABU24189	Abu24189 Protein e
890	42	51.9	703	4	ABW61081	Abw61081 Drosophil	963	38	46.9	266	8	ADU02674	Adu02674 Novel hum
891	41	50.6	118	7	ADD13796	Add13796 Plasmid p	964	38	46.9	306	5	ABG73647	Abg73647 Murine be
892	41	50.6	520	7	ADD13792	Add13792 Plasmid p	965	38	46.9	307	8	ADOS8771	Ados8771 Human MDM
893	41	50.6	521	4	ABW65234	Abw65234 Drosophil	966	38	46.9	310	5	ABG73649	Abg73649 Muvbeta-h
894	41	50.6	719	7	ABW86452	Abw86452 Rice abio	967	38	46.9	332	7	ADG90681	Adg90681 Hepatic s
895	41	50.6	719	7	ABW90154	Abw90154 Rice abio	968	38	46.9	392	5	ABG73651	Abg73651 Murine si
896	40.5	50.0	371	3	AAW27737	Aaw27737 Arabidops	969	38	46.9	395	5	ABG73653	Abg73653 Muvbeta-si
897	40.5	50.0	371	3	AAW37549	Aaw37549 Protein i	970	38	46.9	430	5	ABG73650	Abg73650 Murine si
898	40.5	50.0	392	3	AAW27736	Aaw27736 Arabidops	971	38	46.9	467	9	ADW72192	Adw72192 Arabidops
899	40.5	50.0	502	3	AAW27930	Aaw27930 Arabidops	972	38	46.9	503	8	ADX91284	Adx91284 Plant full
900	40.5	50.0	523	3	AAW27929	Aaw27929 Arabidops	973	38	46.9	580	8	ADR86389	Adr86389 Aspergill

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974 38 46.9 681 8 ADN74353 Thale cre
975 38 46.9 888 4 ABG04248 Novel hum
976 38 46.9 1028 4 ABG62462 Drosophil
977 38 46.9 1031 4 ABG04755 Novel hum
978 38 46.9 1483 4 ABG10809 Novel hum
979 38 46.9 1483 4 ABG09649 Novel hum
980 38 46.9 1483 4 ABG06068 Novel hum
981 38 46.9 2053 4 ABG71118 Drosophil
982 37.5 46.3 51 4 AAM70851 Human
983 37.5 46.3 65 4 AAG74671 Human col
984 37 45.7 69 7 ADF07965 Bacterial
985 37 45.7 83 4 AAU86688 Novel hum
986 37 45.7 83 4 ADB60022 Connectiv
987 37 45.7 91 5 ADK35215 Novel hum
988 37 45.7 101 5 ADJ32178 Human int
989 37 45.7 122 9 AEC04649 Human bre
990 37 45.7 140 7 ADF59586 Human pol
991 37 45.7 141 8 ADY05176 Plant ful
992 37 45.7 173 9 AEB91592 Microbial
993 37 45.7 182 6 ABU18175 Protein e
994 37 45.7 189 3 AAG28160 Arabidops
995 37 45.7 205 8 ADX90313 Plant ful
996 37 45.7 213 3 AAG28159 Arabidops
997 37 45.7 233 3 AAG28158 Arabidops
998 37 45.7 290 8 ABO59480 Human gen
999 37 45.7 331 2 AAY37504 Protein i
1000 37 45.7 335 8 ADS21922 Bacterial
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ALIGNMENTS

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RESULT 1
AD032088
ID AD032088 standard; peptide; 17 AA.
XX
XX AD032088;
AC
XX 12-AUG-2004 (first entry)
DT
XX
XX Mouse anti-CD33 antibody My9-6 light chain CDR1 SEQ ID NO:4.
DE
XX
XX anti-CD33 antibody; epitope-binding fragment;
XX complementarity-determining region; CDR; immunoglobulin; cytostatic;
XX antibody; myelodysplastic syndrome; acute myeloid leukaemia;
XX chronic myeloid leukaemia; pro-myelocytic leukaemia; mouse; My9-6;
XX light chain.
XX
XX Mus musculus:
OS
XX WO2004043344-A2.
XX
XX 27-MAY-2004.
XX
XX 05-NOV-2003; 2003WO-US032737.
XX
XX 07-NOV-2002; 2002US-0424332P.
XX
XX (IMMU-) IMMUNOGEN INC.
XX
XX Hoffee MG, Tavares D, Lutz RJ;
XX
XX WPI; 2004-411619/38.
XX
XX New antibodies that bind to CD33, useful for treating a disease
XX associated with CD33 expression, such as myelodysplastic syndrome, acute
XX or chronic myeloid leukaemia.
XX
XX Claim 1; SEQ ID NO 4; 124pp; English.
XX
XX The present invention describes an isolated anti-CD33 antibody or its
XX epitope-binding fragment comprising: (a) at least one complementarity-
XX determining region (CDR); or (b) at least heavy chain variable region
```

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CC comprising 3 CDRs, and at least one light chain variable region, where
CC the CDR has the ability to bind CD33. Also described: (1) an
CC immunoglobulin comprising the antibody or its epitope-binding fragment
CC linked to a drug or prodrug; (2) a composition comprising the antibody or
CC epitope-binding fragment and a drug or prodrug; (3) a pharmaceutical
CC composition comprising the immunoglobulin, composition or the antibody
CC defined above, or its epitope-binding fragment, and a pharmaceutical
CC agent; (4) a diagnostic reagent comprising the antibody defined above,
CC where the antibody or antibody fragment is labelled; (5) inhibiting the
CC growth of a cell expressing CD33 by contacting the cell with the above
CC defined antibody or its epitope-binding fragment, immunoglobulin, or
CC (pharmaceutical) composition; (6) determining whether a biological sample
CC contains a myelogenous cancer cell; (7) an improved antibody or its
CC epitope-binding fragment that specifically binds to CD33; (8) an isolated
CC polynucleotide encoding the antibody or its epitope-binding fragment
CC defined above; (9) an isolated polynucleotide encoding a light or heavy
CC chain of the antibody defined above or its epitope-binding fragment; (10)
CC a recombinant vector comprising the polynucleotide; (11) a host cell
CC transformed with the recombinant vector; (12) producing an antibody or
CC its epitope-binding fragment having the ability to bind CD33; and (13)
CC obtaining CD33 from a biological material. The anti-CD33 antibody has
CC cytostatic activity. The antibody or its epitope-binding fragment,
CC immunoglobulin, composition can be used for treating a subject having a
CC disease where CD33 is expressed, such as myelodysplastic syndrome, acute
CC myeloid leukaemia, chronic myeloid leukaemia or pro-myelocytic leukaemia.
CC It can also be used for inhibiting the growth of cells expressing CD33,
CC and for in vivo imaging or as affinity purification agents. The present
CC sequence represents the mouse anti-CD33 antibody My9-6 light chain CDR1,
CC which is used in an example from the present invention.
XX
XX SQ Sequence 17 AA;
```

```
Query Match 100.0%; Score 81; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 1,4e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KSSQSVFFSSSQKNYLA 17
DB 1 KSSQSVFFSSSQKNYLA 17
```

```
RESULT 2
AD032132
ID AD032132 standard; peptide; 17 AA.
XX
XX AD032132;
AC
XX 12-AUG-2004 (first entry)
DT
XX
XX Mouse anti-CD33 antibody My9-6 light chain CDR peptide fragment SEQ:48.
DE
XX
XX anti-CD33 antibody; epitope-binding fragment;
XX complementarity-determining region; CDR; immunoglobulin; cytostatic;
XX antibody; myelodysplastic syndrome; acute myeloid leukaemia;
XX chronic myeloid leukaemia; pro-myelocytic leukaemia; mouse; My9-6.
XX
XX Mus musculus.
OS
XX WO2004043344-A2.
XX
XX 27-MAY-2004.
XX
XX 05-NOV-2003; 2003WO-US032737.
XX
XX 07-NOV-2002; 2002US-0424332P.
XX
XX (IMMU-) IMMUNOGEN INC.
XX
XX Hoffee MG, Tavares D, Lutz RJ;
XX
XX WPI; 2004-411619/38.
XX
XX New antibodies that bind to CD33, useful for treating a disease
XX associated with CD33 expression, such as myelodysplastic syndrome, acute
XX or chronic myeloid leukaemia.
```


PT associated with CD33 expression, such as myelodysplastic syndrome, acute
 PT or chronic myeloid leukemia.

PS Example 3; SEQ ID NO 48; 124dp; English.

XX The present invention describes an isolated anti-CD33 antibody or its
 CC epitope-binding fragment comprising: (a) at least one complementarity-
 CC determining region (CDR); or (b) at least heavy chain variable region
 CC comprising 3 CDRs, and at least one light chain variable region, where
 CC the CDR has the ability to bind CD33. Also described: (1) an
 CC immunocjugate comprising the antibody or its epitope-binding fragment
 CC linked to a drug or produg; (2) a composition comprising the antibody or
 CC epitope-binding fragment and a drug or produg; (3) a pharmaceutical
 CC composition comprising the immunocjugate, composition or the antibody
 CC defined above, or its epitope-binding fragment, and a pharmaceutical
 CC agent; (4) a diagnostic reagent comprising the antibody defined above,
 CC where the antibody or antibody fragment is labelled; (5) inhibiting the
 CC growth of a cell expressing CD33 by contacting the cell with the above
 CC defined antibody or its epitope-binding fragment, immunocjugate, or
 CC (pharmaceutical) composition; (6) determining whether a biological sample
 CC contains a myelogenous cancer cell; (7) an improved antibody or its
 CC epitope-binding fragment that specifically binds to CD33; (8) an isolated
 CC polynucleotide encoding the antibody or its epitope-binding fragment
 CC defined above; (9) an isolated polynucleotide encoding a light or heavy
 CC chain of the antibody defined above or its epitope-binding fragment; (10)
 CC a recombinant vector comprising the polynucleotide; (11) a host cell
 CC transformed with the recombinant vector; (12) producing an antibody or
 CC its epitope-binding fragment having the ability to bind CD33; and (13)
 CC obtaining CD33 from a biological material. The anti-CD33 antibody has
 CC cytostatic activity. The antibody or its epitope-binding fragment,
 CC immunocjugate, composition can be used for treating a subject having a
 CC disease where CD33 is expressed, such as myelodysplastic syndrome, acute
 CC myeloid leukaemia, chronic myeloid leukaemia or pro-myelocytic leukaemia.
 CC It can also be used for inhibiting the growth of cells expressing CD33,
 CC and for in vivo imaging or as affinity purification agents. The present
 CC sequence represents a mouse anti-CD33 antibody My9-6 light chain CDR
 CC peptide fragment, which is used in an example from the present invention.

XX Sequence 17 AA:

SO Query Match 100.0%; Score 81; DB 8; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.4e-06;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSSQSVFPSSSQKNTLA 17
 Db 1 KSSQSVFPSSSQKNTLA 17

RESULT 3

ID ADO32094 standard; protein; 113 AA.

XX ADO32094;

XX 12-AUG-2004 (first entry)

DE Humanised mouse anti-CD33 antibody My9-6 light chain SEQ ID NO:10.

XX anti-CD33 antibody; epitope-binding fragment;
 KW complementarity-determining region; CDR; immunocjugate; cytostatic;
 KW antibody; myelodysplastic syndrome; acute myeloid leukaemia;
 KW chronic myeloid leukaemia; pro-myelocytic leukaemia; mouse; humanised;
 KW My9-6; light chain.

OS Mus musculus.
 OS Homo sapiens.
 OS Synthetic.

XX WO2004043344-A2.

XX 27-MAY-2004.

XX PD

PF 05-NOV-2003; 2003WO-US032737.
 XX 07-NOV-2002; 2002US-0424332P.

XX (IMMU-) IMMUNOGEN INC.

XX Hoffee MG, Tavares D, Lutz RJ;

XX WPI; 2004-411619/38.

PT New antibodies that bind to CD33, useful for treating a disease
 PT associated with CD33 expression, such as myelodysplastic syndrome, acute
 PT or chronic myeloid leukemia.

PS Claim 14; SEQ ID NO 10; 124dp; English.

XX The present invention describes an isolated anti-CD33 antibody or its
 CC epitope-binding fragment comprising: (a) at least one complementarity-
 CC determining region (CDR); or (b) at least heavy chain variable region
 CC comprising 3 CDRs, and at least one light chain variable region, where
 CC the CDR has the ability to bind CD33. Also described: (1) an
 CC immunocjugate comprising the antibody or its epitope-binding fragment
 CC linked to a drug or produg; (2) a composition comprising the antibody or
 CC epitope-binding fragment and a drug or produg; (3) a pharmaceutical
 CC composition comprising the immunocjugate, composition or the antibody
 CC defined above, or its epitope-binding fragment, and a pharmaceutical
 CC agent; (4) a diagnostic reagent comprising the antibody defined above,
 CC where the antibody or antibody fragment is labelled; (5) inhibiting the
 CC growth of a cell expressing CD33 by contacting the cell with the above
 CC defined antibody or its epitope-binding fragment, immunocjugate, or
 CC (pharmaceutical) composition; (6) determining whether a biological sample
 CC contains a myelogenous cancer cell; (7) an improved antibody or its
 CC epitope-binding fragment that specifically binds to CD33; (8) an isolated
 CC polynucleotide encoding the antibody or its epitope-binding fragment
 CC defined above; (9) an isolated polynucleotide encoding a light or heavy
 CC chain of the antibody defined above or its epitope-binding fragment; (10)
 CC a recombinant vector comprising the polynucleotide; (11) a host cell
 CC transformed with the recombinant vector; (12) producing an antibody or
 CC its epitope-binding fragment having the ability to bind CD33; and (13)
 CC obtaining CD33 from a biological material. The anti-CD33 antibody has
 CC cytostatic activity. The antibody or its epitope-binding fragment,
 CC immunocjugate, composition can be used for treating a subject having a
 CC disease where CD33 is expressed, such as myelodysplastic syndrome, acute
 CC myeloid leukaemia, chronic myeloid leukaemia or pro-myelocytic leukaemia.
 CC It can also be used for inhibiting the growth of cells expressing CD33,
 CC and for in vivo imaging or as affinity purification agents. The present
 CC sequence represents a humanised mouse anti-CD33 antibody My9-6 light
 CC chain variable region, which is used in an example from the present
 CC invention.

SO Sequence 113 AA:

Query Match 100.0%; Score 81; DB 8; Length 113;
 Best Local Similarity 100.0%; Pred. No. 1.2e-05;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSSQSVFPSSSQKNTLA 17
 Db 24 KSSQSVFPSSSQKNTLA 40

RESULT 4

ID ADO32092 standard; protein; 113 AA.

XX ADO32092;

XX 12-AUG-2004 (first entry)

DE Mouse anti-CD33 antibody My9-6 light chain variable region SEQ ID NO:8.

XX anti-CD33 antibody; epitope-binding fragment;
 KW complementarity-determining region; CDR; immunocjugate; cytostatic;

KW antibody; myelodysplastic syndrome; acute myeloid leukaemia;
 KW chronic myeloid leukaemia; pro-myelocytic leukaemia; mouse; My9-6;
 KW light chain.
 OS Mus musculus;
 PN WO2004043344-A2.
 XX
 XX 27-MAY-2004.
 PD
 XX 05-NOV-2003; 2003WO-US032737.
 PF
 XX 07-NOV-2002; 2002US-0424332P.
 PR
 XX (IMMU-) IMMUNOGEN INC.
 PA
 XX Hoffee MG, Tavares D, Lutz RJ;
 PI WPI; 2004-411619/38.
 DR N-PSDB; ADO32146.
 XX
 XX New antibodies that bind to CD33, useful for treating a disease
 PT associated with CD33 expression, such as myelodysplastic syndrome, acute
 PR or chronic myeloid leukemia.
 XX
 PS Claim 8; SEQ ID NO 8; 124pp; English.
 XX
 CC The present invention describes an isolated anti-CD33 antibody or its
 CC epitope-binding fragment comprising: (a) at least one complementarily-
 CC determining region (CDR); or (b) at least heavy chain variable region
 CC comprising 3 CDRs, and at least one light chain variable region, where
 CC the CDR has the ability to bind CD33. Also described: (1) an
 CC immunocjugate comprising the antibody or its epitope-binding fragment
 CC linked to a drug or prodrug; (2) a composition comprising the antibody or
 CC epitope-binding fragment and a drug or prodrug; (3) a pharmaceutical
 CC composition comprising the immunocjugate, composition or the antibody
 CC defined above, or its epitope-binding fragment, and a pharmaceutical
 CC agent; (4) a diagnostic reagent comprising the antibody defined above,
 CC where the antibody or antibody fragment is labeled; (5) inhibiting the
 CC growth of a cell expressing CD33 by contacting the cell with the above
 CC defined antibody or its epitope-binding fragment, immunocjugate, or
 CC (pharmaceutical) composition; (6) determining whether a biological sample
 CC contains a myelogenous cancer cell; (7) an improved antibody or its
 CC epitope-binding fragment that specifically binds to CD33; (8) an isolated
 CC polynucleotide encoding the antibody or its epitope-binding fragment
 CC defined above; (9) an isolated polynucleotide encoding a light or heavy
 CC chain of the antibody defined above or its epitope-binding fragment; (10)
 CC a recombinant vector comprising the polynucleotide; (11) a host cell
 CC transformed with the recombinant vector; (12) producing an antibody or
 CC its epitope-binding fragment having the ability to bind CD33; and (13)
 CC obtaining CD33 from a biological material. The anti-CD33 antibody has
 CC cytostatic activity. The antibody or its epitope-binding fragment,
 CC immunocjugate, composition can be used for treating a subject having a
 CC disease where CD33 is expressed, such as myelodysplastic syndrome, acute
 CC myeloid leukaemia, chronic myeloid leukaemia or pro-myelocytic leukaemia.
 CC It can also be used for inhibiting the growth of cells expressing CD33,
 CC and for in vivo imaging or as affinity purification agents. The present
 CC sequence represents the mouse anti-CD33 antibody My9-6 light chain
 CC variable region, which is used in an example from the present invention.
 CC
 CC Sequence 113 AA;
 SQ
 Query Match 100.0%; Score 81; DB 8; Length 113;
 Best Local Similarity 100.0%; Pred. No. 1.2e-05;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KSSQSVFFSSSQNYLA 17
 |||||
 DB 24 KSSQSVFFSSSQNYLA 40

ID ADO32146 standard; protein; 114 AA.
 XX
 AC ADO32146;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Mouse anti-CD33 antibody light chain homologous protein SEQ ID NO:62.
 XX
 KW anti-CD33 antibody; epitope-binding fragment;
 KW complementarity-determining region; CDR; immunocjugate; cytostatic;
 KW antibody; myelodysplastic syndrome; acute myeloid leukaemia;
 KW chronic myeloid leukaemia; pro-myelocytic leukaemia; mouse; light chain.
 XX
 OS Mus musculus.
 PN WO2004043344-A2.
 XX
 XX 27-MAY-2004.
 PD
 XX 05-NOV-2003; 2003WO-US032737.
 PF
 XX 07-NOV-2002; 2002US-0424332P.
 PR
 XX (IMMU-) IMMUNOGEN INC.
 PA
 XX Hoffee MG, Tavares D, Lutz RJ;
 PI WPI; 2004-411619/38.
 DR
 XX New antibodies that bind to CD33, useful for treating a disease
 PT associated with CD33 expression, such as myelodysplastic syndrome, acute
 PR or chronic myeloid leukemia.
 XX
 PS Example 3; SEQ ID NO 62; 124pp; English.
 XX
 CC The present invention describes an isolated anti-CD33 antibody or its
 CC epitope-binding fragment comprising: (a) at least one complementarily-
 CC determining region (CDR); or (b) at least heavy chain variable region
 CC comprising 3 CDRs, and at least one light chain variable region, where
 CC the CDR has the ability to bind CD33. Also described: (1) an
 CC immunocjugate comprising the antibody or its epitope-binding fragment
 CC linked to a drug or prodrug; (2) a composition comprising the antibody or
 CC epitope-binding fragment and a drug or prodrug; (3) a pharmaceutical
 CC composition comprising the immunocjugate, composition or the antibody
 CC defined above, or its epitope-binding fragment, and a pharmaceutical
 CC agent; (4) a diagnostic reagent comprising the antibody defined above,
 CC where the antibody or antibody fragment is labeled; (5) inhibiting the
 CC growth of a cell expressing CD33 by contacting the cell with the above
 CC defined antibody or its epitope-binding fragment, immunocjugate, or
 CC (pharmaceutical) composition; (6) determining whether a biological sample
 CC contains a myelogenous cancer cell; (7) an improved antibody or its
 CC epitope-binding fragment that specifically binds to CD33; (8) an isolated
 CC polynucleotide encoding the antibody or its epitope-binding fragment
 CC defined above; (9) an isolated polynucleotide encoding a light or heavy
 CC chain of the antibody defined above or its epitope-binding fragment; (10)
 CC a recombinant vector comprising the polynucleotide; (11) a host cell
 CC transformed with the recombinant vector; (12) producing an antibody or
 CC its epitope-binding fragment having the ability to bind CD33; and (13)
 CC obtaining CD33 from a biological material. The anti-CD33 antibody has
 CC cytostatic activity. The antibody or its epitope-binding fragment,
 CC immunocjugate, composition can be used for treating a subject having a
 CC disease where CD33 is expressed, such as myelodysplastic syndrome, acute
 CC myeloid leukaemia, chronic myeloid leukaemia or pro-myelocytic leukaemia.
 CC It can also be used for inhibiting the growth of cells expressing CD33,
 CC and for in vivo imaging or as affinity purification agents. The present
 CC sequence represents a mouse anti-CD33 antibody light chain homologous
 CC amino acid sequence, which is used in an example from the present
 CC invention.
 CC
 CC Sequence 114 AA;
 SQ
 Query Match 100.0%; Score 81; DB 8; Length 114;
 Best Local Similarity 100.0%; Pred. No. 1.2e-05;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSSQSVFSSSQKNYLA 17
 |||||
 Db 24 KSSQSVFSSSQKNYLA 40

RESULT 6
 ABG31024
 ID ABG31024 standard; protein; 272 AA.
 AC ABG31024;
 XX
 DT 05-NOV-2002 (first entry)
 XX
 DE Synthetic mouse fusion protein.

Immunosuppressive; antirheumatic; antithyroid; antidiabetic; mouse; neuroprotective; gene therapy; single chain antibody; variable fragment; scFv; binding domain-immunoglobulin fusion protein; B-cell disorder; malignant condition; rheumatoid arthritis; myasthenia gravis; psoriasis; Grave's disease; Hashimoto's thyroiditis; type I diabetes mellitus; multiple sclerosis; systemic lupus erythematosus; Sjogrens syndrome; immune thrombocytopenic purpura; scleroderma; cancer; Chron's disease; ulcerative colitis; inflammatory bowel disease; immunological effector; cell mediated cytotoxicity; complement dependent cytotoxicity; complement fixation; mouse.

XX
 OS Mus musculus.
 OS Synthetic.
 XX WO200256910-A1.
 XX 25-JUL-2002.
 PD
 XX 17-JAN-2002; 2002WO-US001487.
 PF
 XX 17-JAN-2001; 2001US-00765208.
 PR
 XX (GENE-) GENE-CRAFT INC.
 PA Ledbetter JA, Hayden-Ledbetter M;
 XX
 DR WPI: 2002-59691/64.
 DR N-PSDB; ABR69856.
 XX
 PT New human binding domain-immunoglobulin fusion protein useful for
 PT treating a subject having or suspected of having a B-cell disorder or
 PT malignant condition e.g. rheumatoid arthritis.
 XX
 PS Disclosure; Page 119; 136pp; English.

The invention describes a binding domain-immunoglobulin fusion protein that is capable of at least one immunological activity, comprising a binding domain polypeptide fused to an immunoglobulin hinge region polypeptide capable of specifically binding to an antigen, or an immunoglobulin heavy chain CH2 or CH3 constant region polypeptide fused to the hinge region polypeptide or to the CH2 constant region polypeptide. The fusion protein is useful for treating a subject having or suspected of having a B-cell disorder or malignant condition e.g. rheumatoid arthritis, myasthenia gravis, Grave's disease, Hashimoto's thyroiditis, type I diabetes mellitus, multiple sclerosis, systemic lupus erythematosus, Sjogrens syndrome, immune thrombocytopenic purpura, psoriasis, scleroderma, cancer and inflammatory bowel disease such as Chron's disease and ulcerative colitis. The fusion protein retains the ability to participate in well known immunological effector activities including antibody dependent cell mediated cytotoxicity and/or complement fixation in complement dependent cytotoxicity, despite having structures that would not be expected to be capable of promoting the effector activities. It can be produced in substantial quantities that are typically greater than those routinely attained with single-chain antibody constructs. This is the amino acid sequence of a synthetic mouse immunoglobulin fusion protein

XX
 SQ Sequence 272 AA;

Query Match 88.9%; Score 72; DB 5; Length 272;
 Best Local Similarity 82.4%; Pred. No. 0.001;
 Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSSQSVFSSSQKNYLA 17
 |||||
 Db 44 KSSQSVFSSSQKNYLA 60

RESULT 7
 ADD25453
 ID ADD25453 standard; protein; 272 AA.
 AC ADD25453;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE Binding domain-immunoglobulin fusion protein-associated protein #4.

XX Binding domain; immunoglobulin; fusion protein; cytostatic;
 XX antiarthritic; immunosuppressive; antidiabetic; antithyroid;
 KW neuroprotective; hinge region; immunoglobulin heavy chain;
 KW CH2 constant region; CH3 constant region; IgG1;
 KW antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
 KW malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;
 KW rheumatoid arthritis; myasthenia gravis; Grave's disease;
 KW type I diabetes mellitus; multiple sclerosis; autoimmune disease.
 XX
 OS Unidentified.
 OS
 XX US2003118592-A1.
 XX 26-JUN-2003.
 PD
 XX 25-JUL-2002; 2002US-00207655.
 PF
 XX 17-JAN-2001; 2001US-0367358P.
 PR 17-JAN-2002; 2002US-00053530.
 PR 03-JUN-2002; 2002US-0386591P.
 PA (GENE-) GENE-CRAFT INC.
 XX
 PT Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;
 PT
 DR WPI: 2003-801317/75.
 XX
 PT New binding domain-immunoglobulin fusion protein, useful for treating a
 PT subject having or suspected of having a malignant condition or a B-cell
 PT disorder, e.g. melanoma, Grave's disease or autoimmune disease.
 XX
 PS Disclosure; SEQ ID NO 14; 157pp; English.

The invention relates to a binding domain-immunoglobulin fusion protein comprising a binding domain polypeptide that is fused to an immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain CH2 constant region polypeptide that is fused to the hinge region polypeptide, and an immunoglobulin heavy chain CH3 constant region polypeptide that is fused to the CH2 constant region polypeptide. The hinge region polypeptide comprises a wild-type human IgG1 immunoglobulin hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge region polypeptide; derived from (a) having 3 or more cysteine residues; where the mutated human IgG1 immunoglobulin hinge region polypeptide contains 2 cysteine residues, where the first cysteine is not mutated; a mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues, where the mutated human IgG1 immunoglobulin hinge region polypeptide contains no more than one cysteine residue; and a mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues; where the mutated human IgG1 immunoglobulin hinge region polypeptide contains no cysteine residues. The binding domain-immunoglobulin fusion protein is

CC capable of at least one immunological activity comprising antibody
CC binding domain polypeptide is capable of specifically binding to an
CC antigen. Also included are an isolated polynucleotide encoding the
CC binding domain-immunoglobulin fusion protein, a recombinant expression
CC construct comprising the polynucleotide (operably linked to a promoter),
CC a host cell transformed or transfected with a recombinant expression
CC construct, producing the binding domain-immunoglobulin fusion protein, a
CC pharmaceutical composition comprising the binding domain-immunoglobulin
CC fusion protein or polynucleotide and a carrier, and treating a subject
CC having or suspected of having a malignant condition or a B-cell disorder.
CC The binding domain-immunoglobulin fusion protein is useful for treating a
CC subject having or suspected of having a malignant condition or a B-cell
CC disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis,
CC myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple
CC sclerosis or autoimmune disease. The present sequence is a binding domain
CC -immunoglobulin fusion protein-associated protein sequence. Note: The
CC sequence data for this patent formed part of the printed specification
CC and is also available in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030118592. The authors have not
CC identified the sequences in the printed specification by their SEQ ID
CC number therefore none of the sequences can be explicitly identified.

XX Sequence 272 AA;

Query Match 88.9%; Score 72; DB 7; Length 272;

Best Local Similarity 82.4%; Pred. No. 0.001; Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSSQSVFSSSQKNTYLA 17
| | | | | : | | | | |
Db 44 KSSQSVFYSSNQRYTALA 60

RESULT 8
ADMA2728 standard; protein; 272 AA.

XX ADMA2728;

XX 03-JUN-2004 (first entry)

DE Synthetic mouse anti-CD22 scFv.

KW Mouse; antibody; single chain antibody; scFv;
KW binding domain-immunoglobulin fusion protein;
KW immunoglobulin hinge region; heavy chain CH2 constant region;
KW heavy chain CH3 constant region;
KW antibody dependent cell-mediated cytotoxicity; complement fixation; Iga;
KW IgG; CD19; CD20; CD37; CD40; L6; CD154; malignant condition; cancer;
KW B-cell disorder; autoantibody; rheumatoid arthritis; myasthenia gravis;
KW Grave's disease; type I diabetes mellitus; multiple sclerosis;
KW autoimmune disease.

XX Mus musculus.
OS Synthetic.

XX US2003133939-A1.

XX 17-JUL-2003.

XX 17-JAN-2002; 2002US-00053530.

XX 17-JAN-2002; 2002US-00053530.

XX (GENE-) GENE-CRAFT INC.

XX Ledbetter JA, Hayden-Ledbetter MS;

XX WPI; 2003-843256/78.

XX N-PSDB; ADMA2724.

XX New binding domain-immunoglobulin fusion protein for treating malignant

PT conditions (e.g. cancer) or B-cell disorders, comprises a binding domain
PT polypeptide and immunoglobulin heavy chain CH2 and CH3 constant region
PT polypeptides.

XX Disclosure; SEQ ID NO 14; 80pp; English.

XX The invention relates to a binding domain-immunoglobulin fusion protein
XX comprising a binding domain polypeptide that is fused to an
XX immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain
XX CH2 constant region polypeptide that is fused to the hinge region
XX polypeptide, and an immunoglobulin heavy chain CH3 constant region
XX polypeptide that is fused to the CH2 constant region polypeptide. The
XX fusion protein is capable of at least one immunological activity such as
XX antibody dependent cell-mediated cytotoxicity and complement fixation,
XX and is capable of specifically binding to an antigen. The hinge region
XX polypeptide is selected from a mutated hinge region polypeptide that
XX contains no cysteine residues (and that is derived from a wild-type
XX immunoglobulin hinge region polypeptide, having one or more cysteine
XX residues), a mutated hinge region polypeptide that contains one cysteine
XX residue (and that is derived from a wild-type immunoglobulin hinge region
XX polypeptide having two or more cysteine residues), a wild-type human
XX immunoglobulin (Ig)A hinge region polypeptide, a mutated human IgA hinge
XX region polypeptide that contains no cysteine residues (and that is
XX derived from a wild-type human IgA region polypeptide) and a mutated
XX human IgA hinge region polypeptide that contains one cysteine residue
XX (and that is derived from a wild-type human IgA region polypeptide). Also
XX included are an isolated polynucleotide encoding the novel fusion
XX protein, a recombinant expression construct comprising the
XX polynucleotide, a host cell transformed or transfected with the
XX expression construct, producing the novel fusion protein (comprising
XX culturing the host cell under conditions that permit expression of the
XX novel fusion protein and isolating the binding domain-immunoglobulin
XX fusion protein from the host cell culture), a pharmaceutical composition
XX comprising the novel fusion protein in combination with a carrier and
XX treating a subject having or suspected of having a malignant condition or
XX a B-cell disorder (comprising administering to the patient an amount of
XX the novel fusion protein). The mutated hinge region polypeptide exhibits
XX a reduced ability to dimerize, relative to a wild-type human
XX immunoglobulin G hinge region polypeptide. The binding domain polypeptide
XX comprises at least one immunoglobulin variable region polypeptide
XX selected from an immunoglobulin light chain variable region polypeptide
XX and an immunoglobulin heavy chain variable region polypeptide, and
XX optionally at least one linker peptide that is fused to the
XX immunoglobulin variable region polypeptide. The immunoglobulin variable
XX and constant region polypeptides are derived from a human immunoglobulin.
XX The immunoglobulin heavy chain constant region CH2 and CH3 polypeptides
XX are of an isotype selected from human IgG and human IgA. The antigen is
XX selected from CD19, CD20, CD37, CD40 and L6. The binding domain
XX polypeptide comprises a CD154 extracellular domain, and optionally, at
XX least one immunoglobulin variable region polypeptide (e.g. mouse V1
XX Vh regions forming single chain antibodies which bind to one of the above
XX antigens). The composition and methods are useful in treating malignant
XX conditions (e.g. cancer) and B-cell disorders, including diseases
XX characterised by autoantibody production, such as rheumatoid arthritis,
XX myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple
XX sclerosis or autoimmune diseases. The present sequence represents a mouse
XX single chain (scFv) antibody binding to one of the above antigens.

XX Sequence 272 AA;

Query Match 88.9%; Score 72; DB 7; Length 272;

Best Local Similarity 82.4%; Pred. No. 0.001; Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSSQSVFSSSQKNTYLA 17
| | | | | : | | | | |
Db 44 KSSQSVFYSSNQRYTALA 60

RESULT 9

XX AEB95396 standard; protein; 272 AA.

XX AEB95396

AC	ABE95396;
XX	
DT	20-OCT-2005 (first entry)
XX	
DE	Mouse G28-7 scFV fusion protein, SEQ ID NO: 14.
XX	
KW	Protein engineering; pharmaceutical; immunotherapy; gene therapy;
KW	rheumatoid arthritis; antiarthritic; antirheumatic; immune disorder;
KW	inflammation; musculoskeletal disease; myasthenia gravis; muscular-gen.;
KW	neuroprotective; immunosuppressive; neurological disease; graves disease;
KW	antithyroid; endocrine disease; insulin dependent diabetes; antidiabetic;
KW	gastrointestinal disease; metabolic disorder; multiple sclerosis;
KW	autoimmune disease; heavy chain variable region;
KW	light chain variable region; CD22; single chain antibody;
KW	monoclonal antibody; G28-7gene fusion protein.
XX	
OS	Mus sp.
XX	
XX	Synthetic.
XX	
EH	Key
FT	Location/Qualifiers
FT	Peptide
FT	1..20
FT	/label= Signal_peptide
FT	Protein
FT	21..272
FT	/note= "Mature mouse G28-7 scFV fusion protein"
FT	Region
FT	21..132
FT	/note= "light chain variable domain for mouse anti-human
FT	CD22, G28-7"
FT	133..148
FT	/note= "(Gly4ser)3 linker peptide"
FT	149..272
FT	/note= "Heavy chain variable domain for mouse anti-human
FT	CD22, G28-7"
XX	
PN	US2005175614-A1.
XX	
PD	11-AUG-2005.
XX	
XX	23-MAR-2005; 2005US-00089511.
XX	
PR	17-JAN-2001; 2001US-0367358P.
PR	17-JAN-2002; 2002US-00053530.
XX	
PA	(TRUBION PHARM INC.
XX	
P1	Ledbetter JA, Hayden-Ledbetter MS;
XX	
DR	WPI; 2005-541746/55.
DR	N-PSDB; ABE95392.
XX	
PT	Treating a malignant condition or a B-cell disorder by administering a
PT	composition comprising a pharmaceutical carrier and an amount of a single
PT	chain protein that binds to vascular endothelial cell growth factor.
XX	
PS	Disclosure; SEQ ID NO 14; 82pp; English.
XX	
CC	The present invention relates to a method of treating cancer. The method
CC	involves administering to a subject in need a composition comprising a
CC	pharmaceutical carrier and an amount of a single chain protein that binds
CC	to vascular endothelial cell growth factor (VEGF), where the single chain
CC	protein is capable of mediating at least one immunological activity
CC	selected from antibody dependent cell-mediated cytotoxicity (ADCC) or
CC	complement fixation. The method is useful for treating a subject having
CC	or suspected of having a malignant condition or a B-cell disorder, e.g.
CC	rheumatoid arthritis, myasthenia gravis, Grave's disease, type I diabetes
CC	mellitus, multiple sclerosis, or an autoimmune disease. The invention is
CC	also useful in immunotherapeutic applications and in gene therapy. The
CC	present sequence is a fusion protein comprising mouse light and heavy
CC	chain variable region (VL & VH) of anti-CD22 scFV (single chain Fv) and
CC	linker peptide. Anti-CD22 is a monoclonal antibody designated as G28-7.
XX	
SO	Sequence 272 AA;

Query Match 88.9%; Score 72; DB 9; Length 272;

[illegible]

QY 1 KSSQSVFFSSQKNYLA 17
 |||||:|||||
 DB 1 KSSQSFYFSTWKNYLA 17

RESULT 13
 ID AEA38785
 AEA38785 standard; peptide; 17 AA.
 AC AEA38785;
 XX
 DT 11-AUG-2005 (first entry)
 XX
 DE Murine 2G7 VL monoclonal antibody protein CDR LI peptide, SEQ ID NO: 48.
 XX
 KM Monoclonal antibody; animal disease model; metastasis; cytostatic;
 KM neoplasia; bone metastases; breast tumor; colorectal tumor; bone disease;
 KM osteolytic; antibody therapy; radiation therapy; immunotherapy;
 KM cancer cell proliferation inhibitor;
 KM transforming growth factor-beta-antagonist; light chain variable region.
 XX
 OS Mus musculus.
 XX
 FN WO2005050200-A2.
 XX
 PD 02-JUN-2005.
 XX
 PF 04-NOV-2004; 2004WO-US036651.
 XX
 PR 13-NOV-2003; 2003US-0520398P.
 XX
 PR 31-MAR-2004; 2004US-0557951P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Filvaroff EH;
 XX
 DR WPI; 2005-41772/42.
 DR N-PSDB; AEA38784.
 XX
 XX Screening compounds useful for treating tumor metastasis involves
 PT administering a test compound to non-human animal model bearing soft
 PT tissue/bone metastasis and identifying compound that inhibits soft tissue
 PT growth/bone metastasis.
 XX
 PS Example 2; SEQ ID NO 48; 109pp; English.
 XX
 CC The present invention relates to the screening of candidate molecules
 CC anti-transforming growth factor (TGF-beta antibodies) for the treatment
 CC of tumor metastasis and treatment methods using such molecules. The
 CC screening method of the invention involves administering several test
 CC substances to a non-human syngeneic immunocompetent animal model bearing
 CC at least one soft tissue or bone metastasis optionally in presence of a
 CC primary tumor, determining the effects of these test substances on the
 CC soft tissue or bone metastasis and growth of the primary tumor and
 CC identifying a test substance inhibiting soft tissue growth or bone
 CC metastasis without adverse effect on the status of the primary tumor. The
 CC invention is useful in the diagnosis and treatment of breast cancer. The
 CC colorectal cancer, liver and lung metastases, bone destruction and bone
 CC loss. The animal models of the present invention is useful to screen
 CC substances useful for the prophylaxis or treatment of soft tissue and/or
 CC bone metastases which may additionally be effective in treating the
 CC primary tumor. The present sequence is murine 2G7 variable light chain
 CC (VL) monoclonal antibody protein complementarity determining region (CDR)
 CC peptide.
 XX
 SQ Sequence 17 AA:
 XX
 Query Match 85.2%; Score 69; DB 9; Length 17;
 Best Local Similarity 82.4%; Pred. No. 0.00015;
 Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DB 1 KSSQSVLYSSNQKNYLA 17
 |||||:|||||
 DB 1 KSSQSVLYSSNQKNYLA 17

RESULT 14
 ID ADO32144
 ADO32144 standard; protein; 99 AA.
 AC ADO32144;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Mouse anti-CD33 antibody 8-27 light chain protein SEQ ID NO:60.
 XX
 KM anti-CD33 antibody; epitope-binding fragment;
 KM complementarity-determining region; CDR; immunoglobulin; cytostatic;
 KM antibody; myelodysplastic syndrome; acute myeloid leukaemia;
 KM chronic myeloid leukaemia; pro-myelocytic leukaemia; mouse; light chain.
 XX
 OS Mus musculus.
 XX
 PN WO2004043344-A2.
 XX
 PD 27-MAY-2004.
 XX
 PF 05-NOV-2003; 2003WO-US032737.
 XX
 PR 07-NOV-2002; 2002US-0424332P.
 XX
 PA (IMMU) IMMUNOGEN INC.
 XX
 PI Hoffee MG, Tavares D, Lutz RJ;
 XX
 DR WPI; 2004-411619/38.
 XX
 PT New antibodies that bind to CD33, useful for treating a disease
 PT associated with CD33 expression, such as myelodysplastic syndrome, acute
 PT or chronic myeloid leukemia.
 XX
 PS Example 3; SEQ ID NO 60; 124pp; English.
 XX
 CC The present invention describes an isolated anti-CD33 antibody or its
 CC epitope-binding fragment comprising: (a) at least one complementarity-
 CC determining region (CDR); or (b) at least heavy chain variable region
 CC comprising 3 CDRs, and at least one light chain variable region, where
 CC the CDR has the ability to bind CD33. Also described: (1) an
 CC immunoglobulin comprising the antibody or its epitope-binding fragment
 CC linked to a drug or prodrug; (2) a composition comprising the antibody or
 CC epitope-binding fragment and a drug or prodrug; (3) a pharmaceutical
 CC composition comprising the immunoglobulin, composition or the antibody
 CC agent; (4) a diagnostic reagent comprising the antibody defined above,
 CC where the antibody or antibody fragment is labelled; (5) inhibiting the
 CC growth of a cell expressing CD33 by contacting the cell with the above
 CC defined antibody or its epitope-binding fragment, immunoglobulin, or
 CC (pharmaceutical) composition; (6) determining whether a biological sample
 CC contains a myelogenous cancer cell; (7) an improved antibody or its
 CC epitope-binding fragment that specifically binds to CD33; (8) an isolated
 CC polynucleotide encoding the antibody or its epitope-binding fragment
 CC defined above; (9) an isolated polynucleotide encoding a light or heavy
 CC chain of the antibody defined above or its epitope-binding fragment; (10)
 CC a recombinant vector comprising the polynucleotide; (11) a host cell
 CC transformed with the recombinant vector; (12) producing an antibody or
 CC its epitope-binding fragment having the ability to bind CD33; and (13)
 CC obtaining CD33 from a biological material. The anti-CD33 antibody has
 CC cytostatic activity. The antibody or its epitope-binding fragment,
 CC immunoglobulin, composition can be used for treating a subject having a
 CC disease where CD33 is expressed, such as myelodysplastic syndrome, acute
 CC myeloid leukaemia, chronic myeloid leukaemia or pro-myelocytic leukaemia.
 CC It can also be used for inhibiting the growth of cells expressing CD33,
 CC and for in vivo imaging or as affinity purification agents. The present
 CC sequence represents the mouse anti-CD33 antibody 8-27 light chain
 CC variable region, which is used in an example from the present invention.

```
SQ Sequence 99 AA;
Query Match 85.2%; Score 69; DB 8; Length 99;
Best Local Similarity 82.4%; Pred. No. 0.001;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSSQSVFSSSQKNYLA 17
   |||||:|:|||||
   24 KSSQSVLYSSNQKNYLA 40

RESULT 15
AAR54932
ID AAR54932 standard; peptide; 112 AA.
XX
AC AAR54932;
XX
DT 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 19-OCT-1994 (first entry)
XX
DE Fc receptor humanized VK chain 022 HuVK.
XX
KW Fc receptor; FcR; humanized antibody; hAb; IgG; cancer; allergy;
KW autoimmune disease; heteroantibody; bifunctional antibody; immunotoxin;
KW CDR; complementarity determining region; VH; heavy chain variable region;
KW VK; kappa chain variable region; mononuclear phagocyte; PCR;
KW polymerase chain reaction; primer; site-directed mutagenesis; HuVK;
KW monoclonal antibody; Mab.
XX
OS Homo sapiens.
OS Mus sp.
XX
PN WO9410332-A1.
XX
PD 11-MAY-1994.
XX
PR 04-NOV-1993; 93WO-US010384.
XX
PR 04-NOV-1992; 92GB-00023377.
XX
PA (MEDA-) MEDAREX INC.
XX
PI Tempest PR, Harris WJ, Carr FJ;
XX
DR WPI; 1994-167486/20.
XX
PT New humanised antibodies to Fc receptors - used for diagnosis or for
PT treatment of e.g. cancer, allergies and infectious and auto-immune
PT diseases.
XX
PS Disclosure; Page 16; 36pp; English.
XX
CC Humanized antibodies (hAbs) for IgG Fc receptors on human phagocytes
CC comprise the CDR of mouse monoclonal antibody 22 (from hybridoma 022WCL-
CC 1), VH chains from human IgG NEMW or KOL, and VK chains from Ig REI.
CC Sequences are provided for mouse 022 VH (AAR54931), humanized NEMW-based
CC VH (022 NMVH, AAR54929), humanized KOL-based VH (022 KLVH, AAR54930),
CC mouse 022 VK (AAR54933) and humanized REI-based VK (022 HuVK, AAR54932).
CC During hAb production, VH and VK cDNAs were PCR amplified using primers
CC given in AA065378-87. Mutagenesis of clone M13VHPCR2 KOL VH (L71R) was
CC performed using oligos AA065388-89. The hAbs can be used in
CC heteroantibody, bifunctional antibody and immunotoxin production.
CC (Updated on 25-MAR-2003 to correct PN field.) (Updated on 27-AUG-2003 to
CC correct OS field.)
XX
SQ Sequence 112 AA;
Query Match 85.2%; Score 69; DB 2; Length 112;
Best Local Similarity 82.4%; Pred. No. 0.0012;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSSQSVFSSSQKNYLA 17
   |||||:|:|||||
   24 KSSQSVLYSSNQKNYLA 40
```

```
DB 24 KSSQSVLYSSNQKNYLA 40
   |||||:|:|||||
RESULT 16
AAR54933
ID AAR54933 standard; peptide; 112 AA.
XX
AC AAR54933;
XX
DT 25-MAR-2003 (revised)
DT 19-OCT-1994 (first entry)
XX
DE Mab 022 VK chain.
XX
KW Fc receptor; FcR; humanized antibody; hAb; IgG; cancer; allergy;
KW autoimmune disease; heteroantibody; bifunctional antibody; immunotoxin;
KW CDR; complementarity determining region; VH; heavy chain variable region;
KW VK; kappa chain variable region; mononuclear phagocyte; PCR;
KW polymerase chain reaction; primer; site-directed mutagenesis;
KW monoclonal antibody; Mab.
XX
OS Mus sp.
XX
PN WO9410332-A1.
XX
PD 11-MAY-1994.
XX
PR 04-NOV-1993; 93WO-US010384.
XX
PR 04-NOV-1992; 92GB-00023377.
XX
PA (MEDA-) MEDAREX INC.
XX
PI Tempest PR, Harris WJ, Carr FJ;
XX
DR WPI; 1994-167486/20.
XX
PT New humanised antibodies to Fc receptors - used for diagnosis or for
PT treatment of e.g. cancer, allergies and infectious and auto-immune
PT diseases.
XX
PS Disclosure; Page 23; 36pp; English.
XX
CC Humanized antibodies (hAbs) for IgG Fc receptors on human phagocytes
CC comprise the CDR of mouse monoclonal antibody 22 (from hybridoma 022WCL-
CC 1), VH chains from human IgG NEMW or KOL, and VK chains from Ig REI.
CC Sequences are provided for mouse 022 VH (AAR54931), humanized NEMW-based
CC VH (022 NMVH, AAR54929), humanized KOL-based VH (022 KLVH, AAR54930),
CC mouse 022 VK (AAR54933) and humanized REI-based VK (022 HuVK, AAR54932).
CC During hAb production, VH and VK cDNAs were PCR amplified using primers
CC given in AA065378-87. Mutagenesis of clone M13VHPCR2 KOL VH (L71R) was
CC performed using oligos AA065388-89. The hAbs can be used in
CC heteroantibody, bifunctional antibody and immunotoxin production.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 112 AA;
Query Match 85.2%; Score 69; DB 2; Length 112;
Best Local Similarity 82.4%; Pred. No. 0.0012;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSSQSVFSSSQKNYLA 17
   |||||:|:|||||
   24 KSSQSVLYSSNQKNYLA 40

RESULT 17
AAE29270
ID AAE29270 standard; protein; 112 AA.
XX
AC AAE29270;
XX
```


DT	27-JAN-2003	(first entry)
DE	S. aureus ClfA specific monoclonal antibody 12-9VL-Hu protein.	
XX		
XX	Clumping factor A; ClfA; fibrinogen; fibrin; Clf40, Clf33; N3 protein;	
XX	immunological; staphylococcal infection; impetigo; pneumonia; furuncle;	
KW	septic arthritis; sepsis; endocarditis; antibacterial; wound; therapy.	
XX		
OS	Staphylococcus aureus.	
XX		
Key	Location/Qualifiers	
FT	Region	24..40
FT		/note= "CDR1"
FT	Region	56..62
FT		/note= "CDR2"
FT	Region	95..102
FT		/note= "CDR3"
XX		
PN	WO200272600-A2.	
XX		
PD	19-SEP-2002.	
XX		
PF	28-JAN-2002; 2002WO-US002236.	
XX		
PR	26-JAN-2001; 2001US-0264072P.	
PR	12-MAR-2001; 2001US-0274611P.	
PR	18-JUN-2001; 2001US-0298413P.	
PR	30-JUL-2001; 2001US-0308116P.	
XX		
PA	(INH1-) INHIBITEX INC.	
XX		
PI	Patti JM, Hutchins JT, Domanski P, Patel P, Hall A;	
XX		
DR	WPI; 2002-759834/82.	
DR	N-PSDB; AAD46869.	
XX		
PT	New anti-clumping factor A (ClfA) monoclonal antibody, useful for	
PT	treating or preventing Staphylococcus aureus infection e.g. wound	
PT	infections, impetigo, furuncles, pneumonia, septic arthritis or sepsis in	
XX	a human or animal.	
PS	Claim 11; Page 42; 80pp; English.	
XX		
CC	The invention relates to monoclonal antibody which binds the clumping	
CC	factor A (ClfA) protein from Staphylococcus aureus. The anti-ClfA	
CC	monoclonal antibody is useful for treating or preventing S. aureus	
CC	infection in a human or animal, and for inhibiting the binding of	
CC	staphylococcal bacteria to fibrinogen or fibrin. The immunogenic fragment	
CC	S. aureus Clf40 protein, S. aureus Clf33 protein, or the S. aureus N3	
CC	protein is useful for inducing an immunological response in a human or	
CC	animal. These staphylococcal infections include wound infections, sepsis,	
CC	impetigo, furuncles, pneumonia, septic arthritis or endocarditis. The	
CC	present sequence is Staphylococcus aureus ClfA specific monoclonal	
CC	antibody 12-9VL-Hu (humanised variable light sequence) protein	
XX		
SQ	Sequence 112 AA;	
XX		
Query Match	85.2%;	Score 69; DB 5; Length 112;
Best Local Similarity	82.4%;	Pred. No. 0.0012;
Matches 14;	Conservative 2;	Mismatches 1; Indels 0; Gaps 0
QY	1 KSSQSVFFSSQKNYLA 17	
	:	
DB	24 KSGCVLYSSNQKNYLA 40	
XX		
RESULT 18		
AAE29264		
ID	AAE29264 standard; protein; 112 AA.	
XX		
AC	AAE29264;	
XX		
DT	27-JAN-2003 (first entry)	

Key	Location/Qualifiers
Region	24..40
FT	/note= "CDR1"
FT	56..62
FT	/note= "CDR2"
FT	95..102
Region	/note= "CDR3"
WT	
PN	WO200272600-A2.
XX	
PD	19-SEP-2002.
XX	
XX	28-JAN-2002; 2002WO-US002296.
PF	
XX	26-JAN-2001; 2001US-0264072P.
PR	12-MAR-2001; 2001US-0274611P.
PR	18-JUN-2001; 2001US-0298413P.
PR	30-JUL-2001; 2001US-0308116P.
PA	(INHI-) INHIBITEX INC.
XX	
PI	Patti JM, Hutchins JT, Domanski P, Patel P, Hall A;
XX	
DR	WPI; 2002-759834/82.
DR	N-PSDB; NAD46863.
XX	
PT	New anti-clumping factor A (ClfA) monoclonal antibody, useful for
PT	treating or preventing Staphylococcus aureus infection e.g. wound
PT	infections, impetigo, furuncles, pneumonia, septic arthritis or sepsis in
PT	a human or animal.
XX	
PS	Claim 11; Page 34; 80pp; English.
XX	
CC	The invention relates to monoclonal antibody which binds the clumping
CC	factor A (ClfA) protein from Staphylococcus aureus. The anti-ClfA
CC	monoclonal antibody is useful for treating or preventing S. aureus
CC	infection in a human or animal, and for inhibiting the binding of
CC	staphylococcal bacteria to fibrinogen of fibrin. The immunogenic fragment
CC	S. aureus ClfA40 protein, S. aureus ClfB protein, or the S. aureus N3
CC	protein is useful for inducing an immunological response in a human or
CC	animal. These staphylococcal infections include wound infections, sepsis,
CC	impetigo, furuncles, pneumonia, septic arthritis or endocarditis. The
CC	present sequence is Staphylococcus aureus ClfA specific monoclonal
CC	antibody 13-2VLA-1 (variable light sequence) protein
XX	
SO	Sequence 112 AA;
Query Match	85.2%; Score 69; DB 5; Length 112;
Best Local Similarity	82.4%; Pred. No. 0.0012;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;	
OY	1 KSSQSVPFSSSQKXYLA 17
DB	24 KSSQSVPFSSSQKXYLA 40
RESULT 19	
AAE29266	
ID	AAE29266 standard; protein; 112 AA.
XX	
AC	AAE29266;
XX	
DT	27-JAN-2003 (first entry)
XX	

```
DE S. aureus ClfA specific monoclonal antibody 12-9VLA-1 protein.
XX
XX Clumping factor A; ClfA, fibrinogen, fibrin, Clf40, Clf33; N3 protein;
KM immunological; staphylococcal infection; impetigo; pneumonia; furuncle;
KM septic arthritis; sepsis; endocarditis; antibacterial; wound; therapy.
XX
XX Staphylococcus aureus.
XX
XX Key Location/Qualifiers
FH Region 24..40
FT /note="CDR1"
FT Region 56..62
FT /note="CDR2"
FT Region 95..102
FT /note="CDR3"
XX
XX WO200272600-A2.
XX
XX 19-SEP-2002.
XX
XX 28-JAN-2002; 2002WO-US002296.
XX
XX 26-JAN-2001; 2001US-0264072P.
XX 12-MAR-2001; 2001US-0274611P.
XX 18-JUN-2001; 2001US-0298413P.
XX 30-JUL-2001; 2001US-0308116P.
XX
XX (INH1-) INHIBITEX INC.
XX
XX Patci JM, Hutchins JT, Domanski P, Patel P, Hall A;
XX
XX WPI; 2002-759834/82.
XX
XX N-PSDB; AAD46865.
XX
XX New anti-clumping factor A (ClfA) monoclonal antibody, useful for
XX treating or preventing Staphylococcus aureus infection e.g. wound
XX infections, impetigo, furuncles, pneumonia, septic arthritis or sepsis in
XX a human or animal.
XX
XX Claim 11; Page 35; 80pp; English.
XX
XX The invention relates to monoclonal antibody which binds the clumping
XX factor A (ClfA) protein from Staphylococcus aureus. The anti-ClfA
XX monoclonal antibody is useful for treating or preventing S. aureus
XX infection in a human or animal, and for inhibiting the binding of
XX staphylococcal bacteria to fibrinogen or fibrin. The immunogenic fragment
XX S. aureus Clf40 protein, S. aureus Clf33 protein, or the S. aureus N3
XX protein is useful for inducing an immunological response in a human or
XX animal. These staphylococcal infections include wound infections, sepsis,
XX impetigo, furuncles, pneumonia, septic arthritis or endocarditis. The
XX present sequence is Staphylococcus aureus ClfA specific monoclonal
XX antibody 12-9VLA-1 (variable light sequence) protein
XX
XX Sequence 112 AA;
SQ
XX
XX Query Match 85.2%; Score 69; DB 5; Length 112;
XX Best Local Similarity 82.4%; Pred. No. 0.0012;
XX Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
OY 1 KSSQSVFFSSQKNYLA 17
XX |||||:|:|||||
XX 24 KSSQSVLYSSNQKNYLA 40
DB
XX
XX RESULT 20
XX ADU39970
XX ID ADU39970 standard; protein; 112 AA.
XX
XX AC ADU39970;
XX
XX 27-JAN-2005 (first entry)
XX
XX Antibody TF9 light chain variable region.
XX
XX
```

```
XX
XX Cyrostatic; gene therapy; human tissue factor; antibody engineering;
KM blood; coagulation; plasma; diagnosing; cancer.
XX
XX Homo sapiens.
OS
XX WO2004094475-A2.
XX
XX 04-NOV-2004.
XX
XX 21-APR-2004; 2004WO-US012206.
XX
XX 22-APR-2003; 2003US-0464363P.
XX 26-JUN-2003; 2003US-0482498P.
XX 05-APR-2004; 2004US-00816938.
XX
XX (EURO-) EUROCELTIQUE SA.
XX (WANG/) WANG B.
XX
XX Wang B;
XX
XX WPI; 2004-795533/78.
XX
XX N-PSDB; ADU39969.
XX
XX New antibodies capable of binding to human tissue factor and do not
XX inhibit tissue factor mediated blood coagulation compared to a normal
XX plasma control, useful for diagnosing, preventing or treating cancer,
XX such as breast cancer.
XX
XX Disclosure; SEQ ID NO 31; 134pp; English.
XX
XX The invention relates to an isolated antibody capable of binding to human
XX tissue factor (TF), which does not inhibit tissue factor mediated blood
XX coagulation compared to a normal plasma control and can initiate an Fc-
XX mediated mechanism. The composition and methods are useful for
XX diagnosing, preventing or treating cancer, such as non-small cell lung
XX cancer, breast cancer, colon cancer or prostate cancer. These may also be
XX used in screening for agents that may treat or prevent cancer. This
XX sequence corresponds to the light chain variable region of an anti-human
XX tissue factor antibody.
XX
XX Sequence 112 AA;
SQ
XX
XX Query Match 85.2%; Score 69; DB 8; Length 112;
XX Best Local Similarity 82.4%; Pred. No. 0.0012;
XX Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
OY 1 KSSQSVFFSSQKNYLA 17
XX |||||:|:|||||
XX 24 KSSQSVLYSSNQKNYLA 40
DB
XX
XX RESULT 21
XX ADB97820
XX ID ADB97820 standard; protein; 113 AA.
XX
XX AC ADB97820;
XX
XX 04-DEC-2003 (first entry)
XX
XX HEV related protein #SEQ ID 14.
XX
XX Hepatitis E virus; HEV; virucide; vaccine; monoclonal antibody; NE2;
XX infection.
XX
XX Unidentified.
XX
XX WO2003040187-A1.
XX
XX 15-MAY-2003.
XX
XX 08-NOV-2002; 2002WO-CN000797.
XX
XX
```

PR 08-NOV-2001; 2001CN-00134643.
 XX (YANG-) YANG SHENG TANG CO LTD.
 XX Xia N, Zhang J, Gu Y, Li S, Ge S, He Z,
 XI WPI; 2003-441530/41.
 DR
 XX Hepatitis E virus monoclonal antibodies and their active fragments, for
 PT use in diagnosis and developing remedies e.g. vaccines for preventing or
 PT treating hepatitis E virus infection.
 PS
 XX Claim 2; Page 141, 165pp; Chinese.
 CC The invention relates to a monoclonal antibody that binds specifically to
 CC hepatitis E virus open-reading frame (ORF) 2. Also disclosed are
 CC nucleotide sequences encoding the heavy-chain and/or light-chain variable
 CC region of their degeneration sequences. The monoclonal antibody is
 CC selected from anti-HEV monoclonal antibody 8C11 secreted by hybridoma
 CC CCTCC-C200116, anti-HEV monoclonal antibody 13D8 secreted by hybridoma
 CC CCTCC-C200114, anti-HEV monoclonal antibody 8H3 secreted by hybridoma
 CC CCTCC-C200117, and anti-HEV monoclonal antibody 16D7 secreted by
 CC hybridoma CCTCC-C200114. The monoclonal antibodies and their active
 CC fragments are useful in diagnosis and developing remedies e.g. vaccines
 CC for preventing or treating hepatitis E virus infection. From the whole
 CC HEV gene obtained in patients, the HEV ORF fragment was prepared by using
 CC the method of Aye et al. The polypeptide NE2 was then expressed and
 CC isolated after biotechnological manipulations, which was characterised.
 CC Its analogs were also produced for immunising mice and construction of
 CC hybridomas. Tests were carried out to confirm usefulness of such
 CC polypeptides and monoclonal antibodies. The current sequence represents a
 CC HEV related protein.
 XX
 SQ Sequence 113 AA;

Query Match 85.2%; Score 69; DB 7; Length 113;
 Best Local Similarity 82.4%; Pred. No. 0.0012;
 Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSSQSVFSSSQKNYLA 17
 |||||:|:|||||
 DB 24 KSSQSVLYSSNQKNYLA 40

RESULT 22

ADX37184
 ID ADX37184 standard; protein; 113 AA.

AC ADX37184;

DT 21-APR-2005 (first entry)

DE Murine SMS-1 antibody, mSM5-1, light chain variable region, SEQ ID 4.

KW Cytostatic; Gene Therapy; light chain variable region; SMS-1; neoplasm;
 melanoma; breast tumor; hepatocellular carcinoma.

OS Mus musculus.

PN US2005031617-A1.

PD 10-FEB-2005.

PF 26-NOV-2003; 2003US-00722849.

PR 06-JUN-2003; 2003CN-00129123.

PR 25-NOV-2003; 2003CN-01119926.

PT (MAJU/) MA J.
 (GUOY/) GUO Y.

PA Ma J, Guo Y;

XX

DR WPI; 2005-131967/14.
 DR N-PSDB; ADX37188.
 XX
 PT New antibody that competitively inhibits the immunospecific binding of a
 PT human SMS-1 specific monoclonal antibody to a SMS-1 target antigen,
 PT useful for diagnosing or treating neoplasms, e.g. melanoma or breast
 PT cancer.
 PS
 XX Claim 11; SEQ ID NO 4; 40pp; English.
 CC The present invention relates to antibodies which are specific for the
 CC cancer associated antigen SMS-1. The antibodies are useful for assaying
 CC for SMS-1 antigen in a sample, which is useful for the prognosis or
 CC diagnosis of a neoplasm, e.g. melanoma, breast cancer, or hepatocellular
 CC carcinoma. The present sequence is a variable region of one such anti-SMS
 CC -1 antibody.
 XX
 SQ Sequence 113 AA;

Query Match 85.2%; Score 69; DB 9; Length 113;
 Best Local Similarity 82.4%; Pred. No. 0.0012;
 Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSSQSVFSSSQKNYLA 17
 |||||:|:|||||
 DB 24 KSSQSVLYSSNQKNYLA 40

RESULT 23

ADX37182
 ID ADX37182 standard; protein; 113 AA.

AC ADX37182;

DT 21-APR-2005 (first entry)

DE SMS-1 humanized antibody, ResMS-1, light chain variable region, SEQ ID 2.

KW Cytostatic; Gene Therapy; light chain variable region;

humanized antibody; SMS-1; neoplasm; melanoma; breast tumor;

hepatocellular carcinoma.

OS Homo sapiens.

OS Mus musculus.

OS Chimeric.

PN US2005031617-A1.

PD 10-FEB-2005.

PF 26-NOV-2003; 2003US-00722849.

PR 06-JUN-2003; 2003CN-00129123.

PR 25-NOV-2003; 2003CN-01119926.

PT (MAJU/) MA J.
 (GUOY/) GUO Y.

PA Ma J, Guo Y;

DR WPI; 2005-131967/14.

DR N-PSDB; ADX37186.

PT New antibody that competitively inhibits the immunospecific binding of a
 PT human SMS-1 specific monoclonal antibody to a SMS-1 target antigen,
 PT useful for diagnosing or treating neoplasms, e.g. melanoma or breast
 PT cancer.

PS Claim 7; SEQ ID NO 2; 40pp; English.

XX The present invention relates to antibodies which are specific for the
CC cancer associated antigen SMS-1. The antibodies are useful for assaying
CC for SMS-1 antigen in a sample, which is useful for the prognosis or
CC diagnosis of a neoplasm, e.g. melanoma, breast cancer, or hepatocellular
CC carcinoma. The present sequence is a variable region of one such anti-SMS
CC -1 antibody.

XX Sequence 113 AA;

Query Match 85.2%; Score 69; DB 9; Length 113;
Best Local Similarity 82.4%; Pred. No. 0.0012;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSSOSVFPSSSQKNYLA 17
|||:|:|:|:|:|
DB 24 KSSOSVLYSSNOKNYLA 40

RESULT 24

ID ADX98401 standard; protein; 113 AA.

AC ADX98401;

DT 05-MAY-2005 (first entry)

DE Human anti-HGF antibody kappa light chain variable region protein SEQ174.

KM antibody; cytostatic; cancer; neoplasm; solid tumor;

KW hepatocyte growth factor; HGF; light chain variable region.

OS Homo sapiens.

PN WO2005017107-A2.

PD 24-FEB-2005.

PF 16-JUL-2004; 2004WO-US018936.

PR 18-JUL-2003; 2003US-0488681P.

PA (ANGE-) AMGEN INC.

PA (ABGE-) ABGENIX INC.

PI Burgess TL, Coxon A, Green LL, Zhang K;

XX WPI; 2005-182350/19.

PT New polypeptide comprising a complementarity determining region (CDR)
PT consisting of CDR1a, CDR2a, CDR3a, CDR1b, CDR2b or CDR3b and capable of
PT binding hepatocyte growth factor, useful in preparing a composition for
PT treating cancer.

XX Example 3; SEQ ID NO 174; 301pp; English.

XX The invention relates to a novel isolated polypeptide comprising at least
CC one complementarity-determining region (CDR) consisting of CDR1a, CDR2a
CC or CDR3a, or CDR1b, CDR2b or CDR3b. The polypeptide, in association with
CC an antibody heavy or light chain, is capable of binding hepatocyte growth
CC factor (HGF); HGF, also known as scatter factor (SF), has been identified
CC as a potent mitogen for hepatocytes and also as a secretory protein of
CC fibroblasts and smooth muscles that acts to induce motility of epithelial
CC cells. The polypeptide demonstrates cytostatic activity and may be useful
CC in preparing a composition for treating cancer or a solid tumor. The
CC current sequence is that of the human anti-HGF antibody kappa light chain
CC variable region protein SEQ174 of the invention.

XX Sequence 113 AA;

Query Match 85.2%; Score 69; DB 9; Length 113;
Best Local Similarity 76.5%; Pred. No. 0.0012;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSSOSVFPSSSQKNYLA 17
|||:|:|:|:|:|
DB 24 KSSOSIFYSSTKNYLA 40

RESULT 25

ID AEA86699 standard; protein; 113 AA.

AC AEA86699;

DT 25-AUG-2005 (first entry)

DE Humanized anti-SMS-1 antibody, ResMS-1 VL region, SEQ ID: 2.

KM cancer; cytostatic; neoplasm; melanoma; breast tumor; endocrine disease;
KW hepatocellular carcinoma; immunotherapy; antibody engineering;
KW light chain variable region; ResMS-1; monoclonal antibody.

OS Homo sapiens.

OS Mus sp.

OS Chimeric.

FH Key Location/Qualifiers

FT Region 24..40

FT /note= "Variable region"

FT /note= "This region is specifically claimed in claim 9,"

FT Misc-difference 41 36, 38, 45, 53, 60, 66"

FT Region /note= "Encoded by GGA"

FT /note= "Variable region"

FT /note= "This region is specifically claimed in claim 9,"

FT Region /note= "Variable region"

FT /note= "This region is specifically claimed in claim 9,"

PN WO2005053604-A2.

PD 16-JUN-2005.

PF 04-JUN-2004; 2004WO-US017855.

PR 06-JUN-2003; 2003CN-00129123.

PR 25-NOV-2003; 2003CN-01119926.

PR 26-NOV-2003; 2003US-00722849.

PR 28-NOV-2003; 2003TW-00133571.

PA (SYMB-) SYMBIGENE ACQUISITION CO INC.

PI Ma J, Guo Y,

XX WPI; 2005-435284/44.

DR N-PSDB; AEA86703.

PT New antibody competitively inhibiting immunospecific binding of a human
PT SMS-1 specific monoclonal antibody to a SMS-1 target antigen, useful in
PT treating malignancies such as melanoma, breast cancer or hepatocellular
PT carcinoma.

XX Claim 7; SEQ ID NO 2; 85pp; English.

XX The present invention relates to an antibody that competitively inhibits
CC the immunospecific binding of a human SMS-1 specific monoclonal antibody
CC (hSMS-1) to a SMS-1 target antigen. The invention is useful in the
CC fields of cancer biology and immunotherapy, in particular for diagnosing
CC and treating malignancies such as melanoma, breast cancer or
CC hepatocellular carcinoma. The present sequence is the humanized anti-SMS-
CC 1 antibody, ResMS-1 light chain variable (VL) region. This sequence is
CC generated by grafting a CDR (complementarity determining region) from

CC mouse SM5-1 light chain into a human Bence-Jones protein I antibody light
 CC chain framework region.
 XX
 SQ Sequence 113 AA;

Query Match 85.2%; Score 69; DB 9; Length 113;
 Best Local Similarity 82.4%; Pred. No. 0.0012;
 Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSSQSVFSSSQKNTLA 17
 |||||:|:|:|
 DB 24 KSSQSVLYSSNQKNTLA 40

RESULT 26

AEA88701
 ID AEA88701 standard; protein; 113 AA.

AC AEA88701;

DT 25-AUG-2005 (first entry)

DE Mouse anti-SM5-1 antibody light chain variable region, SEQ ID: 4.

KW cancer; cytostatic; neoplasm; melanoma; breast tumor; endocrine disease;
 KW hepatocellular carcinoma; immunotherapy; light chain variable region;
 SM5-1.

OS Mus sp.

Key Location/Qualifiers

FT Region 24..40

FT /note= "Variable region"

FT Region 56..62

FT /note= "Variable region"

FT Region 95..102

FT /note= "Variable region"

PN WO2005053604-A2.

PD 16-JUN-2005.

PF 04-JUN-2004; 2004WO-US017855.

PR 06-JUN-2003; 2003CN-00129123.

PR 25-NOV-2003; 2003CN-01119926.

PR 26-NOV-2003; 2003US-00722849.

PR 28-NOV-2003; 2003TW-00133571.

PA (SYMB-) SYMBIGENE ACQUISITION CO INC.

PI Ma J, Guo Y;

DR WPI; 2005-435284/44.

DR N-PSDB; AEA88705.

PT New antibody competitively inhibiting immunospecific binding of a human
 PT SM5-1 specific monoclonal antibody to a SM5-1 target antigen, useful in
 PT treating malignancies such as melanoma, breast cancer or hepatocellular
 PT carcinoma.

PS Claim 11; SEQ ID NO 4; 85pp; English.

CC The present invention relates to an antibody that competitively inhibits
 CC the immunospecific binding of a human SM5-1 specific monoclonal antibody
 CC (hSM5-1) to a SM5-1 target antigen. The invention is useful in the
 CC fields of cancer biology and immunotherapy, in particular for diagnosing
 CC and treating malignancies such as melanoma, breast cancer or
 CC hepatocellular carcinoma. The present sequence is the mouse anti-SM5-1
 CC antibody light chain variable (VL) region.

XX Sequence 113 AA;

SQ

Query Match 85.2%; Score 69; DB 9; Length 113;
 Best Local Similarity 82.4%; Pred. No. 0.0012;
 Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSSQSVFSSSQKNTLA 17
 |||||:|:|:|
 DB 24 KSSQSVLYSSNQKNTLA 40

RESULT 27

AEA38741
 ID AEA38741 standard; protein; 116 AA.

AC AEA38741;

DT 11-AUG-2005 (first entry)

DE Murine anti-TGF-beta antibody (2G7) VL protein, SEQ ID NO: 1.

KW Monoclonal antibody; animal disease model; metastasis; cytostatic;
 KW neoplasm; bone metastases; breast tumor; colorectal tumor; bone disease;
 KW osteopathic; antibody therapy; radiation therapy; immunotherapy;
 KW cancer cell proliferation inhibitor;
 KW transforming growth factor-beta-antagonist; light chain variable region.

OS Mus musculus.

Key Location/Qualifiers

FT Region 24..40

FT /note= "Complementarity determining region (CDR) - L1"

FT Region 56..62

FT /note= "Complementarity determining region (CDR) - L2"

FT Region 95..102

FT /note= "Complementarity determining region (CDR) - L3"

PN WO2005050200-A2.

PD 02-JUN-2005.

PF 04-NOV-2004; 2004WO-US036651.

PR 13-NOV-2003; 2003US-0520398P.

PR 31-MAR-2004; 2004US-0557951P.

PA (GETH) GENENTECH INC.

PI Filvaroff EH;

DR WPI; 2005-417772/42.

PT Screening compounds useful for treating tumor metastasis involves
 PT administering a test compound to non-human animal model bearing soft
 PT tissue/bone metastasis and identifying compound that inhibits soft tissue
 PT growth/bone metastasis.

PS Example 2; SEQ ID NO 1; 109pp; English.

CC The present invention relates to the screening of candidate molecules
 CC [anti-transforming growth factor (TGF)-beta antibodies] for the treatment
 CC of tumor metastasis and treatment methods using such molecules. The
 CC screening method of the invention involves administering several test
 CC substances to a non-human syngeneic immunocompetent animal model bearing
 CC at least one soft tissue or bone metastasis optionally in presence of a
 CC primary tumor, determining the effects of these test substances on the
 CC soft tissue or bone metastasis and growth of the primary tumor and
 CC identifying a test substance inhibiting soft tissue growth or bone
 CC metastasis without adverse effect on the status of the primary tumor. The
 CC invention is useful in the diagnosis and treatment of breast cancer,
 CC colorectal cancer, liver and lung metastases, bone destruction and bone
 CC loss. The animal models of the present invention is useful to screen
 CC substances useful for the prophylaxis or treatment of soft tissue and/or
 CC bone metastases which may additionally be effective in treating the
 CC primary tumor. The present sequence is murine anti-TGF-beta antibody

CC (267) variable light chain (VL) monoclonal antibody protein.
 XX
 SQ Sequence 116 AA;
 Query Match 85.2%; Score 69; DB 9; Length 116;
 Best Local Similarity 82.4%; Pred. No. 0.0012;
 Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KSSQSVFPSSSQKNYLA 17
 |||||:|||||
 DB 24 KSSQSVLYSSNQKNYLA 40
 RESULT 28
 ADV92466
 ID ADV92466 standard; protein; 133 AA.
 AC ADV92466;
 XX
 DT 10-MAR-2005 (first entry)
 XX
 DE Mouse SM5-1 (mSM5-1) light chain variable region protein.
 XX
 KW Antibody engineering; chimeric antibody; cyrostatic; gene therapy;
 KW vaccine; gastrointestinal disease; immune response; melanoma; malignancy;
 KW breast cancer; hepatocellular carcinoma.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..20
 FT /note="Signal peptide"
 FT Region 21..133
 FT /note="Light chain variable region gene (VL)"
 FT Protein 21..133
 FT /note="Mature Mouse SM5-1 (mSM5-1) light chain variable
 FT region protein"
 PN US2004254108-A1.
 XX
 PD 16-DEC-2004.
 XX
 PF 26-NOV-2003; 2003US-00723003.
 XX
 PR 13-JUN-2003; 2003CN-00129290.
 PR 25-NOV-2003; 2003CN-01119930.
 XX
 PA (MAJ/J) MA J,
 PA (GUO/Y) GUO Y.
 XX
 PI Ma J, Guo Y;
 XX
 WP1; 2005-030218/03.
 DR N-PSDB; ADV92465.
 XX
 PT New chimeric protein comprises an Flt3 ligand and a proteinous or
 PT peptidyl tumoricidal agent, useful for treating malignancy or neoplasm,
 PT e.g. melanoma, breast cancer, or hepatocellular carcinoma.
 XX
 Example 3; SEQ ID NO 10; 158pp; English.
 PS
 XX The present invention relates to a chimeric protein having a Flt3 ligand
 CC (FI) or its biologically active fragment and a proteinous or peptidyl
 CC tumoricidal agent. The invention is useful for treating malignancy;
 CC neoplasm e.g. melanoma, breast cancer, hepatocellular carcinoma and as a
 CC vaccine for eliciting an immune response. The invention is also useful in
 CC gene therapy. The present sequence is the mouse SM5-1 (mSM5-1) light
 CC chain variable region protein.
 XX
 SQ Sequence 133 AA;
 Query Match 85.2%; Score 69; DB 9; Length 133;
 Best Local Similarity 82.4%; Pred. No. 0.0015;

Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KSSQSVFPSSSQKNYLA 17
 |||||:|||||
 DB 44 KSSQSVLYSSNQKNYLA 60
 RESULT 29
 ADV98529
 ID ADV98529 standard; protein; 133 AA.
 AC ADV98529;
 XX
 DT 24-MAR-2005 (first entry)
 XX
 DE Novel chimeric protein-related mSM5-1 light chain protein SeqID10.
 XX
 KW protein engineering; pharmaceutical; cyrostatic; vaccine; cancer;
 KW neoplasm; melanoma; breast tumor; hepatocellular carcinoma.
 XX
 OS Mus sp.
 XX
 PN WO2005001048-A2.
 EN
 XX
 PD 06-JAN-2005.
 XX
 PF 04-JUN-2004; 2004WO-US017765.
 XX
 PR 13-JUN-2003; 2003CN-00129290.
 PR 25-NOV-2003; 2003CN-01119930.
 PR 26-NOV-2003; 2003US-00723003.
 PR 28-NOV-2003; 2003TW-00133577.
 XX
 PA (SYMB-) SYMBIGENE ACQUISITION CO INC.
 XX
 PI Ma J, Guo Y;
 XX
 WP1; 2005-075540/08.
 DR N-PSDB; ADV98528.
 XX
 PT New chimeric protein for preventing or treating neoplastic conditions,
 PT e.g. melanoma, breast cancer or hepatocellular carcinoma, comprises an
 PT Flt3 ligand or its fragment, and a proteinous or peptidyl tumoricidal
 PT agent.
 XX
 PS Example 3; SEQ ID NO 10; 147pp; English.
 XX
 CC This invention relates to a novel chimeric protein comprising an Flt3
 CC ligand, or its biological fragment, and a proteinous or peptidyl
 CC tumoricidal agent. The invention may be useful for the production of
 CC compounds with a cyrostatic activity or a vaccine. The composition of
 CC methods are useful for preventing or treating neoplastic conditions, such
 CC as melanoma, breast cancer or hepatocellular carcinoma. The present
 CC sequence is that of a protein which is related to the chimeric proteins
 CC of the invention.
 XX
 SQ Sequence 133 AA;
 Query Match 85.2%; Score 69; DB 9; Length 133;
 Best Local Similarity 82.4%; Pred. No. 0.0015;
 Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KSSQSVFPSSSQKNYLA 17
 |||||:|||||
 DB 44 KSSQSVLYSSNQKNYLA 60
 RESULT 30
 ADX98254
 ID ADX98254 standard; protein; 133 AA.
 AC ADX98254;
 XX

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DT 05-MAY-2005 (first entry)
XX Human anti-HGF antibody kappa light chain variable region protein SEQ 26.
DE antibody; cytostatic; cancer; neoplasm; solid tumor;
XX hepatocyte growth factor; HGF; light chain variable region.
XX Homo sapiens.
XX WO2005017107-A2.
XX
XX 24-FEB-2005.
XX
XX 16-JUL-2004; 2004WO-US018936.
XX
XX 18-JUL-2003; 2003US-0488681P.
XX (AMGE-) AMGEN INC.
XX (ABGE-) ABGENIX INC.
XX
XX Burgess TL, Coxon A, Green LL, Zhang K;
XX WPI, 2005-182350/19.
XX N-PSDB; ADX98231.
XX
XX New polypeptide comprising a complementarity determining region (CDR)
XX consisting of CDRa, CDR2a, CDR3a, CDR1b, CDR2b or CDR3b and capable of
XX binding hepatocyte growth factor, useful in preparing a composition for
XX treating cancer.
XX
XX Claim 2; SEQ ID NO 26; 301pp; English.
XX
XX The invention relates to a novel isolated polypeptide comprising at least
XX one complementarity-determining region (CDR) consisting of CDR1a, CDR2a
XX or CDR3a, or CDR1b, CDR2b or CDR3b. The polypeptide, in association with
XX an antibody heavy or light chain, is capable of binding hepatocyte growth
XX factor (HGF). HGF, also known as scatter factor (SF), has been identified
XX as a potent mitogen for hepatocytes and also as a secretory protein of
XX fibroblasts and smooth muscles that acts to induce motility of epithelial
XX cells. The polypeptide demonstrates cytostatic activity and may be useful
XX in preparing a composition for treating cancer or a solid tumor. The
XX current sequence is that of the human anti-HGF antibody kappa light chain
XX variable region protein SEQ 26 of the invention.
XX
XX Sequence 133 AA;
XX
XX Query Match 85.2%; Score 69; DB 9; Length 133;
XX Best Local Similarity 76.5%; Pred. No. 0.0015;
XX Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 KSSQSVFPSSSQKNYLA 17
Db 44 KSSQSVFPSSSQKNYLA 60

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FH Key Location/Qualifiers
FT Peptide 1..22
FT /label= Signal peptide.
FT Region 23..135
FT /note= "Light chain variable region gene (VL)"
FT Protein 23..135
FT /note= "Mature SMS-1 humanized antibody light chain
FT variable region protein"
FT Misc-difference 63
FT /note= "Encoded by GGA"
XX
XX US2004254108-A1.
XX
XX 16-DEC-2004.
XX
XX 26-NOV-2003; 2003US-00723003.
XX
XX 13-JUN-2003; 2003CN-00129290.
XX 25-NOV-2003; 2003CN-01119930.
XX
XX (MAJY/) MA J.
XX (GUOY/) GUO Y.
XX
XX Ma J, Guo Y;
XX
XX WPI, 2005-030218/03.
XX N-PSDB; ADV92473.
XX
XX New chimeric protein comprises an Flt3 ligand and a proteinous or
XX peptide/tumoricidal agent, useful for treating malignancy or neoplasm,
XX e.g. melanoma, breast cancer, or hepatocellular carcinoma.
XX
XX Example 3; SEQ ID NO 16; 158pp; English.
XX
XX The present invention relates to a chimeric protein having a Flt3 ligand
XX (FL) or its biologically active fragment and a proteinous or peptide/tumoricidal agent. The invention is useful for treating malignancy,
XX neoplasm e.g. melanoma, breast cancer, hepatocellular carcinoma and as a
XX vaccine for eliciting an immune response. The invention is also useful in
XX gene therapy. The present sequence is the SMS-1 humanized antibody (hUSM)
XX light chain variable region protein.
XX
XX Sequence 135 AA;
XX
XX Query Match 85.2%; Score 69; DB 9; Length 135;
XX Best Local Similarity 82.4%; Pred. No. 0.0015;
XX Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 KSSQSVFPSSSQKNYLA 17
Db 46 KSSQSVLYSSNQKNYLA 62

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RESULT 31
ADV92474
ID ADV92474 standard; protein; 135 AA.
XX
XX ADV92474;
XX
XX 10-MAR-2005 (first entry)
XX
XX SMS-1 humanized antibody light chain variable region protein.
XX
XX Antibody engineering; chimeric antibody; cytostatic; gene therapy;
XX vaccine; gastrointestinal disease; immune response; melanoma; malignancy;
XX breast cancer; hepatocellular carcinoma.
XX
XX Homo sapiens.
XX Mus sp.
XX Chimeric.
XX

```

```

RESULT 32
ADV98537
ID ADV98537 standard; protein; 135 AA.
XX
XX ADV98537;
XX
XX 24-MAR-2005 (first entry)
XX
XX Novel chimeric protein-related hUSM light chain protein SeqID18.
XX
XX protein engineering; pharmaceutical; cytostatic; vaccine; cancer;
XX neoplasm; melanoma; breast tumor; hepatocellular carcinoma.
XX
XX Mus sp.
XX Synthetic.
XX
XX WO2005001048-A2.
XX
XX 06-JAN-2005.
XX

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PF 04-JUN-2004; 2004WO-US017765.
XX
PR 13-JUN-2003; 2003CN-00129290.
PR 25-NOV-2003; 2003CN-01119930.
PR 26-NOV-2003; 2003US-00723003.
XX 28-NOV-2003; 2003TW-00133577.
XX
PA (SYMB-) SYMBIGENE ACQUISITION CO INC.
XX
PI Ma J, Guo Y;
XX
DR WPI; 2005-075540/08.
DR N-PSDB; ADV98536.
XX
XX
PT New chimeric protein for preventing or treating neoplastic conditions,
PT e.g. melanoma, breast cancer or hepatocellular carcinoma, comprises an
PT Flt3 ligand or its fragment, and a proteinous or peptidyl tumoricidal
PT agent.
XX
PS Example 3; Fig 13; 147pp; English.
XX
CC This invention relates to a novel chimeric protein comprising an Flt3
CC ligand, or its biological fragment, and a proteinous or peptidyl
CC tumoricidal agent. The invention may be useful for the production of
CC compounds with a cytostatic activity or a vaccine. The composition and
CC methods are useful for preventing or treating neoplastic conditions, such
CC as melanoma, breast cancer or hepatocellular carcinoma. The present
CC sequence is that of a protein which is related to the chimeric proteins
CC of the invention. Note: Two sequences were allocated this Segid number in
CC the specification, the alternative sequence is shown on page 21.
XX
SQ Sequence 135 AA;
XX
Query Match 85.2%; Score 69; DB 9; Length 135;
Best Local Similarity 82.4%; Pred. No. 0.0015;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
OY 1 KSSQSVFPSSSQKNYLA 17
Db 46 KSSQSVLYSSNOKNYLA 62
XX
RESULT 33
ADV92470
ID ADV92470 standard; protein; 239 AA.
XX
AC ADV92470;
XX
DT 10-MAR-2005 (first entry)
XX
DE SMS-1 chimeric antibody (ChSM) light chain protein.
XX
KW Antibody engineering; chimeric antibody; cytostatic; gene therapy;
KW vaccine; gastrointestinal disease; immune response; melanoma; malignancy;
KW breast cancer; hepatocellular carcinoma.
XX
XX Homo sapiens.
OS Mus sp.
OS Chimeric.
OS
XX
FH Key Location/Qualifiers
FT 1..20
FT /label= Signal peptide
FT Protein 21..239
FT /note= "Mature SMS-1 chimeric antibody (ChSM) light chain
FT protein"
FT Region 21..133
FT /note= "Light chain variable region gene (VL)"
FT 134..239
FT /note= "Human kappa chain constant cDNA (CL)"
XX
XX US2004254108-A1.
XX
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```
PD 16-DEC-2004.
XX
PR 26-NOV-2003; 2003US-00723003.
XX
PR 13-JUN-2003; 2003CN-00129290.
PR 25-NOV-2003; 2003CN-01119930.
XX
XX (MATJ/) MA J.
PA (GUOY/) GUO Y.
XX
PI Ma J, Guo Y;
XX
DR WPI; 2005-030218/03.
DR N-PSDB; ADV92469.
XX
XX
PT New chimeric protein comprises an Flt3 ligand and a proteinous or
PT peptidyl tumoricidal agent, useful for treating malignancy or neoplasm,
PT e.g. melanoma, breast cancer, or hepatocellular carcinoma.
XX
PS Example 3; SEQ ID NO 14; 158pp; English.
XX
CC The present invention relates to a chimeric protein having a Flt3 ligand
CC (FL) or its biologically active fragment and a proteinous or peptidyl
CC tumoricidal agent. The invention is useful for treating malignancy,
CC neoplasm e.g. melanoma, breast cancer, hepatocellular carcinoma and as a
CC vaccine for eliciting an immune response. The invention is also useful in
CC gene therapy. The present sequence is the SMS-1 chimeric antibody (ChSM)
CC light chain protein.
XX
SQ Sequence 239 AA;
XX
Query Match 85.2%; Score 69; DB 9; Length 239;
Best Local Similarity 82.4%; Pred. No. 0.0028;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
OY 1 KSSQSVFPSSSQKNYLA 17
Db 44 KSSQSVLYSSNOKNYLA 60
XX
RESULT 34
ADV98533
ID ADV98533 standard; protein; 239 AA.
XX
AC ADV98533;
XX
DT 24-MAR-2005 (first entry)
XX
DE Novel chimeric protein-related ChSM light chain protein Segid14.
XX
KW protein engineering; pharmaceutical; cytostatic; vaccine; cancer;
KW neoplasm; melanoma; breast tumor; hepatocellular carcinoma.
XX
XX Mus sp.
OS Synthetic.
OS
XX
PN WO2005001048-A2.
XX
PD 06-JAN-2005.
XX
PF 04-JUN-2004; 2004WO-US017765.
XX
PR 13-JUN-2003; 2003CN-00129290.
PR 25-NOV-2003; 2003CN-01119930.
PR 26-NOV-2003; 2003US-00723003.
XX 28-NOV-2003; 2003TW-00133577.
XX
XX (SYMB-) SYMBIGENE ACQUISITION CO INC.
XX
PI Ma J, Guo Y;
XX
DR WPI; 2005-075540/08.
DR N-PSDB; ADV98532.
XX
```



```

XX New chimeric protein for preventing or treating neoplastic conditions,
PT e.g. melanoma, breast cancer or hepatocellular carcinoma, comprises an
PT Flt3 ligand or its fragment, and a proteinous or peptidyl tumoricidal
PT agent.
XX
PS Example 3; Fig 9; 147bp; English.
XX
CC This invention relates to a novel chimeric protein comprising an Flt3
CC ligand, or its biological fragment, and a proteinous or peptidyl
CC tumoricidal agent. The invention may be useful for the production of
CC compounds with a cytostatic activity or a vaccine. The composition and
CC methods are useful for preventing or treating neoplastic conditions, such
CC as melanoma, breast cancer or hepatocellular carcinoma. The present
CC sequence is that of a protein which is related to the chimeric proteins
CC of the invention. Note: Two sequences were allocated this Segid number in
CC the specification, the alternative sequence is shown on page 21.
XX
SQ Sequence 239 AA;

Query Match      85.2%; Score 69; DB 9; Length 239;
Best Local Similarity 82.4%; Pred. No. 0.0028; 1; Indels 0; Gaps 0;
Matches 14; Conservative 2; Mismatches 1;

QY      1 KSSQSVFFSSQKNYLA 17
        |||||:|||||
        44 KSSQSVLYSSNQKNYLA 60

RESULT 35
ADV92478
ID ADV92478 standard; protein; 241 AA.
XX
AC ADV92478;
XX
DT 10-MAR-2005 (first entry)
XX
DE SMS-1 humanized antibody (husm) light chain protein.
XX
KW Antibody engineering; chimeric antibody; cytostatic; gene therapy;
KW vaccine; gastrointestinal disease; immune response; melanoma; malignancy;
KW breast cancer; hepatocellular carcinoma.
XX
OS Homo sapiens.
OS Mus sp.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Peptide 1..22
FT Protein /label= Signal peptide 23..241
FT /note= "Mature SMS-1 humanized antibody (husm) light chain protein"
FT Region 23..135
FT /note= "Light chain variable region gene (VL)"
FT Misc-difference 63
FT /note= "Encoded by GGA"
FT Region 136..241
FT /note= "Human kappa chain constant cDNA (CL)"
XX
PN US2004254108-A1.
XX
PD 16-DEC-2004.
XX
PF 26-NOV-2003; 2003US-00723003.
XX
PR 13-JUN-2003; 2003CN-00129290.
XX
PR 25-NOV-2003; 2003CN-01119930.
XX
PA (MAJ/J) MA J.
XX (GUO/Y) GUO Y.
PI Ma J, Guo Y;

```

```

XX WPI; 2005-030218/03.
DR N-PSDB; ADV92477.
XX
PT New chimeric protein comprises an Flt3 ligand and a proteinous or
PT peptidyl tumoricidal agent, useful for treating malignancy or neoplasm,
PT e.g. melanoma, breast cancer, or hepatocellular carcinoma.
XX
PS Example 3; SEQ ID NO 22; 158bp; English.
XX
CC The present invention relates to a chimeric protein having a Flt3 ligand
CC (FL) or its biologically active fragment and a proteinous or peptidyl
CC tumoricidal agent. The invention is useful for treating malignancy,
CC neoplasm e.g. melanoma, breast cancer, hepatocellular carcinoma and as a
CC vaccine for eliciting an immune response. The invention is also useful in
CC gene therapy. The present sequence is the SMS-1 humanized antibody (husm)
CC light chain DNA.
XX
SQ Sequence 241 AA;

Query Match      85.2%; Score 69; DB 9; Length 241;
Best Local Similarity 82.4%; Pred. No. 0.0028; 1; Indels 0; Gaps 0;
Matches 14; Conservative 2; Mismatches 1;

QY      1 KSSQSVFFSSQKNYLA 17
        |||||:|||||
        46 KSSQSVLYSSNQKNYLA 62

RESULT 36
ADV98541
ID ADV98541 standard; protein; 241 AA.
XX
AC ADV98541;
XX
DT 24-MAR-2005 (first entry)
XX
DE Novel chimeric protein-related husm light chain protein Segid22.
XX
KW protein engineering; pharmaceutical; cytostatic; vaccine; cancer;
KW neoplasm; melanoma; breast tumor; hepatocellular carcinoma.
XX
OS Mus sp.
OS Synthetic.
XX
PN WO200501048-A2.
XX
PD 06-JAN-2005.
XX
PF 04-JUN-2004; 2004WO-US017765.
XX
PR 13-JUN-2003; 2003CN-00129290.
XX
PR 25-NOV-2003; 2003CN-01119930.
XX
PR 26-NOV-2003; 2003US-00723003.
XX
PR 28-NOV-2003; 2003TW-00133577.
XX
PA (SYMB-) SYMBIGENE ACQUISITION CO INC.
XX
PI Ma J, Guo Y;

WPI; 2005-075540/08.
DR N-PSDB; ADV98540.
XX
PT New chimeric protein for preventing or treating neoplastic conditions,
PT e.g. melanoma, breast cancer or hepatocellular carcinoma, comprises an
PT Flt3 ligand or its fragment, and a proteinous or peptidyl tumoricidal
PT agent.
XX
PS Example 3; Fig 15; 147bp; English.
XX
CC This invention relates to a novel chimeric protein comprising an Flt3
CC ligand, or its biological fragment, and a proteinous or peptidyl
CC tumoricidal agent. The invention may be useful for the production of

```

CC compounds with a cytostatic activity or a vaccine. The composition and
 CC methods are useful for preventing or treating neoplastic conditions, such
 CC as melanoma, breast cancer or hepatocellular carcinoma. The present
 CC sequence is that of a protein which is related to the chimeric proteins
 CC of the invention. Note: Two sequences were allocated this Segid number in
 CC the specification, the alternative sequence is shown on page 21.

CC Sequence 241 AA;

Query Match 85.2%; Score 69; DB 9; Length 241;
 Best Local Similarity 82.4%; Pred. No. 0.0028;
 Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSSQSVFPSSQKNYLA 17
 |||||:|||||
 DB 46 KSSQSVLYSSNQKNYLA 62

RESULT 37

AAW90226
 ID AAW90226 standard; protein; 263 AA.

XX AAW90226;

XX 10-MAY-1999 (first entry)

XX Anti-B7.2 monospecific triabody 1G10.

XX B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2; CD86;
 KW T cell activation; inhibitor; graft versus host disease;
 KW transplant rejection; allograft rejection; autoimmune disease; allergy;
 KW therapy; human; triabody; antibody; 1G10.

OS Mus sp.
 OS Synthetic.
 OS Chimeric.

FT Key Location/Qualifiers

FT Peptide 1..24

FT Region /note="pe1B signal peptide"

FT Peptide /note="anti B7.2 MAB VH region"

FT Peptide /note="anti B7.2 MAB VL region"

FT Peptide 258..263

FT Peptide /note="His6 tag"

XX WO9858965-A2.

XX 30-DEC-1998.

XX 22-JUN-1998; 98WO-EP003791.

XX 20-JUN-1997; 97EP-00870092.

XX (INNO-) INNOGENETICS NV.

XX Lorre K, Sablon E, Buyse M, Bosman A;

XX WPI; 1999-105615/09.

XX N-PSDB; AAX01660.

XX New molecules which bind B7.1 and B7.2 - useful to prevent and treat

XX immune diseases including allograft rejection.

XX Example 7.3; Fig 34; 182pp; English.

CC This polypeptide comprises a 1G10 monospecific triabody composed of the
 CC VH region of anti-B7.2 monoclonal antibody (Mab) 1G10 joined to the VL
 CC region of 1G10. A triabody is a mono- a bi- or a trispecific molecule
 CC recognising simultaneously e.g. two B7.2 and one B7.1 molecules. It has
 CC a rigid structure that prevents simultaneous binding to the 3 targets.
 CC Each antigen-binding site is formed by pairing of one VH and one VL

CC domain from the same or from two different polypeptides. The invention
 CC relates to novel molecules, including triabodies, which can cross-link
 CC and/or cross-react with the costimulatory molecules B7.1 and B7.2
 CC expressed on professional antigen-presenting cells, leading to the
 CC inhibition of antigen-specific T cell activation. Methods are provided
 CC for the production of such B7-binding molecules, and for their use in the
 CC treatment or prevention of diseases of the immune system, in particular
 CC graft rejection, graft versus host disease, allergy and autoimmune
 CC diseases (claimed)

CC Sequence 263 AA;

Query Match 85.2%; Score 69; DB 2; Length 263;
 Best Local Similarity 82.4%; Pred. No. 0.0031;
 Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSSQSVFPSSQKNYLA 17
 |||||:|||||
 DB 168 KSSQSVLYSSNQKNYLA 184

RESULT 38

AAW90222
 ID AAW90222 standard; protein; 268 AA.

XX AAW90222;

XX 10-MAY-1999 (first entry)

XX Anti-B7.2 monospecific diabody 1G-10.

XX B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2; CD86;
 KW T cell activation; inhibitor; graft versus host disease;
 KW transplant rejection; allograft rejection; autoimmune disease; allergy;
 KW therapy; human; diabody; antibody; 1G-10.

OS Mus sp.
 OS Synthetic.
 OS Chimeric.

FT Key Location/Qualifiers

FT Peptide 1..24

FT Region /note="pe1B signal peptide"

FT Peptide /note="anti B7.2 MAB VH region"

FT Peptide /note="G4S flexible linker"

FT Region /note="anti B7.2 MAB VL region"

FT Peptide 263..268

FT Peptide /note="His6 tag"

XX WO9858965-A2.

XX 30-DEC-1998.

XX 22-JUN-1998; 98WO-EP003791.

XX 20-JUN-1997; 97EP-00870092.

XX (INNO-) INNOGENETICS NV.

XX Lorre K, Sablon E, Buyse M, Bosman A;

XX WPI; 1999-105615/09.

XX N-PSDB; AAX01656.

XX New molecules which bind B7.1 and B7.2 - useful to prevent and treat

XX immune diseases including allograft rejection.

XX Example 7.2; Fig 26; 182pp; English.

CC This polypeptide comprises a 1G-10 monospecific diabody composed of the

CC VH region of anti-B7.2 monoclonal antibody (Mab) 1G-10 joined via a
 CC short, flexible linker to the VL region of 1G-10. Mono- or bispecific
 CC bivalent molecules are generated by shortening the flexible linker
 CC sequence between the VH and VL of the anti-B7.1 scFv B7-24, the anti-B7.2
 CC scFv 1G10 and the scFv molecule with dual specificity for B7.1 and B7.2
 CC (B7.12) to 5-10 residues, and for bispecific molecules by cross-pairing
 CC the VH and VL domains from the 2 scFvs with different antigen recognition
 CC (B7.1/B7.2 and B7.12/B7.12). The invention relates to novel molecules,
 CC including diabodies, which can cross-link and/or cross-react with the
 CC costimulatory molecules B7.1 and B7.2 expressed on professional antigen-
 CC presenting cells, leading to the inhibition of antigen-specific T cell
 CC activation. Methods are provided for the production of such B7-binding
 CC molecules, and for their use in the treatment or prevention of diseases
 CC of the immune system, in particular graft rejection, graft versus host
 CC disease, allergy and autoimmune diseases (claimed)

XX Sequence 268 AA;

Query Match 85.2%; Score 69; DB 2; Length 268;

Best Local Similarity 82.4%; Pred. No. 0.0032; Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSSQSVFSSSQKNTLA 17
 ||||| :||:|||||
 Db 173 KSSQSVLYSSNQKNTLA 189

RESULT 39

AAW90228 AAW90228 standard; protein; 268 AA.

AC AAW90228;

DT 10-MAY-1999 (first entry)

DE Anti-B7.1/anti-B7.2 bispecific triabody II.

XX B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2; CD86;

KM T cell activation; inhibitor; graft versus host disease;

KM transplant rejection; allograft rejection; autoimmune disease; allergy;

KM therapy; human; triabody; antibody; B7-24; 1G10.

XX Mus sp.

OS Synthetic.

OS Chimeric.

XX Key

FT Peptide

FT Region

FT Peptide

FT Peptide

FT Peptide

FT Peptide

FT Peptide

FT Peptide

FT Peptide

FT Peptide

FT Peptide

FT Peptide

FT Peptide

XX This polypeptide comprises a bispecific triabody composed of the VH
 CC region of anti-B7.1 monoclonal antibody (Mab) B7-24 joined to the VL
 CC region of anti-B7.2 Mab 1G10. A triabody is a mono- a bi- or a
 CC trispecific molecule recognising simultaneously e.g. two B7.2 and one
 CC B7.1 molecules. It has a rigid structure that prevents simultaneous
 CC binding to the 3 targets. Each antigen-binding site is formed by pairing
 CC of one VH and one VL domain from the same or from two different
 CC polypeptides. The invention relates to novel molecules, including
 CC triabodies, which can cross-link and/or cross-react with the
 CC costimulatory molecules B7.1 and B7.2 expressed on professional antigen-
 CC presenting cells, leading to the inhibition of antigen-specific T cell
 CC activation. Methods are provided for the production of such B7-binding
 CC molecules, and for their use in the treatment or prevention of diseases
 CC of the immune system, in particular graft rejection, graft versus host
 CC disease, allergy and autoimmune diseases (claimed)

XX Sequence 268 AA;

Query Match 85.2%; Score 69; DB 2; Length 268;

Best Local Similarity 82.4%; Pred. No. 0.0032; Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSSQSVFSSSQKNTLA 17
 ||||| :||:|||||
 Db 179 KSSQSVLYSSNQKNTLA 195

RESULT 40

AAW90224 AAW90224 standard; protein; 273 AA.

AC AAW90224;

DT 10-MAY-1999 (first entry)

DE Anti-B7.1/anti-B7.2 bispecific diabody II.

XX B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2; CD86;

KM T cell activation; inhibitor; graft versus host disease;

KM transplant rejection; allograft rejection; autoimmune disease; allergy;

KM therapy; human; diabody; antibody; B7-24; 1G10.

XX Mus sp.

OS Synthetic.

OS Chimeric.

XX Key

FT Peptide

FT Region

FT Peptide

FT Peptide

FT Peptide

FT Peptide

FT Peptide

FT Peptide

FT Peptide

FT Peptide

FT Peptide

FT Peptide

FT Peptide

```
XX New molecules which bind B7.1 and B7.2 - useful to prevent and treat
PT immune diseases including allograft rejection.
PS Example 7.2; Fig 30; 182pp; English.
XX This polypeptide comprises a bispecific diabody composed of the VH region
CC of anti-B7.1 monoclonal antibody (Mab) B7-24 joined via a short, flexible
CC linker to the VL region of anti-B7.2 Mab 1G10. Mono- or bispecific
CC bivalent molecules are generated by shortening the flexible linker
CC sequence between the VH and VL of the anti-B7.1 scFv B7-24, the anti-B7.2
CC scFv 1G10 and the scFv molecule with dual specificity for B7.1 and B7.2
CC (B7.12) to 5-10 residues, and for bispecific molecules by cross-pairing
CC the VH and VL domains from the 2 scFvs with different antigen recognition
CC (B7.1/B7.2 and B7.12/B7.12). The invention relates to novel molecules,
CC including diabodies, which can cross-link and/or cross-react with the
CC costimulatory molecules B7.1 and B7.2 expressed on professional antigen-
CC presenting cells, leading to the inhibition of antigen- specific T cell
CC activation. Methods are provided for the production of such B7-binding
CC molecules, and for their use in the treatment or prevention of such B7-binding
CC of the immune system, in particular graft rejection, graft versus host
CC disease, allergy and autoimmune diseases (claimed)
XX
SQ Sequence 273 AA;
Query Match 85.2%; Score 69; DB 2; Length 273;
Best Local Similarity 82.4%; Pred. No. 0.0032; Mismatches 1; Indels 0; Gaps 0;
Matches 14; Conservative 2;
QY 1 KSSQSVFFSSQKNYLA 17
Db 184 KSSQSVLYSSNQKNYLA 200
RESULT 41
AAW11507
ID AAW11507 standard; protein; 301 AA.
XX
AC AAW11507;
XX
DT 24-SEP-1997 (first entry)
XX
DE Single chain, humanised anti-Fc gamma RI antibody H22.
XX
KM Humanised antibody; anti-Fc receptor; H22; bifunctional; bispecific;
KW fusion protein; chimera; carcinoembryonic antigen; CEA.
XX
OS Mus musculus.
OS Homo sapiens.
OS Synthetic.
OS Chimeric.
XX
XX Key Location/Qualifiers
FH 1..19
FT /label= signal_peptide
FT 20..139
FT /label= VH
FT /note= "H22 heavy chain variable region"
FT Region 140..154
FT /label= linker
FT 155..266
FT /label= VL
FT /note= "H22 light chain variable domain"
FT 267..281
FT /label= linker
FT 282..292
FT /label= c-myc_tag
FT 296..301
FT /label= His-6_tail
FT /note= "6 histidine residues"
XX
XX WO9640789-A1.
```

```
PD 19-DEC-1996.
XX
XX 07-JUN-1996; 96WO-US009988.
XX
PR 07-JUN-1995; 95US-00484172.
XX
XX (MEDA-) MEDAREX INC.
XX
PI Deo YM, Goldstein J, Graziano R, Somasundaram C;
XX
DR WPI; 1997-052242/05.
DR N-PSDB; AAT58129.
XX
PT Recombinant, multi-specific anti-Fc receptor antibody molecules - also
PT comprise an anti-target portion, used for the treatment of cancer,
PT autoimmune disease and pathogenic infection.
XX
PS Example 8; Fig 39; 115pp; English.
XX
CC A mammalian expression construct encoding a single chain antibody having
CC binding specificity for Fc gamma RI, derived from the humanised anti-Fc
CC gamma RI monoclonal antibody H22 was prepared (see AAT58129). A
CC bispecific single chain polypeptide was produced by fusing the H22 ScFv
CC to an anti-carcinoembryonic antigen (CEA) antibody. The H22-anti-CEA
CC fusion protein was shown to bind both Fc gamma RI and CEA
XX
SQ Sequence 301 AA;
Query Match 85.2%; Score 69; DB 2; Length 301;
Best Local Similarity 82.4%; Pred. No. 0.0036; Mismatches 1; Indels 0; Gaps 0;
Matches 14; Conservative 2;
QY 1 KSSQSVFFSSQKNYLA 17
Db 178 KSSQSVLYSSNQKNYLA 194
RESULT 42
AAW73217
ID AAW73217 standard; protein; 301 AA.
XX
AC AAW73217;
XX
DT 25-JAN-1999 (first entry)
XX
DE Multispecific single chain antibody H22.
XX
KM Multispecific single chain antibody; antibody H22; tumour cell; therapy;
KW antibody-dependent cellular cytotoxicity; ADCC; HER 2/neu; infection;
KW epidermal growth factor receptor; breast cancer; ovarian cancer.
XX
XX Homo sapiens.
XX
XX US5837243-A.
XX
PD 17-NOV-1998.
XX
PF 07-JUN-1996; 96US-00661052.
XX
PR 07-JUN-1995; 95US-00484172.
XX
PA (MEDA-) MEDAREX INC.
XX
PI Somasundaram C, Graziano R, Deo YM, Goldstein J;
XX
XX WPI; 1999-023374/02.
XX
DR N-PSDB; AAV08175.
XX
PT Specific killing of tumour cells - using a multi-specific molecule
PT comprising an anti-Fc receptor antibody and a portion which binds to a
PT target cell.
XX
XX Claim 14; Fig 39; 57pp; English.
XX
```

XX This sequence is the multispecific single chain antibody designated H22.
 CC The antibody can be used in the method of the invention for inducing
 CC antibody-dependent cellular cytotoxicity (ADCC) against a tumour cell
 CC which is characterised by overexpression of HER 2/neu or epidermal growth
 CC factor receptor (EGFR), comprises contacting the tumour cell with a
 CC multispecific protein molecule (preferably a single chain antibody)
 CC comprising: (a) an anti-Fc receptor antibody or an antigen binding
 CC fragment; (b) a portion which binds to HER 2/neu; and (c) a portion which
 CC binds to EGFR. The method can be used for treating cancers especially
 CC breast cancer or ovarian cancer. The multispecific antibody can also be
 CC administered prophylactically to vaccinate a subject against infection by
 CC a target cell
 CC
 XX Sequence 301 AA;
 SQ
 Query Match 85.2%; Score 69; DB 2; Length 301;
 Best Local Similarity 82.4%; Pred. No. 0.0036;
 Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 KSSQSVFFSSSQKNYLA 17
 |||||:|||||
 Db 178 KSSQSVLYSSNQKNYLA 194
 RESULT 43
 AAB61959
 ID AAB61959 standard; protein; 301 AA.
 AC AAB61959;
 XX
 DT 14-MAY-2001 (first entry)
 XX
 DE Single chain humanised anti-Fc gamma RI antibody H22.
 XX
 DE Fc alpha receptor; epidermal growth factor; EGF; HER2 receptor; tumour;
 KW immune thrombocytopenia purpura; systemic lupus erythematosus; vaccine;
 KW cytostatic; antiviral; protozoaside; antifungal; immunosuppressive;
 KW antiinflammatory; dermatological; hemostatic.
 XX
 OS Mus musculus.
 XX
 PN WO200109186-A2.
 PD
 XX 08-FEB-2001.
 PD
 XX 25-JUL-2000; 2000WO-US020158.
 PF
 XX 30-JUL-1999; 99US-00364088.
 PR
 XX 10-MAR-2000; 2000US-00523279.
 PR
 XX (MEDA-) MEDAREX INC.
 PA
 XX Deo YM, Goldstein J, Graziano R, Keler T;
 PI
 XX WPI; 2001-123318/13.
 DR
 XX N-PSDB; AAC85182.
 DR
 XX Bispecific molecule comprising specific binding sites for an Fc-alpha
 PT receptor and an epidermal growth factor, used to induce effector cell
 PT killing of tumor cells.
 PT
 XX Example 8; Fig 39A-C; 183pp; English.
 PS
 XX The invention relates to a bispecific molecule (I) comprising specific
 CC binding sites for an Fc alpha receptor and an epidermal growth factor
 CC (EGF) receptor. It also provides bispecific molecule (II) comprising a
 CC human antibody, preferably a single chain antibody, specific for an
 CC Fc alpha receptor, linked to EGF; a bispecific molecule (III) comprising
 CC specific binding sites for an Fc alpha receptor and a HER2 receptor; (3) a
 CC multispecific molecule (IV) comprising specific binding sites for Fc alpha
 CC receptor, HER2 receptor and EGF receptor; (4) a multispecific molecule
 CC (V) comprising a human antibody specific for an Fc alpha receptor, a human

CC antibody specific for a HER2 receptor, and EGF. (I)-(V) can be used for
 CC inducing effector cell killing of tumour cells. The molecules can be used
 CC to treat or prevent viral, protozoal, or fungal infections, or autoimmune
 CC diseases such as immune thrombocytopenia purpura and systemic lupus
 CC erythematosus. The present sequence represents the amino acid sequence of
 CC a single chain humanised anti-Fc gamma RI antibody H22
 CC
 XX Sequence 301 AA;
 SQ
 Query Match 85.2%; Score 69; DB 4; Length 301;
 Best Local Similarity 82.4%; Pred. No. 0.0036;
 Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 KSSQSVFFSSSQKNYLA 17
 |||||:|||||
 Db 178 KSSQSVLYSSNQKNYLA 194
 RESULT 44
 AAB85454
 ID AAB85454 standard; protein; 301 AA.
 AC AAB85454;
 XX
 DT 25-SEP-2001 (first entry)
 XX
 DE Single chain humanised anti-Fc gamma RI antibody sequence.
 XX
 DE HER 2/neu; epidermal growth factor receptor; EGFR; multispecific protein;
 KW Fc receptor; FcR; tumor cell; breast; cancer; sarcoma; carcinoma; HIV;
 KW pathogenic; Toxoplasma gondii; candidiasis; systemic lupus; cytostatic;
 KW immune thrombocytopenia purpura; immunosuppressive; antiviral;
 KW antifungal; antiprotozoal.
 XX
 XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT /note= "signal sequence"
 FT Protein 20..139
 FT /note= "H22 Vh"
 FT Peptide 140..154
 FT /note= "linker"
 FT Peptide 155..266
 FT /note= "H22 V1"
 FT Peptide 267..281
 FT /note= "linker"
 FT Peptide 282..292
 FT /note= "C-mys tag"
 FT Peptide 296..301
 FT /note= "His-6 tail"
 FT
 XX US6270765-B1.
 PN
 XX 07-AUG-2001.
 PD
 XX 06-NOV-1998; 98US-00188082.
 PE
 XX 07-JUN-1995; 95US-00484172.
 PR
 XX 07-JUN-1996; 96US-00661052.
 PR
 XX (MEDA-) MEDAREX INC.
 PA
 XX Deo YM, Goldstein J, Graziano R, Somasundaram C;
 PI
 XX WPI; 2001-475189/51.
 DR
 XX N-PSDB; AAH23382.
 DR
 XX Inducing killing of tumor cells which expresses HER 2/neu or epidermal
 PT growth factor receptor (EGFR) by contacting the cell with multispecific
 PT proteins comprising an anti-Fc receptor, -Her 2/neu or -EGFR antibody,
 PT useful for treating cancer.
 FT

PS Example 8; Fig 39A-B; 57bp; English.
XX
CC The invention relates to a new method for inducing killing of a tumor
CC cell which expresses HER 2/neu or epidermal growth factor receptor
CC (EGFR). The method comprises contacting the tumor cell with a
CC multispecific protein comprising a component, preferably an antibody,
CC which binds to an Fc receptor (FcR), Her 2/neu or EGFR. The method is
CC useful for inducing killing of a tumor cell from breast cancer, sarcoma,
CC carcinoma, or ovarian cancer. Specific multispecific proteins can also be
CC administered to a subject to treat or prevent other diseases or
CC conditions, including pathogenic infections (e.g., viral (such as HIV)),
CC protozoan infections (such as Toxoplasma gondii), fungal infections (such
CC as candidiasis), and an autoimmunity (e.g. immune thrombocytopenia
CC purpura and systemic lupus). The present sequence represents the amino
CC acid sequence of a single chain humanised anti-FcgammaRI antibody H22
CC encoded by construct 225
XX
SQ Sequence 301 AA;
Query Match 85.2%; Score 69; DB 4; Length 301;
Best Local Similarity 82.4%; Pred. No. 0.0036; Mismatches 1; Indels 0; Gaps 0;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 1 KSSQSVFFSSQKNYLA 17
|||:|:|:|:|
Db 178 KSSQSVLYSSNQKNYLA 194
RESULT 45
AAy06272
ID AAY06272 standard; protein; 352 AA.
XX
AC AAY06272;
XX
DT 23-AUG-1999 (first entry)
XX
DE Anti-Fc gamma receptor scFv H22-PDGR-R TM fusion.
XX
KW Single chain antibody; scFv; H22; IgG receptor; Fc receptor;
KW Fc gamma receptor; platelet derived growth factor receptor;
KW antibody engineering; cell surface expression; therapy; cancer; tumour;
KW vaccine; human.
XX
OS Homo sapiens,
OS Synthetic.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Domain 1..21
FT /note= "Ig K-chain SP"
FT Peptide 22..30
FT /note= "HA epitope"
FT Domain 38..149
FT /note= "H22 VL"
FT Peptide 150..166
FT /note= "linker"
FT Domain 167..286
FT /note= "H22 VH"
FT Peptide 293..302
FT /note= "Myc epitope"
FT Domain 303..352
FT /note= "PDGFR transmembrane domain"
XX
FN WO9928349-A2.
XX
PD 10-JUN-1999.
XX
PF 02-DEC-1998; 98WO-US025556.
XX
PR 02-DEC-1997; 97US-0067232P.
XX
PA (MEDA-) MEDAREX INC.
XX

PI Keller T, Goldstein J, Graziano R, Deo YW;
XX
XX WPI; 1999-371099/31.
DR N-PSDB; AAX58935.
XX
PT Cells expressing anti-Fc receptor binding components.
XX
PS Example 1; Fig 4A-E; 68bp; English.
XX
CC This sequence represents a fusion protein comprising anti-Fc gamma
CC receptor antibody H22 sfv and the transmembrane domain of platelet
CC derived growth factor receptor (PDGFR-TM). H22 is a humanised monoclonal
CC antibody produced by cell line HA022CL1 (ATCC CRL 11177). The fusion
CC protein is encoded by expression vector pJG717 (see AAX58935). The H22
CC sfv was expressed on the surface of murine tumour cells transformed with
CC this vector. These transformed tumour cells, when in the presence of
CC macrophages, engaged and activated Fc gamma RI, resulting in specific
CC lysis of the tumour cells. Induction of cytokines by H22-TM transformed
CC tumour cells was also demonstrated. This is an example of cells of the
CC invention that have been transformed to express on their surface a
CC component which binds to an Fc receptor of an effector cell. The
CC transformed cell is targeted to an effector cell via the Fc binding
CC component, and can be used as a vehicle to increase an effector cell-
CC mediated immune response, such as cell lysis and phagocytosis, against an
CC antigen associated with the cell. The transformed cells are used to treat
CC cancer and infectious diseases or used as vaccines. The method allows for
CC killing of target cells without targeting any particular antigen on the
CC cell. This is advantageous since many tumour cells and other target cells
CC do not have defined antigens for targeting
XX
SQ Sequence 352 AA;
Query Match 85.2%; Score 69; DB 2; Length 352;
Best Local Similarity 82.4%; Pred. No. 0.0043; Mismatches 1; Indels 0; Gaps 0;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 1 KSSQSVFFSSQKNYLA 17
|||:|:|:|:|
Db 61 KSSQSVLYSSNQKNYLA 77
RESULT 46
AAW11508
ID AAW11508 standard; protein; 553 AA.
XX
AC AAW11508;
XX
DT 24-SEP-1997 (first entry)
XX
DE Single chain anti-Fc gamma RI antibody fused to anti-CEA antibody.
XX
KW Humanised antibody; anti-Fc receptor; H22; bifunctional; bispecific;
KW fusion protein; chimera; carcinoembryonic antigen; CEA.
XX
OS Mus musculus.
OS Homo sapiens.
OS Synthetic.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT /label= signal_peptide
FT Domain 20..139
FT /label= H22 VH
FT /note= "Anti-Fc gamma RI antibody H22 heavy chain
FT variable domain"
FT Region 140..154
FT /label= linker
FT Domain 155..266
FT /label= H22 VL
FT /note= "Anti-Fc gamma RI antibody H22 light chain
FT variable domain"
FT Region 267..276
XX

Accession	Region	Label	Score	DB	Length	Indels	Gaps
FT	Domain	/label= linker	277.396				
FT	Domain	/label= MFE-23_VH					
FT	Domain	/note= "Anti-CEA antibody MFE-23 heavy chain variable domain"					
FT	Region	/label= linker	397.411				
FT	Region	/label= linker	412.520				
FT	Domain	/label= MFE-23_VL					
FT	Domain	/note= "Anti-CEA antibody MFE-23 light chain variable domain"					
FT	Region	/label= linker	521.533				
FT	Peptide	/label= linker	534.544				
FT	Region	/label= C-myc_tag	548.553				
FT	Region	/label= His-6_tail					
FT	Region	/note= "6 histidine residues"					
PN	WO9640789-A1.						
XX	19-DEC-1996.						
PD	07-JUN-1996;	96WO-US009988.					
PF	07-JUN-1996;	96WO-US009988.					
PR	07-JUN-1995;	95US-00484172.					
PA	(MEDA-) MEDAREX INC.						
PI	Dec YM, Goldstein J, Graziano R, Somaundaram C;						
XX	WPI, 1997-052242/05.						
DR	N-PSDB; AAT58130.						
XX	Recombinant, multi-specific anti-Fc receptor antibody molecules - also comprise an anti-target portion, used for the treatment of cancer, autoimmune disease and pathogenic infection.						
PT	Example 8; Fig 40; 115pp; English.						
PS	A mammalian expression construct encoding a single chain antibody having binding specificity for Fc gamma RI, derived from the humanised anti-Fc gamma RI monoclonal antibody H22 was prepared (see AAT58129). A bispecific single chain polypeptide was produced by fusing the H22 ScFv to an anti-carcinoembryonic antigen (CEA) antibody. The H22-anti-CEA fusion protein was shown to bind both Fc gamma RI and CEA						
CC	Sequence 553 AA;						
CC	Query Match	85.2%;	Score 69;	DB 2;	Length 553;		
CC	Best Local Similarity	82.4%;	Pred. No. 0.007;				
CC	Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;						
QY	1 KSSGSVFPSSSQKNTLA 17						
DB	178 KSSGSVLYSSNQKNTLA 194						
RESULT 47							
AAW73223							
AAW73223	standard; protein; 553 AA.						
AAW73223;							
25-JAN-1999	(first entry)						
H22-anti-CEA	antibody construct 321.						
antibody-specific	single chain antibody; antibody H22; tumour cell; therapy;						
antibody-dependent	cellular cytotoxicity; ADCC; HER 2/neu; infection;						
epidermal growth	factor receptor; breast cancer; ovarian cancer.						
Synthetic.							

```

XX  US5637243-A.
XX
XX
XX  17-NOV-1998.
XX
XX
XX  07-JUN-1996; 96US-00661052.
XX
XX
XX  07-JUN-1995; 95US-00484172.
XX
XX
XX  (MEDA-) MEDAREX INC.
XX
XX
XX  Somasundaram C, Graziano R, Deo YM, Goldstein J;
XX
XX  WPI; 1999-023374/02.
XX
XX  N-PSDB; AAV08176.
XX
XX
XX  Specific killing of tumour cells - using a multi-specific molecule
XX  comprising an anti-Fc receptor antibody and a portion which binds to a
XX  target cell.
XX
XX
XX  Example 8; Fig 40; 57pp; English.
XX
XX
XX  This sequence represents the construct 321, which is a fusion between an
XX  anti-CEA antibody and a multispecific single chain antibody designated
XX  H22. The antibody can be used in the method of the invention for inducing
XX  antibody-dependent cellular cytotoxicity (ADCC) against a tumour cell
XX  which is characterised by overexpression of HER 2/neu or epidermal growth
XX  factor receptor (EGFR), comprises contacting the tumour cell with a
XX  multispecific protein molecule (preferably a single chain antibody)
XX  comprising: (a) an anti-Fc receptor antibody or an antigen binding
XX  fragment; (b) a portion which binds to HER 2/neu; and (c) a portion which
XX  binds to EGFR. The method can be used for treating cancers especially
XX  breast cancer or ovarian cancer. The multispecific antibody can also be
XX  administered prophylactically to vaccinate a subject against infection by
XX  a target cell
XX
XX
XX  Sequence 553 AA;
XX
XX
XX  Query Match 85.2%; Score 69; DB 2; Length 553;
XX  Best Local Similarity 82.4%; Pred. No. 0.007;
XX  Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0
XX
XX  QY 1 KSSQSVFFSSSQKNYLA 17
XX  ||||| :||:|||||
XX  Db 178 KSSQSVLYSSNQKNYLA 194
XX
XX
XX  RESULT 48
XX  AAB61960
XX  ID AAB61960 standard; protein; 553 AA.
XX
XX  AC AAB61960;
XX
XX  DT 14-MAY-2001 (first entry)
XX
XX
XX  Bispecific single chain molecule H22-anti-CEA.
XX
XX  DE Fcalpha receptor; epidermal growth factor; EGF; HER2 receptor; tumour;
XX  KW immune thrombocytopenia purpura; systemic lupus erythematosus; vaccine;
XX  KW cyclostatic; antiviral; protozoacide; antifungal; immunosuppressive;
XX  KW antinflammatory; dermatological; hemostatic.
XX
XX  OS Mus musculus.
XX
XX  PN WO200109186-A2.
XX
XX  PD 08-FEB-2001.
XX
XX  PF 25-JUL-2000; 2000WO-US020158.
XX
XX  PR 30-JUL-1999; 99US-00364088.
XX  PR 10-MAR-2000; 2000US-00523279.
XX

```

```

PA (MEDA-) MEDAREX INC.
XX Deo YM, Goldstein J, Graziano R, Keler T;
XX WPI; 2001-123318/13.
DR N-PSDB; AAC65183.
XX Bispecific molecule comprising specific binding sites for an Fc-alpha
PT receptor and an epidermal growth factor, used to induce effector cell
PT killing of tumor cells.
XX
PS Example 8; Fig 40 A-D; 1833p; English.
XX
CC The invention relates to a bispecific molecule (I) comprising specific
CC binding sites for an Fc-alpha receptor and an epidermal growth factor
CC (EGF) receptor. It also provides bispecific molecule (II) comprising a
CC human antibody, preferably a single chain antibody, specific for an
CC Fc-alpha receptor, linked to EGF; a bispecific molecule (III) comprising
CC multiple binding sites for an Fc-alpha receptor and a HER2 receptor; (3) a
CC multispecific molecule (IV) comprising specific binding sites for Fc-alpha
CC receptor, HER2 receptor and EGF receptor; (4) a multispecific molecule
CC (V) comprising a human antibody specific for an Fc-alpha receptor, a human
CC antibody specific for a HER2 receptor, and EGF. (1)-(V) can be used for
CC inducing effector cell killing of tumour cells. The molecules can be used
CC to treat or prevent viral, protozoal, or fungal infections, or autoimmune
CC diseases such as immune thrombocytopenia purpura and systemic lupus
CC erythematosus. The present sequence represents the amino acid sequence of
CC a bispecific single chain molecule H22-anti-CEA, having one binding
CC specificity for the Fc-gamma RI and one binding specificity for CEA
XX
SQ Sequence 553 AA;

Query Match      85.2%; Score 69; DB 4; Length 553;
Best Local Similarity 82.4%; Pred. No. 0.007;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy      1 KSSQSVFSSSQKNYLA 17
        ||||| :||:|||||
Db      178 KSSQSVLYSSNQKNYLA 194

RESULT 49
AAB85455
ID AAB85455 standard; protein; 553 AA.
XX
AC AAB85455;
XX
DT 25-SEP-2001 (first entry)
XX
DE Bispecific single chain H22-anti-CEA amino acid sequence.
XX
KW HER 2/neu; epidermal growth factor receptor; EGFR; multispecific protein;
KW Fc receptor; FcR; tumor cell; breast; cancer; sarcoma; carcinoma; HIV;
KW pathogenic; Toxoplasma gondii; candidiasis; systemic lupus; cytostatic;
KW immune thrombocytopenia purpura; immunosuppressive; antiviral;
KW antifungal; antiprotozoal.
XX
XX Homo sapiens.
XX
FH Key
FT Peptide
FT /note= "signal sequence"
FT 20..139
FT Protein
FT /note= "H22 Vh"
FT 140..154
FT Peptide
FT /note= "linker"
FT 155..266
FT Peptide
FT /note= "H22 V1"
FT 267..276
FT Peptide
FT /note= "linker"
FT 277..396
FT Protein
FT /note= "MFR-23 Vh"
FT 397..411
FT Peptide

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FT /note= "linker"
FT Peptide
FT 412..520
FT /note= "MFR-23 V1"
FT 521..533
FT Peptide
FT /note= "linker"
FT 534..544
FT Peptide
FT /note= "C-mys tag"
FT 548..553
FT /note= "His-6 tail"
XX
XX US6270765-B1.
XX
XX 07-AUG-2001.
XX
XX 06-NOV-1998; 98US-00188082.
XX
XX 07-JUN-1995; 95US-00484172.
XX 07-JUN-1996; 96US-00661052.
XX
PA (MEDA-) MEDAREX INC.
XX
XX Deo YM, Goldstein J, Graziano R, Somasundaram C;
XX WPI; 2001-475189/51.
XX N-PSDB; AAH23383.
XX
XX Inducing killing of tumor cells which expresses HER 2/neu or epidermal
PT growth factor receptor (EGFR) by contacting the cell with multispecific
PT proteins comprising an anti-Fc receptor; Her 2/neu or -EGFR antibody,
PT useful for treating cancer.
XX
XX
PS Example 8; Fig 40A-C; 57pp; English.
XX
CC The invention relates to a new method for inducing killing of a tumor
CC cell which expresses HER 2/neu or epidermal growth factor receptor
CC (EGFR). The method comprises contacting the tumor cell with a
CC multispecific protein comprising a component, preferably an antibody,
CC which binds to an Fc receptor (FcR), Her 2/neu or EGFR. The method is
CC useful for inducing killing of a tumor cell from breast cancer, sarcoma,
CC carcinoma, or ovarian cancer. Specific multispecific proteins can also be
CC administered to a subject to treat or prevent other diseases or
CC conditions, including pathogenic infections (e.g., viral (such as HIV),
CC protozoan infections (such as Toxoplasma gondii), fungal infections (such
CC as candidiasis), and an autoimmunity (e.g., immune thrombocytopenia
CC purpura and systemic lupus). The present sequence represents the amino
CC acid sequence of a bispecific single chain molecule H22-anti-CEA encoded
CC by construct 321
XX
SQ Sequence 553 AA;

Query Match      85.2%; Score 69; DB 4; Length 553;
Best Local Similarity 82.4%; Pred. No. 0.007;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy      1 KSSQSVFSSSQKNYLA 17
        ||||| :||:|||||
Db      178 KSSQSVLYSSNQKNYLA 194

RESULT 50
AAW90218
ID AAW90218 standard; protein; 556 AA.
XX
AC AAW90218;
XX
DT 10-MAY-1999 (first entry)
XX
DE Bispecific tetraivalent antibody B17B1G10-B7-24H6.
XX
XX B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2; CD86;
XX T cell activation; inhibitor; graft versus host disease;
XX transplant rejection; allograft rejection; autoimmune disease; allergy;
KW therapy; human; bispecific tetraivalent antibody; B17b;

```


KW BitB1G10-B7-24H6.

Db 159 KSSQSVLYSSNQKNTLA 175

XX Mus sp.

Search completed: May 4, 2006, 12:58:13

OS Homo sapiens.

Job time : 161.111 secs

OS Synthetic.

OS Chimeric.

XX Location/Qualifiers

Key 1..120

Region /note= "VH region anti B7.2 Mab"

Peptide 121..135

Region /note= "(G4S3) flexible linker"

Region 136..248

Region /note= "VL region anti B7.2 Mab"

Region 249..259

Domain /note= "human IgG3 hinge region"

Domain 260..285

Domain /note= "helix-turn-helix dimerisation domain"

Domain 286..305

Region /note= "human IgG3 hinge domain"

Region 306..426

Peptide /note= "VH region anti B7.1 Mab"

Region 427..441

Region /note= "(G4S3) flexible linker"

Region 442..550

Peptide /note= "VL region anti B7.1 Mab"

Peptide 551..556

/note= "His6 tag"

W09858965-A2.

30-DEC-1998.

22-JUN-1998; 98MO-EP003791.

20-JUN-1997; 97EP-00870092.

(INNO-) INNOGENETICS NV.

Lorrie K, Sablon E, Buyse M, Bosman A;

WPI; 1999-105615/09.

N-PSDB; AAX01652.

New molecules which bind B7.1 and B7.2 - useful to prevent and treat

immune diseases including allograft rejection.

Example 7.1; Fig 18; 182pp; English.

This polypeptide comprises the bispecific tetravalent antibody BitB1G10-

B7-24H6. The molecule consists of 4 scFvs, i.e. 2 anti B7.1 scFvs and 2

anti B7.2 scFvs (tetravalency). One single BitB1 is a homodimer of 2

identical molecules, each containing both an anti B7.1 and anti B7.2 scFv

(bispecificity). An anti-B7.1 and anti-B7.2 scFv are linked using a

dimerisation domain (see AAW90219), which drives the homodimerisation of

the molecule. DNA (see AAX01652) encoding the BitB1 has been constructed

to allow expression of the BitB1 in transformed E. coli cells. The BitB1

cross-links, and/or cross-reacts, with the costimulatory molecules B7.1

and B7.2 that are expressed on the membrane of professional antigen-

presenting cells, leading to the inhibition of antigen-specific T cell

activation. The invention relates to such B7-binding molecules, methods

for their production, and their use for treating or preventing diseases

of the immune system, in particular graft rejection, graft versus host

disease, allergy and autoimmune diseases (claimed)

Sequence 556 AA;

Query Match 85.2%; Score 69; DB 2; Length 556;

Best Local Similarity 82.4%; Pred. NO. 0.0071;

Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

1 KSSQSVLYSSNQKNTLA 17

|||||:|:|:|

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 4, 2006, 13:00:03 ; Search time 24.2857 Seconds
(Without alignments)
67.352 Million cell updates/sec

Title: US-10-700-632-4

Perfect score: 81
Sequence: 1 KSSQSVFSSSQKNYLA 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Length	DB ID	Description
1	69	85.2	101	2 S26337	Ig light chain V r
2	69	85.2	103	2 PH1054	Ig light chain V r
3	69	85.2	111	2 G30502	Ig kappa chain V r
4	68	84.0	240	2 S06084	Ig kappa chain pre
5	67	82.7	113	2 S30520	Ig kappa chain V r
6	66	81.5	112	2 S41393	Ig kappa chain V r
7	66	81.5	118	2 PT0356	Ig kappa chain V r
8	64	79.0	92	2 S37532	Ig kappa chain V r
9	64	79.0	92	2 S37533	Ig kappa chain V r
10	64	79.0	92	2 S37530	Ig kappa chain V r
11	64	79.0	92	2 S37535	Ig kappa chain V r
12	64	79.0	92	2 S37534	Ig kappa chain V r
13	64	79.0	92	2 S37529	Ig kappa chain V r
14	64	79.0	106	2 A49138	Ig kappa chain V r
15	64	79.0	113	2 S34002	Ig kappa chain V r
16	64	79.0	113	2 S34003	Ig kappa chain V r
17	64	79.0	113	2 S30523	Ig kappa chain V r
18	64	79.0	114	1 K4HULN	Ig kappa chain V-I
19	64	79.0	120	2 S51147	antibody light cha
20	64	79.0	121	1 K4HU	Ig kappa chain pre
21	64	79.0	133	1 K4HUT	Ig kappa chain pre
22	64	79.0	134	1 S49531	anti-Sm antibody V
23	63	77.8	96	2 G38601	Ig kappa chain V r
24	63	77.8	112	2 S09970	Ig kappa chain V-J
25	63	77.8	114	2 S44119	Ig kappa chain V-J
26	63	77.8	134	2 PC1214	Ig kappa chain pre
27	63	77.8	138	2 S26040	Ig kappa chain pre
28	62	76.5	113	2 A49260	Ig kappa chain pre
29	62	76.5	134	1 K4HUL7	Ig kappa chain pre

30	62	76.5	135	2 S38807	Ig light chain V-J
31	61	75.3	138	2 A53261	Ig kappa chain pre
32	60	74.1	97	2 A42575	Ig kappa chain V r
33	60	74.1	101	2 PH0869	Ig kappa chain V r
34	60	74.1	104	2 PH1053	Ig light chain V r
35	60	74.1	113	2 UC2270	PL7-6 antibody lig
36	59	72.8	107	2 B30535	Ig kappa chain V r
37	59	72.8	132	2 S46373	Ig kappa chain V-J
38	58	71.6	129	2 S40347	Ig kappa chain - h
39	57	70.4	112	2 PL0265	Ig kappa chain V r
40	56	69.1	105	2 C30535	Ig kappa chain V r
41	56	69.1	107	2 F30535	Ig kappa chain V r
42	56	69.1	107	2 D30535	Ig kappa chain V r
43	56	69.1	107	2 G30535	Ig kappa chain V r
44	56	69.1	108	2 G30535	Ig kappa chain V r
45	56	69.1	112	2 F30538	Ig kappa chain V r
46	56	69.1	112	2 E30538	Ig kappa chain V r
47	56	69.1	124	2 S40364	Ig kappa chain - h
48	55	67.9	92	2 S37531	Ig heavy chain V r
49	55	67.9	94	2 S20648	Ig light chain V r
50	55	67.9	109	2 S26336	Ig kappa chain V r
51	55	67.9	113	2 PL0264	Ig kappa chain V r
52	55	67.9	114	2 S44116	Ig kappa chain V-J
53	55	67.9	145	2 PL0014	Ig kappa chain pre
54	55	67.9	214	2 S68212	Ig kappa chain (Ma
55	54	66.7	102	2 A34153	Ig kappa chain V-I
56	54	66.7	102	2 B34153	Ig kappa chain V-I
57	52	64.2	113	2 PL0263	Ig kappa chain V r
58	52	64.2	220	2 A31790	Ig kappa chain V r
59	52	63.0	81	2 PH1048	Ig light chain V r
60	51	63.0	101	2 PH1046	Ig light chain V r
61	51	63.0	103	2 PH1047	Ig light chain V r
62	51	63.0	103	2 PH1050	Ig light chain V r
63	51	63.0	104	2 PH1101	Ig light chain V r
64	51	63.0	104	2 PH1102	Ig light chain V r
65	51	63.0	104	2 PH1103	Ig light chain V r
66	51	63.0	104	2 S41103	Ig light chain V r
67	51	63.0	112	2 S41103	Ig kappa chain V-J
68	51	63.0	113	2 PT0408	Ig light chain V r
69	51	63.0	113	2 PT0407	Ig light chain V r
70	51	63.0	120	2 G33932	Ig kappa chain pre
71	51	63.0	134	2 S21917	Ig kappa chain V r
72	46	56.8	103	2 PH1051	Ig light chain V r
73	46	56.8	103	2 PH1052	Ig light chain V r
74	46	56.8	133	2 S03304	Ig kappa chain pre
75	45	55.6	111	2 UB0241	Ig kappa chain V r
76	45	55.6	216	2 T23132	Ig kappa chain Am3
77	44	54.3	497	2 D71361	probable alpha-amy
78	42	51.9	621	2 T15859	probable alpha-amy
79	42	51.9	621	2 B96908	hypothetical prote
80	41	50.6	232	2 S38329	(FS) similar to AB
81	41	50.6	527	2 T18680	probable ATP-depen
82	40.5	50.0	294	2 A71490	hypothetical prote
83	40.5	50.0	400	2 G86349	aromatic-amino-aci
84	40.5	50.0	203	2 S54622	hypothetical prote
85	40	49.4	527	2 S74008	24.1K protein homo
86	40	49.4	292	2 F70102	hypothetical prote
87	40	49.4	347	2 S19974	DNA-binding protei
88	39.5	48.8	98	2 F38601	Ig kappa chain V r
89	39	48.1	104	2 S70890	Ig kappa chain V r
90	39	48.1	136	1 D85915	hypothetical prote
91	39	48.1	136	2 A91071	hypothetical prote
92	39	48.1	140	2 T10589	hypothetical prote
93	39	48.1	140	2 C64434	hypothetical prote
94	39	48.1	337	2 T50801	hypothetical prote
95	39	48.1	517	2 A64697	conserved hypotnet
96	39	48.1	535	2 A71823	hypothetical prote
97	39	48.1	553	2 C71826	hypothetical prote
98	39	48.1	972	2 T22762	hypothetical prote
99	39	48.1	1049	2 A61195	probable heat shoc
100	38.5	47.5	304	2 PT0409	Ig light chain V r
101	38	46.9	113	2 A49137	Ig kappa chain V r
102	38	46.9	136	2 A49137	Ig kappa chain V r

103	38	46.9	137	2	T1939	MHC class II I-A-b
104	38	46.9	141	2	H27577	T cell receptor be
105	38	46.9	249	2	H97161	cell division sept
106	38	46.9	322	2	B84635	hypothetical prote
107	38	46.9	336	2	A64378	hypothetical prote
108	38	46.9	368	2	B88065	protein T16Al.8 fi
109	38	46.9	456	2	T19817	hypothetical prote
110	38	46.9	457	2	T04444	cytochrome P450 -
111	38	46.9	533	2	E86207	hypothetical prote
112	38	46.9	757	2	T16609	hypothetical prote
113	38	46.9	996	2	AG2366	hypothetical prote
114	38	46.9	1241	2	H84486	probable helicase
115	37	45.7	95	2	A83715	hypothetical prote
116	37	45.7	126	2	T38715	very hypothetical
117	37	45.7	173	2	A71872	hypothetical prote
118	37	45.7	266	2	D90131	hypothetical prote
119	37	45.7	304	2	A11552	probable heat shoc
120	37	45.7	398	2	S29819	serpin - barley
121	37	45.7	399	1	DXBHZ	protein Z4 - barle
122	37	45.7	402	2	E86038	probable LPS biosy
123	37	45.7	402	2	D91191	lipid A-core surfa
124	37	45.7	453	2	AF2401	cytochrome P450 f1
125	37	45.7	478	1	SGHUV	vitronectin precur
126	37	45.7	490	2	E71486	glucose s/t prote
127	37	45.7	612	2	I64241	probable DNA-direc
128	37	45.7	959	2	T37263	probable GTPase ac
129	37	45.7	1031	2	T38411	probable membrane
130	37	45.7	1071	2	S48378	kinesin-related pr
131	37	45.7	1111	1	A42640	cyclic beta 1-2 gl
132	37	45.7	2831	2	T31419	cellobiose-phospho
133	37	45.7	2867	2	AG3481	homeotic protein z
134	37	45.7	3005	2	S33642	Ig kappa chain V-1
135	36.5	45.1	124	2	S03876	Ig kappa chain V r
136	36	44.4	105	2	A10534	hypothetical CDS 1
137	36	44.4	114	2	A11356	insulin-related pr
138	36	44.4	145	2	S43224	hypothetical prote
139	36	44.4	258	2	G84824	lectin light chain
140	36	44.4	278	2	A49505	hypothetical prote
141	36	44.4	342	2	T22192	hypothetical prote
142	36	44.4	343	2	A64513	hypothetical prote
143	36	44.4	397	2	T06183	serpin - barley
144	36	44.4	405	2	F81373	hypothetical prote
145	36	44.4	408	2	G81373	hypothetical prote
146	36	44.4	428	2	T37560	hypothetical prote
147	36	44.4	455	2	H84955	UDP-N-acetyluramo
148	36	44.4	468	2	B75053	dinf related PAB14
149	36	44.4	472	2	C71172	hypothetical prote
150	36	44.4	516	2	S34525	hypothetical prote
151	36	44.4	543	2	H86739	hypothetical prote
152	36	44.4	562	2	A96773	hypothetical prote
153	36	44.4	566	2	T15866	hypothetical prote
154	36	44.4	699	2	T12667	NADH2 dehydrogenas
155	36	44.4	746	2	T13678	NADH2 dehydrogenas
156	36	44.4	763	2	AE2443	penicillin-binding
157	36	44.4	805	2	T40739	rm3-pif1 helicase
158	36	44.4	805	2	T47241	RRM3/Pif1 helicase
159	36	44.4	823	2	C81739	conserved hypotet
160	36	44.4	876	2	B72856	late expression fa
161	36	44.4	895	2	T32374	hypothetical prote
162	36	44.4	1039	2	A34269	integrin alpha-2b
163	36	44.4	1127	2	T32404	hypothetical prote
164	36	44.4	1277	2	T30532	neural cell adhesi
165	36	44.4	1360	2	T34302	cell polarity prot
166	36	44.4	1452	2	T17157	Cl2Aa protein - ra
167	36	44.4	1467	2	T17160	Cl2BA protein - ra
168	36	44.4	1714	2	E71609	Ser/thr protein ki
169	36	44.4	1817	2	H71611	probably secreted
170	36	44.4	3413	2	T17467	ifamycin polyketi
171	35	43.2	116	2	F81031	protein-export mem
172	35	43.2	165	2	D86526	hypothetical prote
173	35	43.2	165	2	F72097	hypothetical prote
174	35	43.2	193	2	AE1561	weakly molybdopter
175	35	43.2	196	2	AD0004	conserved hypotet
176	35	43.2	176	2	E91064	chaperone-like pro
177	35	43.2	177	2	A85909	probable chaperone
178	35	43.2	178	2	A86761	competence chaperone
179	35	43.2	216	2	T23318	hypothetical prote
180	35	43.2	218	2	T01076	transcription fact
181	35	43.2	238	2	JC1124	33K protein - Chlo
182	35	43.2	238	2	H89830	hypothetical prote
183	35	43.2	238	2	A12178	hypothetical prote
184	35	43.2	247	2	T26045	hypothetical prote
185	35	43.2	262	2	D90136	hypothetical prote
186	35	43.2	276	2	G69627	cell-division prot
187	35	43.2	292	2	E87146	probable hydrolase
188	35	43.2	304	2	B85070	hypothetical prote
189	35	43.2	328	2	C96612	hypothetical prote
190	35	43.2	352	2	C96583	hypothetical prote
191	35	43.2	366	2	A95862	hypothetical prote
192	35	43.2	367	2	B82897	hypothetical prote
193	35	43.2	393	2	S50486	hypothetical prote
194	35	43.2	399	2	T28913	cut repeat and hom
195	35	43.2	429	2	T15303	hypothetical prote
196	35	43.2	431	2	T09048	probable mannan en
197	35	43.2	437	2	T21518	kyurenine-oxogluc
198	35	43.2	439	2	F96592	probable zinc fing
199	35	43.2	445	1	RSBSMT	probable site-spec
200	35	43.2	445	2	B89783	hypothetical prote
201	35	43.2	462	2	S76693	hypothetical prote
202	35	43.2	494	2	S67166	PAC1 protein - yea
203	35	43.2	495	2	S30838	hypothetical prote
204	35	43.2	518	2	F85856	hypothetical prote
205	35	43.2	518	2	D91012	hypothetical prote
206	35	43.2	518	2	G64986	hypothetical prote
207	35	43.2	530	2	F96491	hypothetical prote
208	35	43.2	573	2	E90560	probable membrane
209	35	43.2	747	2	A71440	hypothetical prote
210	35	43.2	747	2	H82943	hypothetical prote
211	35	43.2	835	2	JC6140	cell surface-assoc
212	35	43.2	870	2	AB0570	outer membrane uah
213	35	43.2	887	2	T03939	potassium channel
214	35	43.2	913	2	T18503	hypothetical prote
215	35	43.2	953	2	S54478	probable membrane
216	35	43.2	978	2	T50221	put polyprotein -
217	35	43.2	982	2	S00954	cul1 protein - fi
218	35	43.2	997	2	T43523	DNA repair protein
219	35	43.2	1196	2	S35994	SIL protein - huma
220	35	43.2	1287	2	A41685	protein-tyrosine k
221	35	43.2	1368	2	T16287	rhnd protein precu
222	35	43.2	1426	2	H64780	hypothetical prote
223	35	43.2	1435	2	S59384	hypothetical prote
224	35	43.2	1691	2	T15564	hypothetical prote
225	35	43.2	2489	2	S59782	probable membrane
226	35	43.2	3216	2	C90538	hypothetical prote
227	35	43.2	109	2	F44151	Ig kappa chain V r
228	34.5	42.6	302	2	F90526	hypothetical prote
229	34.5	42.6	397	2	C38888	COI intron 10 prot
230	34.5	42.6	497	2	F71472	cysteine-tRNA liga
231	34.5	42.6	553	1	ORECM4	aspartate chemorec
232	34.5	42.6	553	2	H85801	hypothetical prote
233	34.5	42.6	553	2	D90953	metmyl-accepting c
234	34.5	42.6	750	2	T37829	ATP synthase chain
235	34.5	42.6	96	2	T39503	hypothetical prote
236	34	42.0	116	2	S50805	hypothetical prote
237	34	42.0	118	2	D72524	hypothetical prote
238	34	42.0	124	2	D97512	hypothetical prote
239	34	42.0	131	2	S10863	T-cell receptor be
240	34	42.0	136	1	RWMSLB	aspartate carboxamoy
241	34	42.0	155	2	AB2067	flagellar basal-bo
242	34	42.0	173	2	AB3648	40S ribosomal prot
243	34	42.0	187	2	T49491	hypothetical prote
244	34	42.0	219	2	F90103	hypothetical prote
245	34	42.0	223	2	AF1345	hypothetical prote
246	34	42.0	226	2	AB6316	protein T10022.3 l
247	34	42.0	249	2	T52142	RING finger protei
248	34	42.0				

249	34	42.0	252	2	E86576	CT481 hypothetical	322	34	42.0	5005	2	P82884	hypothetical prote
250	34	42.0	252	2	F72047	conserved hypothet	323	33.5	41.4	121	2	S40371	Ig kappa chain - h
251	34	42.0	257	2	E71450	hypothetical prote	324	33.5	41.4	258	2	A97991	hypothetical prote
252	34	42.0	272	2	T24709	hypothetical prote	325	33.5	41.4	258	2	E95121	phosphoesterase, p
253	34	42.0	273	2	S57766	diocorin class A	326	33.5	41.4	358	2	S45911	hypothetical prote
254	34	42.0	273	2	B71355	probable ribosomal	327	33.5	41.4	1139	1	E64234	cytochrome-c-acc
255	34	42.0	278	2	D96513	unknown protein, 6	328	33	40.7	73	2	B84768	hypothetical prote
256	34	42.0	286	2	E82202	hypothetical prote	329	33	40.7	92	2	G86731	exodeoxyribonuclea
257	34	42.0	294	2	DB1430	UDP-3-O-[3-hydroxy	330	33	40.7	104	2	C30534	Ig kappa chain V r
258	34	42.0	311	2	G64238	hypothetical prote	331	33	40.7	122	1	RNBY29	DNA-directed RNA p
259	34	42.0	332	2	B90522	hypothetical prote	332	33	40.7	123	2	S64368	probable membrane
260	34	42.0	350	2	G95097	lipoprotein [limpo	333	33	40.7	127	2	AE1445	hypothetical prote
261	34	42.0	364	2	H71440	hypothetical prote	334	33	40.7	133	2	S74640	hypothetical prote
262	34	42.0	372	2	S44858	hypothetical prote	335	33	40.7	136	2	AF0841	Nrd1 protein [limo
263	34	42.0	374	2	C97965	conserved hypothet	336	33	40.7	142	2	A11197	hypothetical prote
264	34	42.0	379	2	T44360	transcription acti	337	33	40.7	145	2	AB7574	hypothetical prote
265	34	42.0	380	2	T04343	L-ascorbate oxidas	338	33	40.7	146	2	B97039	hypothetical prote
266	34	42.0	380	2	T09661	ascorbate oxidase	339	33	40.7	148	2	S48314	hypothetical prote
267	34	42.0	406	2	G70167	phosphoribosyl pyr	340	33	40.7	152	2	G86691	hypothetical prote
268	34	42.0	414	2	C86236	protein F14N23.3 [341	33	40.7	155	2	S58178	T cell antigen rec
269	34	42.0	418	2	S55018	CEM-1 protein - Ca	342	33	40.7	160	2	F75450	hypothetical prote
270	34	42.0	430	2	T28318	ORF MSY157 hypoth	343	33	40.7	181	2	S23418	lambiotic epide
271	34	42.0	441	2	C81344	probable periplasm	344	33	40.7	185	2	F72723	hypothetical prote
272	34	42.0	457	2	T04226	hypothetical prote	345	33	40.7	192	2	T40448	translocation prot
273	34	42.0	461	2	H90090	hypothetical prote	346	33	40.7	192	2	F71169	hypothetical prote
274	34	42.0	463	2	B81725	frumate hydratase	347	33	40.7	193	2	E95402	hypothetical prote
275	34	42.0	473	2	H84550	probable obtusifol	348	33	40.7	193	2	AE2316	hypothetical prote
276	34	42.0	475	2	A38340	66k glycoprotein p	349	33	40.7	194	2	G11038	hypothetical prote
277	34	42.0	478	2	G90514	nadh oxidase (nox)	350	33	40.7	204	2	S11460	late U3 23K protei
278	34	42.0	478	2	D66990	transmembrane prot	351	33	40.7	204	2	C97084	hypothetical prote
279	34	42.0	491	2	F87793	protein C27A12.6 [352	33	40.7	205	2	B89567	protein T08A9.7 [I
280	34	42.0	494	2	S07276	flagellin H-1A - S	353	33	40.7	207	2	B85649	hypothetical prote
281	34	42.0	506	2	S71591	aspartic proteins	354	33	40.7	207	2	A99789	hypothetical prote
282	34	42.0	508	2	T32847	hypothetical prote	355	33	40.7	212	2	H97826	hypothetical prote
283	34	42.0	513	2	T41011	hypothetical prote	356	33	40.7	214	2	T11966	lipote biosynthes
284	34	42.0	514	2	JB3137	activin receptor p	357	33	40.7	223	2	AB2339	hypothetical prote
285	34	42.0	525	2	AB3539	bacterial peptid	358	33	40.7	227	2	T21901	hypothetical prote
286	34	42.0	528	2	D97270	ATP-dependent RNA	359	33	40.7	230	2	C71337	conserved hypothet
287	34	42.0	543	2	G96570	hypothetical prote	360	33	40.7	235	2	B96565	F6D8.31 [imported]
288	34	42.0	555	2	T08869	protein p2 - Acyrt	361	33	40.7	246	1	F64148	hypothetical prote
289	34	42.0	561	2	T07649	hypothetical prote	362	33	40.7	249	2	A48325	phosphogluconate d
290	34	42.0	585	2	T50325	probable ubiqutin	363	33	40.7	253	2	T41539	probable short cna
291	34	42.0	614	2	T23790	hypothetical prote	364	33	40.7	261	2	S40210	chlorophyll a/b-i
292	34	42.0	632	2	T16128	hypothetical prote	365	33	40.7	262	2	D88196	protein XK1127.8 [
293	34	42.0	645	2	T28867	hypothetical prote	366	33	40.7	278	2	B90099	hypothetical prote
294	34	42.0	665	2	G96961	exonuclease ABC c	367	33	40.7	278	2	A42400	probable transcrip
295	34	42.0	666	2	H88098	protein F18A12.7 [368	33	40.7	281	2	A30471	hypothetical prote
296	34	42.0	710	2	S72497	oligopeptidase trans	369	33	40.7	284	2	T33860	hypothetical prote
297	34	42.0	718	2	T22329	hypothetical prote	370	33	40.7	290	2	T10104	maturase-like prot
298	34	42.0	730	2	B85013	hypothetical prote	371	33	40.7	301	2	B71330	hypothetical prote
299	34	42.0	730	2	T10539	hypothetical prote	372	33	40.7	319	2	B96715	protein FAN2.12 [I
300	34	42.0	730	2	T43317	pgl-1 protein - Ca	373	33	40.7	321	2	S62015	SOL1 protein - yea
301	34	42.0	771	2	T29177	hypothetical prote	374	33	40.7	322	2	T44020	hypothetical prote
302	34	42.0	797	2	E84642	hypothetical prote	375	33	40.7	328	2	E86837	two-component syst
303	34	42.0	803	2	G96640	hypothetical prote	376	33	40.7	328	2	T15555	G protein-coupled
304	34	42.0	802	2	B56277	DNA-directed DNA p	377	33	40.7	329	2	A30760	1-phosphatidylinos
305	34	42.0	810	1	S57196	calpain (BC 3.4.22	378	33	40.7	331	2	S74456	regulatory protein
306	34	42.0	873	2	H85134	polyubiquitin-like	379	33	40.7	331	2	AH2077	transcription regu
307	34	42.0	901	2	A48227	staiidase - Actino	380	33	40.7	333	2	T52594	squamosa promoter
308	34	42.0	913	2	S20590	exo-alpha-stalidas	381	33	40.7	335	2	T39391	mei14. RING zinc f
309	34	42.0	934	2	G86548	polymorphic outer	382	33	40.7	336	2	T24237	hypothetical prote
310	34	42.0	934	2	A72075	polymorphic membra	383	33	40.7	338	2	T23365	hypothetical prote
311	34	42.0	952	2	DB1593	hypothetical prote	384	33	40.7	358	2	DB1345	probable periplasm
312	34	42.0	964	2	T05382	hypothetical prote	385	33	40.7	363	2	S49222	adenosylmethionine
313	34	42.0	964	2	T41547	hypothetical prote	386	33	40.7	365	2	T15478	hypothetical prote
314	34	42.0	964	2	JC6027	115k outer membran	387	33	40.7	369	2	T42295	hypothetical prote
315	34	42.0	1111	2	A59000	transcription-limpo	388	33	40.7	380	2	F81449	8-amino-7-oxononan
316	34	42.0	1122	2	A97814	reverse transcript	389	33	40.7	383	2	JC2472	brain and reproduc
317	34	42.0	1191	2	AP2501	reverse transcript	390	33	40.7	387	2	B71611	hypothetical prote
318	34	42.0	1258	2	T14855	reverse transcript	391	33	40.7	392	2	DB8949	protein R09B5.12 [
319	34	42.0	1258	2	T14853	reverse transcript	392	33	40.7	397	2	T39507	kappa-caraghenase
320	34	42.0	1465	2	DB6478	protein F1504.11 [393	33	40.7	403	2	T49294	hypothetical prote
321	34	42.0	1501	2	T45623	hypothetical prote	394	33	40.7	406	2	T48103	mRNA binding prote

395	33	40.7	413	2	C69259	conserved hypotet
396	33	40.7	415	2	D95248	conserved hypotet
397	33	40.7	415	2	A98113	conserved hypotet
398	33	40.7	421	2	S33998	K421R protein - Af
399	33	40.7	425	2	D90535	DNA-damage repair
400	33	40.7	434	2	T37521	nifs homolog - fis
401	33	40.7	444	2	T20803	hypothetical prote
402	33	40.7	446	2	A95140	exodeoxyribonuclea
403	33	40.7	448	2	H96007	exodeoxyribonuclea
404	33	40.7	462	1	S31195	polysialacturonase
405	33	40.7	463	2	H71462	probable fumarate
406	33	40.7	465	2	S59426	hypothetical prote
407	33	40.7	468	2	B72351	clostritpain-relate
408	33	40.7	473	2	E64120	exodeoxyribonuclea
409	33	40.7	486	2	D70932	probable monoxigen
410	33	40.7	488	2	T09138	phosphoglycerate m
411	33	40.7	493	2	AB0588	PPR2-family transp
412	33	40.7	495	2	E70198	hypothetical prote
413	33	40.7	501	2	T43375	cell division cont
414	33	40.7	502	2	E85767	hypothetical prote
415	33	40.7	502	2	H90918	hypothetical prote
416	33	40.7	502	2	H64917	probable membrane
417	33	40.7	503	2	T40997	probable short-cha
418	33	40.7	504	2	B71620	monosaccharide tra
419	33	40.7	506	2	I38915	histidyl-tRNA synt
420	33	40.7	506	2	B87102	conserved membrane
421	33	40.7	511	2	P84968	virulence factor m
422	33	40.7	512	2	S23344	hypothetical prote
423	33	40.7	516	2	T00974	probable SP16 prot
424	33	40.7	522	2	B45268	interleukin-9 rece
425	33	40.7	530	2	JC6030	3-oxo-5-alpha-ster
426	33	40.7	545	2	C82014	probable capsule b
427	33	40.7	555	2	C71414	hypothetical prote
428	33	40.7	564	2	AD1550	conserved hypotet
429	33	40.7	564	2	E81735	heat shock protein
430	33	40.7	571	2	S58356	pept protein - Sta
431	33	40.7	581	1	A37913	seitin/threonine-s
432	33	40.7	585	2	G86200	protein F12K1.15
433	33	40.7	596	2	S61146	probable membrane
434	33	40.7	597	2	T25547	hypothetical prote
435	33	40.7	602	2	G97293	ATP-dependent Zn p
436	33	40.7	603	2	E71444	probable EREBP-4
437	33	40.7	607	2	AB0915	probable transfera
438	33	40.7	617	2	C90121	DNA repair helicase
439	33	40.7	640	2	B84887	probable SCARECROW
440	33	40.7	646	2	T23039	hypothetical prote
441	33	40.7	666	2	T44207	DNA-packaging prot
442	33	40.7	667	1	Q08EH6	12L protein - huma
443	33	40.7	673	2	T05619	hypothetical prote
444	33	40.7	676	2	T46870	protoporphyrin IX
445	33	40.7	676	2	S74635	protoporphyrin IX
446	33	40.7	684	2	G82495	probable Ca-dicarb
447	33	40.7	702	2	S48754	major surface prot
448	33	40.7	740	2	P98057	GMP diposphokinas
449	33	40.7	744	2	AB1719	exodeoxyribonuclea
450	33	40.7	766	2	AF2279	hypothetical prote
451	33	40.7	784	2	E72515	probable DNA-direc
452	33	40.7	785	2	S46672	hypothetical prote
453	33	40.7	804	2	T37821	probable dna repai
454	33	40.7	825	2	T27852	hypothetical prote
455	33	40.7	843	2	S78352	DNA-directed RNA p
456	33	40.7	858	2	S56205	probable membrane
457	33	40.7	859	2	C90088	hypothetical prote
458	33	40.7	859	2	S66827	aluminum resistan
459	33	40.7	872	2	JC7380	DNA-directed DNA p
460	33	40.7	877	2	T41794	RNA polymerase LEF
461	33	40.7	900	2	E71623	protein with DnaJ
462	33	40.7	905	2	AH2892	hypothetical prote
463	33	40.7	905	2	C97668	ABC transporter re
464	33	40.7	914	2	S46593	finger protein AZF
465	33	40.7	929	2	T34206	hypothetical prote
466	33	40.7	950	2	T25088	hypothetical prote
467	33	40.7	971	2	A70179	exodeoxyribonuclea
468	33	40.7	974	2	P96635	unknown protein, 6
469	33	40.7	981	2	T41029	probable aminoacid
470	33	40.7	986	2	T33135	hypothetical prote
471	33	40.7	989	2	T02568	hypothetical prote
472	33	40.7	1026	2	A89696	protein T21H8.1 (I
473	33	40.7	1131	2	T16217	hypothetical prote
474	33	40.7	1133	1	S43938	endopeptidase La-1
475	33	40.7	1237	2	S64385	probable membrane
476	33	40.7	1245	2	D71613	GAP domain protein
477	33	40.7	1261	2	E59430	PTPL1-associated R
478	33	40.7	1272	2	C96637	hypothetical prote
479	33	40.7	1275	2	B28096	line-1 protein ORF
480	33	40.7	1279	2	A47363	RNA helicase A - h
481	33	40.7	1317	2	T11661	phosphoribosylform
482	33	40.7	1423	2	A57570	Bloom's syndrome r
483	33	40.7	1466	2	T32791	hypothetical prote
484	33	40.7	1500	2	G84922	probable retroelem
485	33	40.7	1501	2	C84512	glucosyltransferase
486	33	40.7	1599	2	S22737	protein T04G9.1 (I
487	33	40.7	1610	2	D88451	head-activator bin
488	33	40.7	1661	2	T31330	Yeast Bem3 cell w
489	33	40.7	1679	2	T50091	cell division prot
490	33	40.7	1720	2	T07258	ritamycin polyketi
491	33	40.7	1728	2	T17466	sodium channel alp
492	33	40.7	1835	2	I54323	breast/ovarian can
493	33	40.7	1863	1	A58881	probable receptor
494	33	40.7	2062	2	G96602	myosin heavy chain
495	33	40.7	2116	2	A26655	hypothetical prote
496	33	40.7	2326	2	T29140	hypothetical prote
497	33	40.7	2539	2	B71619	probable polyketid
498	33	40.7	4451	2	G70944	polyketide synthas
499	33	40.7	4447	2	A69679	partial CDS - Caen
500	33	40.7	5107	2	T29144	probable peptide s
501	33	40.7	10797	2	T30192	Ig light chain V r
502	33	40.7	103	2	PH1056	Ig light chain V r
503	33	40.7	103	2	PH1055	hypothetical prote
504	33	40.7	1559	2	B96648	protein F09B12.1 (
505	33	40.7	573	2	T00548	hypothetical prote
506	33	40.7	637	2	D97011	sensory transducti
507	33	40.7	683	2	D97011	type I fatty acid
508	33	40.7	8243	2	T07307	hypothetical prote
509	33	40.7	8243	2	T07307	Ig kappa chain - m
510	33	40.7	66	2	S59083	hoer factor I prot
511	33	40.7	66	2	S24215	serum amyloid A -
512	33	40.7	81	2	C97126	hypothetical prote
513	33	40.7	83	2	T17951	DNA primase homolo
514	33	40.7	105	2	A34167	Nrd1 protein homol
515	33	40.7	127	2	T31159	hypothetical prote
516	33	40.7	134	2	AD0323	hypothetical prote
517	33	40.7	138	2	S74872	hypothetical prote
518	33	40.7	141	2	T34511	photosystem I chai
519	33	40.7	143	2	T16963	hypothetical prote
520	33	40.7	143	2	T29840	hypothetical prote
521	33	40.7	144	2	B86521	hypothetical prote
522	33	40.7	144	2	F72100	photosystem I chai
523	33	40.7	147	2	T15056	hypothetical prote
524	33	40.7	156	2	D96818	hypothetical prote
525	33	40.7	164	2	A97364	small protein A (I
526	33	40.7	167	2	AB3400	hypothetical prote
527	33	40.7	169	2	S07748	protein C18B10.3 (
528	33	40.7	172	2	F89103	probable ppe prote
529	33	40.7	176	2	F70738	hypothetical prote
530	33	40.7	177	2	D90449	ribosomal protein
531	33	40.7	177	2	S53852	coenzyme f390 synt
532	33	40.7	180	2	D90318	conserved hypotet
533	33	40.7	183	2	B70183	hypothetical prote
534	33	40.7	183	2	T28711	hypothetical prote
535	33	40.7	184	2	A82631	hypothetical prote
536	33	40.7	184	2	B90592	hypothetical prote
537	33	40.7	184	2	F84904	hypothetical prote
538	33	40.7	197	2	T32254	hypothetical prote
539	33	40.7	198	2	S37970	succinate dehydrog
540	33	40.7	200	2	I46051	secreted phosphopr

541	32	39.5	201	2	AD0283	[acyl-carrier-prot	614	32	39.5	386	2	E71001	probable transamin
542	32	39.5	209	2	B64168	hypothetical prote	615	32	39.5	391	1	VPXRIB	major inner capsid
543	32	39.5	212	2	T18943	hypothetical prote	616	32	39.5	395	2	T13756	NADH2 dehydrogenas
544	32	39.5	213	2	A86654	hypothetical prote	617	32	39.5	404	2	F64238	hypothetical prote
545	32	39.5	217	2	S01095	hypothetical prote	618	32	39.5	407	2	S47660	CDC2/CDC13 suppres
546	32	39.5	219	2	C69439	sugar fermentation	619	32	39.5	408	2	T32237	hypothetical prote
547	32	39.5	220	2	B81333	probable membrane	620	32	39.5	412	2	AD3641	glucose/galactose
548	32	39.5	224	2	A86734	hypothetical prote	621	32	39.5	415	2	C84709	hypothetical prote
549	32	39.5	225	2	C86869	hypothetical prote	622	32	39.5	427	2	A84826	hypothetical prote
550	32	39.5	225	2	A88991	protein C36C5.3 li	623	32	39.5	429	2	D90428	hypothetical prote
551	32	39.5	240	2	E81653	conserved hypotnet	624	32	39.5	438	2	A71531	probable ATP synth
552	32	39.5	240	2	H69932	hypothetical prote	625	32	39.5	438	2	D81687	ATP synthase, chal
553	32	39.5	242	2	B86293	F7H2.20 protein -	626	32	39.5	439	1	TVRIMC	transforming prote
554	32	39.5	249	2	T46031	hypothetical prote	627	32	39.5	441	2	A71677	tail-specific prot
555	32	39.5	250	2	AB3401	glycine hydroxymet	628	32	39.5	445	2	A88956	protein K04F1.3 li
556	32	39.5	254	2	F84977	deoxyribonuclease	629	32	39.5	448	2	A38445	EV12B protein prec
557	32	39.5	254	2	F90087	ATP-dependent Clp	630	32	39.5	448	2	C83793	hypothetical prote
558	32	39.5	261	2	I39853	glucose 1-dehydrog	631	32	39.5	450	2	S73139	hypothetical prote
559	32	39.5	262	2	AB0593	probable exported	632	32	39.5	450	2	S69942	probable membrane
560	32	39.5	263	2	B85577	hypothetical prote	633	32	39.5	459	2	JC5139	vitronectin precur
561	32	39.5	263	2	A99726	hypothetical prote	634	32	39.5	459	2	H82426	serine/threonine k
562	32	39.5	263	2	E64810	hypothetical prote	635	32	39.5	461	2	AD2088	hypothetical prote
563	32	39.5	265	2	S69335	YbgF protein precu	636	32	39.5	462	2	S54572	hypothetical prote
564	32	39.5	266	2	C95072	carcinembryonic a	637	32	39.5	462	2	S69915	sodium-phosphate t
565	32	39.5	271	2	F86171	hypothetical prote	638	32	39.5	466	2	T45269	fumarate hydratase
566	32	39.5	271	2	A97940	hypothetical prote	639	32	39.5	466	2	E90046	hypothetical prote
567	32	39.5	274	2	T07393	myb-related transc	640	32	39.5	466	2	AH1126	endo-1,4-beta-xyla
568	32	39.5	278	2	T04504	hypothetical prote	641	32	39.5	469	2	F97738	tail-specific prot
569	32	39.5	278	2	S06173	development-specif	642	32	39.5	470	2	D84658	hypothetical prote
570	32	39.5	283	2	AD1429	sugar ABC transpor	643	32	39.5	471	2	C71089	hypothetical prote
571	32	39.5	283	2	AC1803	sugar ABC transpor	644	32	39.5	472	2	T25511	hypothetical prote
572	32	39.5	288	2	G82205	chemotaxis protein	645	32	39.5	474	2	A34024	F4P protein - yeas
573	32	39.5	288	2	A48452	galactose-inhibita	646	32	39.5	483	2	A97295	fusion of Uroporph
574	32	39.5	290	2	H64591	signal peptidase I	647	32	39.5	485	2	E72115	hypothetical prote
575	32	39.5	290	2	D90075	intercellular adhe	648	32	39.5	489	2	S66564	acetyl CoA carboxy
576	32	39.5	292	2	F97082	transcription regu	649	32	39.5	493	2	A71875	hypothetical prote
577	32	39.5	294	2	T33931	hypothetical prote	650	32	39.5	495	2	S36114	pituitary adenylat
578	32	39.5	296	2	T20005	hypothetical prote	651	32	39.5	497	2	T15872	hypothetical prote
579	32	39.5	299	2	T27984	hypothetical prote	652	32	39.5	498	2	H85040	hypothetical prote
580	32	39.5	301	2	T26550	hypothetical prote	653	32	39.5	501	2	T48336	hypothetical prote
581	32	39.5	308	2	H82936	hpr serine/threoni	654	32	39.5	502	2	S77331	NADH2 dehydrogenas
582	32	39.5	317	2	A45107	DNA-directed RNA p	655	32	39.5	508	2	H98016	hypothetical prote
583	32	39.5	318	2	C71173	hypothetical prote	656	32	39.5	513	2	S47631	pituitary adenylat
584	32	39.5	319	2	T01546	hypothetical prote	657	32	39.5	514	2	AF0275	probable exported
585	32	39.5	320	2	H90478	hypothetical prote	658	32	39.5	519	2	A95149	ABC transporter. A
586	32	39.5	320	2	T38301	probable mitotic c	659	32	39.5	527	1	S69203	teichoic acid tran
587	32	39.5	321	1	J00288	cytochrome c-type	660	32	39.5	535	2	T24309	hypothetical prote
588	32	39.5	324	2	A69934	chloroethoxin reduct	661	32	39.5	541	2	T46423	hypothetical prote
589	32	39.5	327	2	F86813	xylose operon regu	662	32	39.5	547	2	E91135	probable alkaline
590	32	39.5	328	2	A13600	UDPglucose 4-epime	663	32	39.5	547	2	H85980	probable alkaline
591	32	39.5	331	2	A85430	peroxidase like pr	664	32	39.5	547	2	H65107	hypothetical 61.6
592	32	39.5	332	2	T21249	hypothetical prote	665	32	39.5	560	2	D90571	conserved hypotnet
593	32	39.5	342	2	T22018	hypothetical prote	666	32	39.5	571	2	H89866	hypothetical prote
594	32	39.5	345	2	UC4025	opioid-binding cel	667	32	39.5	581	2	S09140	coit intron protei
595	32	39.5	348	2	S73742	cell division prot	668	32	39.5	589	2	AD2263	polyhydroxyalkanoi
596	32	39.5	350	2	JN0621	G protein-coupled	669	32	39.5	590	2	I39685	glucose-6-phosphat
597	32	39.5	352	2	E89844	hypothetical prote	670	32	39.5	591	1	NUZOP	hypothetical prote
598	32	39.5	357	2	C97744	hypothetical prote	671	32	39.5	594	2	T04783	hypothetical prote
599	32	39.5	361	2	S68089	actin 2 - Arabidop	672	32	39.5	594	2	T16387	hypothetical prote
600	32	39.5	362	2	S68090	actin 8 - Arabidop	673	32	39.5	595	2	G96491	hypothetical prote
601	32	39.5	364	2	G72331	N-acetylglucosamin	674	32	39.5	596	2	D84972	ABC transporter AT
602	32	39.5	365	2	A85475	hypothetical prote	675	32	39.5	597	2	H71809	glutamine-fructose
603	32	39.5	369	2	T05013	hypothetical prote	676	32	39.5	597	2	D64711	glutamine-fructose
604	32	39.5	371	2	T48760	hypothetical prote	677	32	39.5	599	2	T48450	hypothetical prote
605	32	39.5	381	2	S33449	pituitary adenylat	678	32	39.5	615	2	A53616	lamin B receptor -
606	32	39.5	382	2	C85725	probable outer mem	679	32	39.5	617	2	S48160	metallopeptidase
607	32	39.5	382	2	F90892	probable outer mem	680	32	39.5	625	2	T01929	probable cellulase
608	32	39.5	382	2	D64904	outer membrane ush	681	32	39.5	644	2	H64675	virulence associat
609	32	39.5	383	2	H75129	flagellar P-ring p	682	32	39.5	645	2	A47081	triacylglycerol li
610	32	39.5	385	2	A84970	hypothetical prote	683	32	39.5	646	2	T19104	conserved hypotnet
611	32	39.5	385	2	G86552	conserved hypotnet	684	32	39.5	647	2	F90595	transferrin-bindin
612	32	39.5	385	2	H81595	hypothetical prote	685	32	39.5	648	2	S70907	myb-related protei
613	32	39.5	385	2	E72070	hypothetical prote	686	32	39.5	670	1	S50591	

687	32	39.5	673	2	B86437	E2K20.8 protein -	760	32	39.5	2016	2	A38195	sodium channel pro
688	32	39.5	674	2	B86388	76.0K hypothetical	761	32	39.5	2019	2	A33996	sodium channel pro
689	32	39.5	680	2	H64206	fructose-permease	762	32	39.5	2025	2	T03884	hypothetical prote
690	32	39.5	681	2	AC0455	thiamin biosynthes	763	32	39.5	2180	2	T29764	hypothetical prote
691	32	39.5	688	2	T05352	hypothetical prote	764	32	39.5	2324	1	A29924	acetyl-CoA carboxy
692	32	39.5	691	2	S46585	outward-rectifier	765	32	39.5	2339	2	S41121	acetyl-CoA carboxy
693	32	39.5	701	2	C84972	hypothetical prote	766	32	39.5	2340	2	B17104	cell surface antig
694	32	39.5	731	2	A99106	hypothetical prote	767	32	39.5	2345	1	A35578	acetyl-CoA carboxy
695	32	39.5	734	2	T13685	NADH2 dehydrogenas	768	32	39.5	2346	2	T38928	acetyl-CoA carboxy
696	32	39.5	736	2	C69451	cationic amino aci	769	32	39.5	3147	2	T21328	hypothetical prote
697	32	39.5	743	2	T47849	hypothetical prote	770	32	39.5	3225	2	I52300	hypothetical prote
698	32	39.5	750	2	HYHUN	neprilysin (EC 3.4	771	32	39.5	3259	1	A56539	giantin - human
699	32	39.5	751	1	HYRBN	neprilysin (EC 3.4	772	32	39.5	3259	1	T29165	giantin - human
700	32	39.5	751	2	AD2168	phytylchome-like p	773	32	39.5	5762	2	A41819	hypothetical prote
701	32	39.5	760	2	B84953	penicillin-binding	774	32	39.5	10223	2	T30225	polypeptide synthas
702	32	39.5	778	2	T44761	probable preprotei	775	32	39.5	109	2	S47181	Ig kappa chain - h
703	32	39.5	781	2	JC7382	DNA-directed DNA p	776	31.5	38.9	111	2	S20709	Ig kappa chain v r
704	32	39.5	804	2	D81281	probable nucleotid	777	31.5	38.9	112	2	PL0273	Ig kappa chain v r
705	32	39.5	804	2	T18014	hypothetical prote	778	31.5	38.9	120	2	S42266	Ig kappa chain v r
706	32	39.5	808	2	A82877	hypothetical prote	779	31.5	38.9	203	2	C97773	ribonuclease III (
707	32	39.5	809	2	A55547	quinate-shikimate	780	31.5	38.9	274	2	T33371	hypothetical prote
708	32	39.5	815	2	T00546	serine/threonine-s	781	31.5	38.9	285	2	AC1537	hypothetical prote
709	32	39.5	821	2	H71475	probable chlcx pho	782	31.5	38.9	314	2	S38165	hypothetical prote
710	32	39.5	846	2	AT2336	primosomal protein	783	31.5	38.9	346	2	T13179	hypothetical prote
711	32	39.5	847	2	T19544	DNA polymerase I (784	31.5	38.9	517	2	T11665	probable cell divi
712	32	39.5	882	2	F90201	DNA-directed DNA p	785	31.5	38.9	559	2	T40764	serine-threonine p
713	32	39.5	883	2	S23019	probable fibrial	786	31.5	38.9	581	2	T19261	p45 NF-E2 related
714	32	39.5	882	2	B85725	unknown protein, 4	787	31.5	38.9	604	2	D90523	lipoprotein (impor
715	32	39.5	884	2	E86244	DLP2 protein - yea	788	31.5	38.9	629	2	G83251	probable acetyltra
716	32	39.5	943	2	S58317	hypothetical prote	789	31.5	38.9	829	2	T40239	probable helicase
717	32	39.5	955	2	T48515	hypothetical prote	790	31.5	38.9	880	2	T21538	hypothetical prote
718	32	39.5	972	2	F71608	isooleucyl-t-tna syn	791	31.5	38.3	26	2	A81209	hypothetical prote
719	32	39.5	973	2	T41201	transcription regu	792	31	38.3	72	2	AD0096	probable membrane
720	32	39.5	974	2	A44484	hypothetical prote	793	31	38.3	75	2	B89582	protein C18A11.2 [
721	32	39.5	975	2	T48107	myosin heavy chain	794	31	38.3	100	2	D86636	hypothetical prote
722	32	39.5	994	1	U00151	hypothetical prote	795	31	38.3	101	2	S51384	hypothetical prote
723	32	39.5	1008	2	T33672	hypothetical prote	796	31	38.3	107	2	C69354	hypothetical prote
724	32	39.5	1014	2	F96501	hypothetical prote	797	31	38.3	113	2	H30534	Ig kappa chain v r
725	32	39.5	1039	2	F71427	hypothetical prote	798	31	38.3	113	2	R30534	Ig kappa chain v r
726	32	39.5	1040	2	S50617	BEH1 protein - yea	799	31	38.3	113	2	S64781	hypothetical prote
727	32	39.5	1054	2	T30901	cyclic nucleotide	800	31	38.3	114	1	KVMS7A	hypothetical prote
728	32	39.5	1066	2	T06501	hypothetical prote	801	31	38.3	114	2	A32967	Ig kappa chain v r
729	32	39.5	1083	2	S54293	regulator protein	802	31	38.3	115	2	S51429	Ig kappa chain V-I
730	32	39.5	1099	2	H83210	probable phospholi	803	31	38.3	115	2	T08958	hypothetical prote
731	32	39.5	1120	2	H71664	transcription-repa	804	31	38.3	116	2	F90024	glycine-rich prote
732	32	39.5	1142	2	T00022	B120 protein - hum	805	31	38.3	124	2	AT1362	hypothetical prote
733	32	39.5	1150	2	A41641	mannosyl-Oligosacc	806	31	38.3	127	2	H75186	hypothetical prote
734	32	39.5	1222	2	B90593	hypothetical prote	807	31	38.3	128	2	T05491	hypothetical prote
735	32	39.5	1259	4	GNHUL1	retrovirus-related	808	31	38.3	129	2	A97094	uncharacterized pr
736	32	39.5	1275	2	T33369	hypothetical prote	809	31	38.3	135	2	G83845	hypothetical prote
737	32	39.5	1275	2	I38588	reverse transcript	810	31	38.3	139	2	G83845	hypothetical prote
738	32	39.5	1275	2	S65824	reverse transcript	811	31	38.3	140	1	Q0MSIG	hypothetical prote
739	32	39.5	1275	2	T49362	hypothetical prote	812	31	38.3	140	2	G81276	hypothetical prote
740	32	39.5	1280	2	B34087	hypothetical prote	813	31	38.3	144	2	G87514	hypothetical prote
741	32	39.5	1333	2	B88257	protein Iec-23 [lm	814	31	38.3	148	2	B90115	hypothetical prote
742	32	39.5	1365	2	T18419	hypothetical prote	815	31	38.3	150	2	F86299	hypothetical prote
743	32	39.5	1374	2	S70712	protein-tyrosine k	816	31	38.3	155	2	G69987	hypothetical prote
744	32	39.5	1404	2	F86470	probable retroelem	817	31	38.3	157	1	Q0ECPL	creb protein [smi
745	32	39.5	1469	2	T19168	hypothetical prote	818	31	38.3	157	2	C91298	creb protein [smi
746	32	39.5	1494	2	C70152	senory transducti	819	31	38.3	157	2	B86139	hypothetical prote
747	32	39.5	1614	2	T29861	hypothetical prote	820	31	38.3	168	2	H89886	DNA repair protei
748	32	39.5	1765	2	T42388	sodium channel alp	821	31	38.3	175	2	C90227	hypothetical prote
749	32	39.5	1802	2	G1616	hypothetical prote	822	31	38.3	181	2	T46017	hypothetical prote
750	32	39.5	1827	2	T76270	genome polyprotein	823	31	38.3	189	2	E90789	hypothetical prote
751	32	39.5	1874	1	J00533	sodium channel pro	824	31	38.3	192	2	S28254	NADH2 dehydrogen
752	32	39.5	1951	2	S00320	sodium channel pro	825	31	38.3	199	2	S54407	embryonic fibrobla
753	32	39.5	1957	2	S68453	sodium channel pro	826	31	38.3	195	2	A99346	hypothetical prote
754	32	39.5	1976	2	I56555	sodium channel alp	827	31	38.3	197	2	S74851	hypothetical prote
755	32	39.5	1977	2	S54771	sodium channel alp	828	31	38.3	198	2	H95042	hypothetical prote
756	32	39.5	1983	2	A60054	sodium channel pro	829	31	38.3	198	2	B97913	recombination prot
757	32	39.5	2005	2	A46269	sodium channel alp	830	31	38.3	198	2	AH0099	general secretion
758	32	39.5	2005	2	B25019	sodium channel pro	831	31	38.3	202	2	A82160	hypothetical prote
759	32	39.5	2009	2	A25019	sodium channel pro	832	31	38.3	203	2	B96670	hypothetical prote

833	31	38.3	204	2	T24771	hypothetical prote	906	31	38.3	322	2	F90748	NADH oxidoreductas
834	31	38.3	210	2	I49294	CD7 antigen - mous	907	31	38.3	323	2	C70205	hypothetical prote
835	31	38.3	212	2	F83255	3-isopropylmalate	908	31	38.3	327	2	T33540	hypothetical prote
836	31	38.3	214	2	A1371	hypothetical prote	909	31	38.3	328	2	T40910	probable tyrosine
837	31	38.3	215	2	G82564	3-isopropylmalate	910	31	38.3	329	2	S53833	cytochrome-c oxida
838	31	38.3	215	2	T51640	myd-related transc	911	31	38.3	329	2	AF1891	hypothetical prote
839	31	38.3	217	2	C86350	protein F8X7.12 (1	912	31	38.3	334	2	C70955	cell division prot
840	31	38.3	222	2	B64211	hypothetical prote	913	31	38.3	332	2	T27089	hypothetical prote
841	31	38.3	223	2	B71514	hypothetical prote	914	31	38.3	334	2	F89008	protein W08A12.4 (
842	31	38.3	224	2	T28136	butyrophilin 2, B	915	31	38.3	335	2	S53352	2,4-dienoyl-CoA re
843	31	38.3	235	2	G49338	flagellar hook-len	916	31	38.3	335	2	C70196	flagellar P-ring p
844	31	38.3	237	2	A99103	26S proteasome iot	917	31	38.3	338	2	UC1238	oploid-binding pro
845	31	38.3	238	2	E81957	3-demethylubiquino	918	31	38.3	339	2	T23086	hypothetical prote
846	31	38.3	238	2	T30864	stb protein - Sal	919	31	38.3	339	2	T19555	hypothetical prote
847	31	38.3	238	2	T02118	hypothetical prote	920	31	38.3	339	2	T19261	hypothetical prote
848	31	38.3	242	2	H81015	3-demethylubiquino	921	31	38.3	339	2	T19600	hypothetical prote
849	31	38.3	246	2	T17432	probable chaparon	922	31	38.3	339	2	T18783	probable transposi
850	31	38.3	246	2	AB0234	probable pill asse	923	31	38.3	339	2	T26396	hypothetical prote
851	31	38.3	246	2	T25978	hypothetical prote	924	31	38.3	339	2	T15721	hypothetical prote
852	31	38.3	248	2	C89472	protein ZC53.3 (Im	925	31	38.3	339	2	T29362	hypothetical prote
853	31	38.3	249	2	T50162	hypothetical prote	926	31	38.3	339	2	T27715	hypothetical prote
854	31	38.3	251	2	F87454	hypothetical prote	927	31	38.3	339	2	T19660	hypothetical prote
855	31	38.3	251	2	H85649	probable fatty acy	928	31	38.3	339	2	T22780	hypothetical prote
856	31	38.3	251	2	B86647	hypothetical prote	929	31	38.3	339	2	T28781	hypothetical prote
857	31	38.3	252	2	T15300	hypothetical prote	930	31	38.3	339	2	T20442	hypothetical prote
858	31	38.3	252	2	C86796	hypothetical prote	931	31	38.3	339	2	T32676	hypothetical prote
859	31	38.3	253	2	C83906	hypothetical prote	932	31	38.3	339	2	T15113	hypothetical prote
860	31	38.3	258	2	AH0360	probable dimethyl	933	31	38.3	339	2	T24136	hypothetical prote
861	31	38.3	260	2	G64690	type IIS restriction	934	31	38.3	339	2	C68035	protein W01D1.4 (l
862	31	38.3	260	2	F96584	hypothetical prote	935	31	38.3	339	2	T25335	hypothetical prote
863	31	38.3	262	1	UC4803	venombin A (EC 3.4	936	31	38.3	339	2	T25365	hypothetical prote
864	31	38.3	264	1	T18998	hypothetical prote	937	31	38.3	340	2	T42684	hypothetical prote
865	31	38.3	265	2	G81377	probable transmemb	938	31	38.3	341	2	G87593	conserved hypothet
866	31	38.3	267	2	T23978	hypothetical prote	939	31	38.3	345	2	S03199	oploid-binding pro
867	31	38.3	274	2	A26050	exfoliative toxin	940	31	38.3	345	2	UC1239	oploid-binding pro
868	31	38.3	276	2	T46198	hypothetical prote	941	31	38.3	346	2	B71651	probable ferredox
869	31	38.3	283	2	T01096	hypothetical prote	942	31	38.3	349	2	A75612	phosphate ABC tran
870	31	38.3	285	2	T29832	hypothetical prote	943	31	38.3	352	2	T27281	hypothetical prote
871	31	38.3	286	2	S55901	probable tagatose	944	31	38.3	353	2	T07805	alternative oxidas
872	31	38.3	286	2	G64976	tagatose-bisphosph	945	31	38.3	355	2	T20782	hypothetical prote
873	31	38.3	286	2	C90991	tagatose-bisphosph	946	31	38.3	357	2	E71708	hypothetical prote
874	31	38.3	286	2	B85836	tagatose-bisphosph	947	31	38.3	359	2	UC1049	glucose-glutamine
875	31	38.3	290	1	T26139	hypothetical prote	948	31	38.3	359	2	E64425	hypothetical prote
876	31	38.3	292	1	DXHUBH	libeta-hydroxyster	949	31	38.3	362	2	E72002	aromatic amino aci
877	31	38.3	293	2	T24095	hypothetical prote	950	31	38.3	362	2	C86621	aromatic amino aci
878	31	38.3	297	2	C70251	hypothetical prote	951	31	38.3	363	2	T39726	mannopine biosynth
879	31	38.3	298	2	T45527	ECM29 homolog (Imp	952	31	38.3	364	2	AD1400	hypothetical prote
880	31	38.3	300	2	A71645	protein p34 (p34)	953	31	38.3	365	2	S58197	probable membrane
881	31	38.3	301	2	T39401	probable ribose me	954	31	38.3	365	2	A72574	probable acyl carr
882	31	38.3	301	2	T18788	hypothetical prote	955	31	38.3	365	2	T04247	hypothetical prote
883	31	38.3	301	2	T31472	hypothetical prote	956	31	38.3	366	2	S03770	pectinesterase (BC
884	31	38.3	301	2	S13095	p34 protein - Rick	957	31	38.3	366	2	UN0799	pectinesterase (BC
885	31	38.3	303	2	T34112	hypothetical prote	958	31	38.3	367	2	AG0480	aspartate semialde
886	31	38.3	305	2	E75122	hypothetical prote	959	31	38.3	368	2	T22361	adenosylmethionine
887	31	38.3	306	2	S32834	methylviologen-red	960	31	38.3	370	2	F82125	aspartate-semialde
888	31	38.3	306	2	F97860	protein p34 (impor	961	31	38.3	371	2	S60903	hypothetical prote
889	31	38.3	307	2	T27915	hypothetical prote	962	31	38.3	374	2	H75002	methyl-accepting c
890	31	38.3	308	2	S73847	yabc protein homol	963	31	38.3	377	2	S21302	succinate dehydrog
891	31	38.3	308	2	F95087	hypothetical prote	964	31	38.3	381	2	G97114	unsaturatedized me
892	31	38.3	308	2	H71008	probable ATP-bind	965	31	38.3	383	2	E70156	lipopolysaccharide
893	31	38.3	312	2	AG1789	secreted protein w	966	31	38.3	383	2	T00674	conserved hypothet
894	31	38.3	312	2	AH1413	secreted protein w	967	31	38.3	384	2	H81198	hypothetical prote
895	31	38.3	313	2	T28728	hypothetical prote	968	31	38.3	390	2	C84984	hypothetical prote
896	31	38.3	314	2	T29396	hypothetical prote	969	31	38.3	392	2	G97330	probable aminopt
897	31	38.3	314	2	T18991	hypothetical prote	970	31	38.3	393	2	T12608	NADH2 dehydrogenas
898	31	38.3	316	2	D90585	hypothetical prote	971	31	38.3	393	2	T13501	NADH2 dehydrogenas
899	31	38.3	317	2	D64220	methyltransferase	972	31	38.3	393	2	T13565	NADH2 dehydrogenas
900	31	38.3	317	2	T25003	hypothetical prote	973	31	38.3	393	2	T13775	NADH2 dehydrogenas
901	31	38.3	318	2	T15869	hypothetical prote	974	31	38.3	393	2	T12630	NADH2 dehydrogenas
902	31	38.3	321	2	F84597	probable prolina-r	975	31	38.3	393	2	T12609	NADH2 dehydrogenas
903	31	38.3	322	2	B88452	protein ZC155.1 (i	976	31	38.3	394	2	T13721	NADH2 dehydrogenas
904	31	38.3	322	2	H64825	hypothetical prote	977	31	38.3	395	2	T13779	NADH2 dehydrogenas
905	31	38.3	322	2	B85599	probable enzyme Z1	978	31	38.3	395	2	T51774	acetyl-CoA C-acety

979 31 38.3 396 2 T27946 hypothetical prote
980 31 38.3 396 2 D97140 probable TPR-repa
981 31 38.3 398 2 T06597 sepin homolog WZ
982 31 38.3 400 2 T25605 hypothetical prote
983 31 38.3 400 2 B81775 hypothetical integ
984 31 38.3 401 2 S63227 hypothetical prote
985 31 38.3 404 2 C96549 hypothetical prote
986 31 38.3 405 2 D96614 hypothetical prote
987 31 38.3 408 2 B64237 nitrogen fixation
988 31 38.3 415 2 T21532 hypothetical prote
989 31 38.3 417 2 P66731 exodeoxyribonuclea
990 31 38.3 418 2 T25092 hypothetical prote
991 31 38.3 422 2 H70481 hemolysin homolog
992 31 38.3 425 2 JC6557 podosporepsin (E
993 31 38.3 425 2 AH1264 histidyl-tRNA synt
994 31 38.3 428 2 F85437 patatin-like prote
995 31 38.3 429 2 T00857 probable receptor-
996 31 38.3 431 2 B37802 crx protein - Brw
997 31 38.3 433 2 AD1164 H+-transporting AT
998 31 38.3 433 2 AD1523 H+-transporting AT
999 31 38.3 434 2 A42512 G5R protein - Vacc
1000 31 38.3 434 2 T37350 probable 49.8K pro

ALIGNMENTS

RESULT 1

1g light chain V region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 20-Jun-2000

C:Accession: S26337; S78449

R:Stark, S.E.; Caton, A.J.

U:Exp. Med. 174, 613-624, 1991

A:Title: Antibodies that are specific for a single amino acid interchange in a protein

A:Reference number: S26309; MUID:91341421; PMID:1908510

A:Accession: S26337

A:Molecule type: mRNA

A:Residues: 1-101 <STA>

A:Cross-references: UNIPARC:UPI0000176980; EMBL:X59193

R:Caton, A.J.

submitted to the EMBL Data Library, April 1991

A:Reference number: S78447

A:Accession: S78449

A:Molecule type: mRNA

A:Residues: 1-60, 'T', 62-91, 'S', 93-101 <CAT>

A:Cross-references: UNIPARC:UPI0000115F7F; EMBL:X59193; NID:G52323; PIDN:CAA41903.1; PID

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:8-86/Domain: immunoglobulin homology <IMM>

Query Match 85.2%; Score 69; DB 2; Length 101;

Best Local Similarity 82.4%; Pred. No. 4.6e-05; Mismatches 1; Indels 0; Gaps 0;

Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

1 KSSQSVFFSSQKNYLA 17

16 KSSQSVLYSSNQKNYLA 32

RESULT 2

PH1054

1g light chain V region (clone 202.135) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000

C:Accession: PH1054

R:Fillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B

A:Reference number: PH0971; MUID:92381444; PMID:1512540

A:Accession: PH1054

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA
A:Residues: 1-103 <TIL>
A:Cross-references: UNIPARC:UPI0000176AAE
A:Experimental source: B cell, strain [NZB x NZW]P1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 85.2%; Score 69; DB 2; Length 103;

Best Local Similarity 82.4%; Pred. No. 4.7e-05; Mismatches 1; Indels 0; Gaps 0;

Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

1 KSSQSVFFSSQKNYLA 17

24 KSSQSVLYSSNQKNYLA 40

RESULT 3

3g kappa chain V region (A52) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 03-Nov-1988 #sequence_revision 03-Nov-1988 #text_change 21-Jan-2000

C:Accession: G30502

R:Ellat, D.; Webster, D.M.; Rees, A.R.

U:Immunol. 141, 1745-1753, 1988

A:Title: V region sequences of anti-DNA and anti-RNA autoantibodies from NZB/NZW F-1 mice

A:Reference number: A30502; MUID:88315787; PMID:2457627

A:Accession: G30502

A:Molecule type: mRNA

A:Residues: 1-111 <EIL>

A:Cross-references: UNIPARC:UPI0000176AF0

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 85.2%; Score 69; DB 2; Length 111;

Best Local Similarity 82.4%; Pred. No. 5.1e-05; Mismatches 1; Indels 0; Gaps 0;

Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

1 KSSQSVFFSSQKNYLA 17

24 KSSQSVLYSSNQKNYLA 40

RESULT 4

S06084

Ig kappa chain precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000

C:Accession: S06084

R:Crowe, J.S.; Smith, M.A.; Cooper, H.J.

Nucleic Acids Res. 17, 7992, 1989

A:Title: Nucleotide sequence of V3-Ag 1.2.3. rat myeloma immunoglobulin kappa chain cDNA

A:Reference number: S06084; MUID:90016888; PMID:2508067

A:Accession: S06084

A:Molecule type: mRNA

A:Residues: 1-240 <CRO>

A:Cross-references: UNIPARC:UPI0000113764; EMBL:X16129; NID:G56457; PIDN:CAA34256.1; PID

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-240/Product: Ig kappa chain #status predicted <MAT>

F:153-222/Domain: immunoglobulin homology <IMM>

Query Match 84.0%; Score 68; DB 2; Length 240;

Best Local Similarity 76.5%; Pred. No. 0.00017; Mismatches 3; Indels 0; Gaps 0;

Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

1 KSSQSVFFSSQKNYLA 17

44 KSSQSVLYSSNQKNYLA 60

RESULT 5

S30520
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C:Accession: S30520
R:Marlette, X.
submitted to the EMBL Data Library, October 1992
A:Reference number: S30520
A:Accession: S30520
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-113 <MAR>
A:Cross-references: UNIPARC:UPI0000176AR4; EMBL:Z18325
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keyword: heterotetramer; immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 82.7%; Score 67; DB 2; Length 113;
Matches 13; Conservativity 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSSQVFPSSSQKNYLA 17
|||||:|:|:|:|:|
DB 24 KSSQSLVYSSNNKNYLA 40

RESULT 6

S41393
Ig kappa chain V region (12.5H VL) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Mar-2001
C:Accession: S41393
R:Margaritte, C.; Gilbert, D.; Brard, P.; Tron, F.
submitted to the EMBL Data Library, January 1994
A:Description: Structural characterization of an (NZB X NZW) F1 mouse-derived IGM anti-DN
A:Reference number: S41393
A:Accession: S41393
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-112 <MAR>
A:Cross-references: UNIPARC:UPI0000176CCB; EMBL:Z29536
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 81.5%; Score 66; DB 2; Length 112;
Matches 13; Conservativity 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSSQVFPSSSQKNYLA 17
|||||:|:|:|:|:|
DB 24 KSSQSLVYSSNNKNYLA 40

RESULT 7

PT0356
Ig kappa chain V region (2B1.1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 21-Jan-2000
C:Accession: PT0356
R:Shefner, R.; Kleiner, G.; Turken, A.; Papazian, L.; Diamond, B.
J. Exp. Med. 173, 287-296, 1991
A>Title: A novel class of anti-DNA antibodies identified in BALB/c mice.
A:Reference number: PT0356; MVID:91108325; PMID:1988536
A:Accession: PT0356
A:Molecule type: mRNA
A:Residues: 1-118 <SHS>
A:Cross-references: UNIPARC:UPI0000176791
A:Experimental source: strain BALB/c
A>Note: the authors translated the codon CTT for residue 32 as Ser
C:Comment: This protein is an anti-double-stranded DNA antibody.

C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:19-99/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 81.5%; Score 66; DB 2; Length 118;
Matches 13; Conservativity 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSSQVFPSSSQKNYLA 17
|||||:|:|:|:|:|
DB 27 KSSQSLVYSSNNKNYLA 43

RESULT 8

S37532
Ig kappa chain V region (V-kappa 4) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37532
R:Klein, U.; Kuepers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A:Description: Human IGM(+) IGD(+) cells, the major B cell subset in the peripheral blood
A:Reference number: S37501
A:Accession: S37532
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-92 <KLE>
A:Cross-references: UNIPARC:UPI000011658C; EMBL:Z26628; NID:9405706; PIDN:CAA81381.1; PI
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match

Best Local Similarity 79.0%; Score 64; DB 2; Length 92;
Matches 13; Conservativity 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KSSQVFPSSSQKNYLA 17
|||||:|:|:|:|:|
DB 2 KSSQSLVYSSNNKNYLA 18

RESULT 9

S37533
Ig kappa chain V region (V-kappa 4) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37533
R:Klein, U.; Kuepers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A:Description: Human IGM(+) IGD(+) cells, the major B cell subset in the peripheral blood
A:Reference number: S37501
A:Accession: S37533
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-92 <KLE>
A:Cross-references: UNIPARC:UPI000011658B; EMBL:Z26627; NID:9405708; PIDN:CAA81380.1; PI
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match

Best Local Similarity 79.0%; Score 64; DB 2; Length 92;
Matches 13; Conservativity 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KSSQVFPSSSQKNYLA 17
|||||:|:|:~|:|:|
DB 2 KSSQSLVYSSNNKNYLA 18

RESULT 10

S37530
Ig kappa chain V region (V-kappa 4) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37530
R:Klein, U.; Kuepers, R.; Rajewsky, K.

submitted to the EMBL Data Library, September 1993
A:Description: Human IGM(+)IgD(+) cells, the major B cell subset in the peripheral blood
A:Reference number: S37501
A:Accession: S37530
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-92 <KLE>
A:Cross-references: UNIPARC:UPI000011658E; EMBL:Z26630; NID:G405702; PIDN:CAA81383.1; PI
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 79.0%; Score 64; DB 2; Length 92;
Best Local Similarity 76.5%; Pred. No. 0.00032;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KSSQSVFFSSSQKNYLA 17
|||||:|:|:|
Db 2 KSSQSVLYSSNNKNYLA 18

RESULT 11
S37535
Ig kappa chain V region (V-kappa 4) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37535
R:Klein, U.; Kuipers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A:Description: Human IGM(+)IgD(+) cells, the major B cell subset in the peripheral blood
A:Reference number: S37501
A:Accession: S37535
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-92 <KLE>
A:Cross-references: UNIPARC:UPI0000116589; EMBL:Z26625; NID:G405712; PIDN:CAA81378.1; PI
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 79.0%; Score 64; DB 2; Length 92;
Best Local Similarity 76.5%; Pred. No. 0.00032;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KSSQSVFFSSSQKNYLA 17
|||||:|:|:|
Db 2 KSSQSVLYSSNNKNYLA 18

RESULT 12
S37534
Ig kappa chain V region (V-kappa 4) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37534
R:Klein, U.; Kuipers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A:Description: Human IGM(+)IgD(+) cells, the major B cell subset in the peripheral blood
A:Reference number: S37501
A:Accession: S37534
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-92 <KLE>
A:Cross-references: UNIPARC:UPI000011658A; EMBL:Z26626; NID:G405710; PIDN:CAA81379.1; PI
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 79.0%; Score 64; DB 2; Length 92;
Best Local Similarity 76.5%; Pred. No. 0.00032;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KSSQSVFFSSSQKNYLA 17
|||||:|:|:|
Db 2 KSSQSVLYSSNNKNYLA 18

RESULT 13
S37529
Ig kappa chain V region (V-kappa 4) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37529
R:Klein, U.; Kuipers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A:Description: Human IGM(+)IgD(+) cells, the major B cell subset in the peripheral blood
A:Reference number: S37501
A:Accession: S37529
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-92 <KLE>
A:Cross-references: UNIPARC:UPI000011658F; EMBL:Z26631; NID:G405700; PIDN:CAA81384.1; PI
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 79.0%; Score 64; DB 2; Length 92;
Best Local Similarity 76.5%; Pred. No. 0.00032;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KSSQSVFFSSSQKNYLA 17
|||||:|:|:|
Db 2 KSSQSVLYSSNNKNYLA 18

RESULT 14
A49138
IGA kappa rheumatoid factor variable - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: A49138
R:Gaube, A.; Kuipers, R.; Meriau, R.
Clin. Exp. Immunol. 88, 430-434, 1992
A:Title: A somatically mutated V kappa IV gene encoding a human rheumatoid factor light
A:Reference number: A49138; MUID:92298590; PMID:1606727
A:Accession: A49138
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-106 <GAU>
A:Cross-references: UNIPARC:UPI0000176810; GB:S37926; NID:G298207; PIDN:AA82366.1; PID:
A>Note: sequence inconsistent with the nucleotide translation
A>Note: sequence extracted from NCBI backbone (NCBI:106633, NCBI:P:106637)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:20-99/Domain: immunoglobulin homology <1MW>

Query Match 79.0%; Score 64; DB 2; Length 106;
Best Local Similarity 76.5%; Pred. No. 0.00037;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KSSQSVFFSSSQKNYLA 17
|||||:|:|:|
Db 28 KSSQSVLYSSNNKNYLA 44

RESULT 15
S34002
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C>Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S34002; S30522
R:Marlette, X.; Tsapis, A.; Brunet, J.C.
Eur. J. Immunol. 23, 846-851, 1993
A:Title: Nucleotide sequence analysis of the variable domains of four human monoclonal
A:Reference number: S34001; MUID:93209281; PMID:7681398
A:Accession: S34002
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-113 <MAR>
A:Cross-references: UNIPARC:UPI0000176D32; EMBL:Z18328
C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 79.0%; Score 64; DB 2; Length 113;
Best Local Similarity 76.5%; Pred. No. 0.0004; 2; Indels 0; Gaps 0;
Matches 13; Conservative 2; Mismatches 2;

QY 1 KSSQSVFPSSQKNYLA 17
|||||:|:|:|
Db 24 KSSQSVLYSSNNKNYLA 40

RESULT 16

S34003
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C>Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C:Accession: S34003
R:Marielette, X.; Tsapis, A.; Brouet, J.C.

Eur. J. Immunol. 23, 846-851, 1993

A:Title: Nucleotide sequence analysis of the variable domains of four human monoclonal
A:Reference number: S34003; MUID:93209281; PMID:7681398

A:Accession: S34003

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-113 <MAR>

A:Cross-references: UNIPARC:UPI0000176CCA

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 79.0%; Score 64; DB 2; Length 113;
Best Local Similarity 76.5%; Pred. No. 0.0004; 2; Indels 0; Gaps 0;
Matches 13; Conservative 2; Mismatches 2;

QY 1 KSSQSVFPSSQKNYLA 17
|||||:|:|:|
Db 24 KSSQSVLYSSNNKNYLA 40

RESULT 17

S30523
Ig kappa chain V region - human

C:Species: Homo sapiens (man)

C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000

C:Accession: S30523

R:Marielette, X.
submitted to the EMBL Data Library, October 1992

A:Reference number: S30520

A:Accession: S30523

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-113 <MAR>

A:Cross-references: UNIPARC:UPI0000176AE2; EMBL:Z18329

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 79.0%; Score 64; DB 2; Length 113;
Best Local Similarity 76.5%; Pred. No. 0.0004; 2; Indels 0; Gaps 0;
Matches 13; Conservative 2; Mismatches 2;

QY 1 KSSQSVFPSSQKNYLA 17
|||||:|:|:|
Db 24 KSSQSVLYSSNNKNYLA 40

RESULT 18

K4HUNL

Ig kappa chain V-IV region (len) - human

C:Species: Homo sapiens (man)

C>Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 01-Dec-2000

C:Accession: A01903; F61458

R:Schneider, M.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 356, 507-547, 1975

A:Title: Die Primärstruktur einer monoklonalen Immunoglobulin-L-Kette der Subgruppe IV v

A:Reference number: A01903; MUID:76004342; PMID:50995

A:Accession: A01903

A:Molecule type: protein

A:Residues: 1-114 <SCH>

A:Cross-references: UNIPARC:UPI0000173708

A>Note: this is the first completely sequenced V region of a new kappa chain subgroup, a

R:Brouet, J.C.; Delagrè, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Minasco, E.

J. Exp. Med. 170, 1551-1558, 1989

A:Title: Expression of a public idiotype by human monoclonal IgM directed to myelin-asso

A:Reference number: A61458; MUID:90039128; PMID:2478651

A:Accession: F61458

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-13 <BRO>

A:Cross-references: UNIPARC:UPI0000173709

C:Comment: This is a Bence Jones protein.

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kaf

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-96/Domain: immunoglobulin homology <IMM>

F:23-94/Disulfide bonds: #status predicted

Query Match 79.0%; Score 64; DB 1; Length 114;
Best Local Similarity 76.5%; Pred. No. 0.0004; 2; Indels 0; Gaps 0;
Matches 13; Conservative 2; Mismatches 2;

QY 1 KSSQSVFPSSQKNYLA 17
|||||:|:|:|
Db 24 KSSQSVLYSSNNKNYLA 40

RESULT 19

S51147

antibody light chain V region - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000

C:Accession: S51147

R:de Kruijf, J.; Boel, E.; Logtenberg, T.

submitted to the EMBL Data Library, January 1995

A:Description: Selection and application of human SCFV antibody fragments from a semi-sy

A:Reference number: S51147

A:Accession: S51147

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-120 <DEK>

A:Cross-references: UNIPARC:UPI0000116210; EMBL:X83714; NID:G633227; PIDN:CAA58689.1; PI

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 79.0%; Score 64; DB 2; Length 120;
Best Local Similarity 76.5%; Pred. No. 0.00043; 2; Indels 0; Gaps 0;
Matches 13; Conservative 2; Mismatches 2;

QY 1 KSSQSVFPSSQKNYLA 17
|||||:|:~|:|
Db 24 KSSQSVLYSSNNKNYLA 40

RESULT 20

K4HUNL

Ig kappa chain precursor V-IV region - human

C:Species: Homo sapiens (man)

C>Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004

C:Accession: A01902

R:Klobeck, H.G.; Bornkamm, G.W.; Combiato, G.; Mochkat, R.; Pohlenz, H.D.; Zachau, H.G.

Nucleic Acids Res. 13, 6515-6529, 1985

A:Title: Subgroup IV of human immunoglobulin K light chains is encoded by a single germ l

A:Reference number: A93589; MUID:86041853; PMID:2997712

A:Accession: A01902
A:Molecule type: DNA
A:Residues: 1-121 <KLO>
A:Cross-references: UNIPROT:P06312; UNIPARC:UPI0000113B70
A>Note: the sequence was determined from the germline gene
C:Genetics:
A:Introns: 17/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as Iga and IgM, the subunits associate into 1a C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-121/Product: Ig kappa chain precursor V-IV region #status predicted <MAT>
F:21-43/Region: framework 1
F:36-116/Domain: immunoglobulin homology <IMM>
F:44-60/Region: complementarity-determining 1
F:61-75/Region: framework 2
F:76-82/Region: complementarity-determining 2
F:83-114/Region: framework 3
F:115-121/Region: complementarity-determining 3
F:43-114/Disulfide bonds: #status predicted
Query Match 79.0%; Score 64; DB 1; Length 121;
Best Local Similarity 76.5%; Pred. No. 0.00043;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 KSSQSVFFSSQKNYLA 17
DB 44 KSSQSVLYSSNNKNYLA 60

RESULT 21
K4HU1
Ig kappa chain precursor V-IV region (VI) - human
C:Species: Homo sapiens (man)
C>Date: 30-Jun-1987 #revision 30-Jun-1987 #text_change 09-Jul-2004
C:Accession: A01904
R:Klodeck, H.G.; Bornkamm, G.W.; Combricato, G.; Mochkat, R.; Pohlenz, H.D.; Zachau, H.G.
Nucleic Acids Res. 13, 6515-6529, 1985
A>Title: Subgroup IV of human immunoglobulin K light chains is encoded by a single germ
A:Reference number: A93589; MUID:86041853; PMID:2937712
A:Accession: A01904
A:Molecule type: DNA
A:Residues: 1-133 <KLO>
A:Cross-references: UNIPROT:P06313; UNIPARC:UPI000012E165; GB:Z00022; GB:X51570; NID:933
A>Note: the sequence was determined from the differentiated gene
C:Genetics:
A:Gene: GDB:IGKV
A:Cross-references: GDB:119341; OMIM:146980
A:Map position: 2p12-2p12
A:Introns: 17/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as Iga and IgM, the subunits associate into 1a C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-133/Product: Ig kappa chain V-IV region (VI) #status predicted <MAT>
F:21-43/Region: framework 1
F:36-116/Domain: immunoglobulin homology <IMM>
F:44-60/Region: complementarity-determining 1
F:61-75/Region: framework 2
F:76-82/Region: complementarity-determining 2
F:83-114/Region: framework 3
F:115-122/Region: complementarity-determining 3
F:123-133/Region: framework 4
F:43-114/Disulfide bonds: #status predicted

Query Match 79.0%; Score 64; DB 1; Length 133;
Best Local Similarity 76.5%; Pred. No. 0.00047;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 KSSQSVFFSSQKNYLA 17

DB 44 KSSQSVLYSSNNKNYLA 60
RESULT 22
S49531
anti-Sm antibody VL chain (V kappa 4/J kappa 3) - human
C:Species: Homo sapiens (man)
C>Date: 01-Feb-1995 #revision 12-May-1995 #text_change 21-Jan-2000
C:Accession: S49531
R:Mamoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
submitted to the EMBL Data Library, October 1994
A:Description: Molecular characterization of natural human anti-Sm autoantibodies.
A:Reference number: S48797
A:Accession: S49531
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-134 <MAH>
A:Cross-references: UNIPARC:UPI00001166FE; EMBL:Z46347; NID:G560841; PIDN:CAA86466.1; PI
F:36-116/Domain: immunoglobulin homology <IMM>
Query Match 79.0%; Score 64; DB 2; Length 134;
Best Local Similarity 76.5%; Pred. No. 0.00048;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 KSSQSVFFSSQKNYLA 17
DB 44 KSSQSVLYSSNNKNYLA 60

RESULT 23
G38601
Ig kappa chain V region (4A9) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 30-Aug-1991 #revision 30-Aug-1991 #text_change 23-Jul-1999
C:Accession: G38601
J: Biol. Chem. 266, 2134-2142, 1991
R:Goshorn, S.C.; Retzel, E.; Jemerson, R.
A>Title: Common structural features among monoclonal antibodies binding the same antigen
A:Reference number: A38601; MUID:91115823; PMID:1703527
A:Accession: G38601
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-96 <GOS>
A:Cross-references: UNIPARC:UPI000011517B; GB:M57984; NID:9196414; PIDN:AA63365.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 77.8%; Score 63; DB 2; Length 96;
Best Local Similarity 76.5%; Pred. No. 0.00051;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 KSSQSVFFSSQKNYLA 17
DB 6 KSSQSVLYSSNNKNYLA 22

RESULT 24
S09970
Ig kappa chain V-J region (4C8) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 12-Feb-1993 #revision 12-Feb-1993 #text_change 21-Jan-2000
C:Accession: S09970
R:Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jacon, J.C.; Izui, S.
Eur. J. Immunol. 20, 771-777, 1990
A>Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodies
A:Reference number: S09955; MUID:90269328; PMID:2347362
A:Accession: S09970
A:Molecule type: mRNA
A:Residues: 1-112 <REI>
A:Cross-references: UNIPARC:UPI0000115B69; EMBL:X51858; NID:G55406; PIDN:CAA36151.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin
F;16-96/Domain: immunoglobulin homology <IMM>

Query Match 77.8%; Score 63; DB 2; Length 112;
Best Local Similarity 70.6%; Pred. No. 0.0006;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSSQSVFFSSSQKNYLA 17
|||||:|:|:|
Db 24 KSSQSLVSSNNQKNYLA 40

RESULT 25

S44119

Ig kappa chain V-J region - human

C;Species: Homo sapiens (man)

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001

C;Accession: S44119

R;Hawkins, R.B.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.

submitted to the EMBL Data Library, March 1994

A;Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable

A;Reference number: S44105

A;Accession: S44119

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-114 <HAM>

A;Cross-references: UNIPARC:UPI000011636; EMBL:Z31396; NID:9472973; PIDN:CAA83271.1; PI

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;16-96/Domain: immunoglobulin homology <IMM>

Query Match 77.8%; Score 63; DB 2; Length 114;
Best Local Similarity 70.6%; Pred. No. 0.00061;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 KSSQSVFFSSSQKNYLA 17
|||||:|:|:|
Db 24 KSSQSLVSSNNQKNYLA 40

RESULT 26

PCI214

Ig kappa chain precursor V region (mAb H8) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000

C;Accession: PCI214

R;Hong, H.J.; Kim, A.K.; Ryu, C.J.; Park, S.S.; Chung, H.K.; Kwon, K.S.; Kim, K.L.; Kim,

Gene 121, 331-335, 1992

A;Title: Cloning and characterization of cDNAs coding for heavy and light chains of a mo

A;Reference number: PCI213; MUID:93077049; PMID:1446832

A;Accession: PCI214

A;Molecule type: mRNA

A;Residues: 1-114 <HON>

A;Cross-references: UNIPARC:UPI000011530; GB:M98042; NID:9196749; PIDN:AAA38777.1; PID:

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-20/Domain: signal sequence #status predicted <SIG>

F;21-134/Product: Ig light chain V region #status predicted <MAT>

F;36-116/Domain: immunoglobulin homology <IMM>

Query Match 77.8%; Score 63; DB 2; Length 134;
Best Local Similarity 76.5%; Pred. No. 0.00072;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KSSQSVFFSSSQKNYLA 17
|||||:|:|:|
Db 44 KSSQSLVSSNNQKNYLA 60

RESULT 27

S26040

Ig kappa chain precursor - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 21-Jan-2000

C;Accession: S26040; S78098

R;Okamoto, M.; Honjo, T.

Nucleic Acids Res. 18, 1895, 1990

A;Title: Nucleotide sequences of the gene/cDNA coding for anti-murine erythrocyte autoa

A;Reference number: S09216; MUID:90245589; PMID:2336368

A;Accession: S26040

A;Molecule type: DNA

A;Residues: 1-138 <OKA>

A;Cross-references: UNIPARC:UPI00001769D0; EMBL:X51742

A;Note: the authors translated the codon AGC for residue 107 as Thr and AGT for residue

R;Okamoto, M.

submitted to the EMBL Data Library, February 1990

A;Reference number: S78098

A;Accession: S78098

A;Molecule type: DNA

A;Residues: 1-87, 'W', 89-138 <OKM>

A;Cross-references: UNIPARC:UPI0000116D53; EMBL:X51742; NID:952697; PIDN:CAA36032.1; PI

C;Accession: S26040

C;Keywords: 22/1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;1-25/Domain: signal sequence #status predicted <SIG>

F;26-138/Product: Ig kappa chain (fragment) #status predicted <MAT>

F;41-121/Domain: immunoglobulin homology <IMM>

Query Match 77.8%; Score 63; DB 2; Length 138;
Best Local Similarity 70.6%; Pred. No. 0.00074;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSSQSVFFSSSQKNYLA 17
|||||:|:|:|
Db 49 KSSQSLVSSNNQKNYLA 65

RESULT 28

A49260

antitumor monoclonal CC49 light chain variable region, mAb CC49 VL - mouse

C;Species: Mus musculus (house mouse)

C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000

C;Accession: A49260

R;Bergerel, C.; Padian, E.A.; Kashmiri, S.V.; Milenic, D.; Calvo, B.; Schlom, J.

Proteins 17, 438-443, 1993

A;Title: Crystallographic studies and primary structure of the antitumor monoclonal CC49

A;Reference number: A49260; MUID:94151295; PMID:8108385

A;Accession: A49260

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: nucleic acid

A;Residues: 1-113 <ABE>

A;Cross-references: UNIPARC:UPI00002FCCF

A;Note: sequence extracted from NCBI backbone (NCBI:147720)

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;16-96/Domain: immunoglobulin homology <IMM>

Query Match 76.5%; Score 62; DB 2; Length 113;
Best Local Similarity 70.6%; Pred. No. 0.00091;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 KSSQSVFFSSSQKNYLA 17
|||||:|:|:|
Db 24 KSSQSLVSSNNQKNYLA 40

RESULT 29

K4H17

Ig kappa chain precursor V-IV region (B17) - human

C;Species: Homo sapiens (man)

C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 21-Jan-2000

C;Accession: A01905

R;Marsh, P.; Miller, F.; Gould, H.

Nucleic Acids Res. 13, 6531-6544, 1985

A;Title: Detection of a unique human Vkapapay germ-line gene by a cloned cDNA probe.

A;Reference number: A01905; MUID:86041854; PMID:2997713

Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KSSQSVFFSSSQKNYLA 16
 |||||:|:|:|
 Db 24 KSSQSVLSSNNKNYLA 39

RESULT 34
 PH1053
 Ig light chain V region (clone 163.100) - mouse (fragment)

C:Species: Mus musculus (house mouse)
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
 C:Accession: PH1053
 R:Fillman, D.M.; You, N.T.; Hill, R.J.; Marion, T.N.
 J. Exp. Med. 176, 761-779, 1992
 A:Title: Both IGM and IGG anti-DNA antibodies are the products of clonally selective B
 A:Reference number: PH0971; MUID:92381444; PMID:1512540
 A:Accession: PH1053
 A>Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-104 <TIL>
 A:Cross-references: UNIPARC:UPI0000176AAD
 A:Experimental source: B cell, strain [NZB x NZW]F1
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 74.1%; Score 60; DB 2; Length 104;
 Best Local Similarity 76.5%; Pred. No. 0.0019;
 Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KSSQSVFFSSSQKNYLA 17
 |||||:|:|:|
 Db 24 KSSQSVLSSNNKNYLA 40

RESULT 35
 JIC2270
 PL7-6 antibody light chain - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 21-Jan-2000
 C:Accession: JIC2270; PC2187
 R:Kurume, T.; Katayama, M.; Murakami, K.; Hashino, K.; Yamamoto, M.; Kato, J. Biochem. 115, 608-614, 1994
 A:Title: Expression of recombinant mouse/human chimeric antibody specific to human GMP-1
 A:Reference number: JIC2269; MUID:94334310; PMID:7520038
 A:Accession: JIC2270
 A:Molecule type: mRNA
 A:Residues: 1-113 <KUR>
 A:Cross-references: UNIPARC:UPI0000156488
 A:Accession: PC2187
 A:Molecule type: protein
 A:Residues: 1-21 <KUR>
 A:Cross-references: UNIPARC:UPI0000156488
 A:Experimental source: hybridoma cell
 C:Comment: This protein is specific to human P-selectin.
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 F:1-101/Region: V segment
 F:16-96/Domain: immunoglobulin homology <IMM>
 F:102-113/Region: J segment

Query Match 74.1%; Score 60; DB 2; Length 113;
 Best Local Similarity 76.5%; Pred. No. 0.0021;
 Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KSSQSVFFSSSQKNYLA 17
 |||||:|:|:|
 Db 24 KSSQSVLSSNNKNYLA 40

RESULT 36
 B30535
 Ig kappa chain V region (5C8) - mouse (fragment)

C:Species: Mus musculus (house mouse)
 C>Date: 23-Feb-1989 #sequence_revision 23-Feb-1989 #text_change 21-Jan-2000
 C:Accession: B30535
 R:Clafin, J.L.; Berry, J.; Flaherty, D.; Dunnick, W.
 J. Immunol. 138, 3060-3068, 1987

A:Title: Somatic evolution of diversity among anti-phosphocholine antibodies induced wit
 A:Reference number: A30556; MUID:87196439; PMID:3106498
 A:Accession: B30535
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-107 <CLA>
 A:Cross-references: UNIPARC:UPI0000176AF5
 A>Note: the sequence was determined from the differentiated gene
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 72.8%; Score 59; DB 2; Length 107;
 Best Local Similarity 70.6%; Pred. No. 0.0029;
 Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KSSQSVFFSSSQKNYLA 17
 |||||:|:|:|
 Db 24 KSSQSVLSSNNKNYLA 40

RESULT 37
 S46373
 Ig kappa chain V-J region (724-9) - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
 C:Accession: S46373; S38647
 R:Bensimon, C.; Chastagner, P.; Zouali, M.
 EMBO J. 13, 2951-2962, 1994
 A:Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene rea
 A:Reference number: S46369; MUID:94313975; PMID:8039491
 A:Accession: S46373
 A:Molecule type: mRNA
 A:Residues: 1-132 <BEN>
 A:Cross-references: UNIPARC:UPI00001155A6; EMBL:Z27174; NID:9415963; PIDN:CAAG1698.1; PI
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:34-114/Domain: immunoglobulin homology <IMM>

Query Match 72.8%; Score 59; DB 2; Length 132;
 Best Local Similarity 76.5%; Pred. No. 0.0037;
 Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KSSQSVFFSSSQKNYLA 17
 |||||:|:|:|
 Db 42 KSSQSVLSSNNKNYLA 58

RESULT 38
 S40347
 Ig kappa chain - human
 C:Species: Homo sapiens (man)
 C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C:Accession: S40347
 R:Klein, R.; Jaenichen, R.; Zachau, H.G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
 A:Reference number: S40342; MUID:94080891; PMID:8258341
 A:Accession: S40347
 A>Status: preliminary; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-129 <KLE>
 A:Cross-references: UNIPARC:UPI0000116141; EMBL:X72457; NID:9441382; PIDN:CAAG1125.1; PI
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:33-113/Domain: immunoglobulin homology <IMM>

Query Match 71.6%; Score 58; DB 2; Length 129;

Best Local Similarity 70.6%; Pred. No. 0.0054;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 KSSQSVFPSSSQKNYLA 17
|||||:|:|||||
Db 41 KSSQSVLNSGNQKNYLA 57

RESULT 39

PL0265

Ig kappa chain V region (anti-DNA, DP13VK and DP18VK) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000

C:Accession: P10265

R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Platsky, D.; Marshak-Rothstein, A

J. Exp. Med. 171, 265-297, 1990

A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic

A:Reference number: P10231; MUID:9011618; PMID:2104919

A:Accession: P10265

A:Molecule type: mRNA

A:Residues: 1-112 <SHL>

A:Cross-references: UNIPARC:UPI0000176AF3

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-23/Region: framework 1

F:16-96/Domain: immunoglobulin homology <IMM>

F:24-40/Region: complementarity-determining 1

F:41-55/Region: framework 2

F:56-62/Region: complementarity-determining 2

F:63-94/Region: framework 3

F:95-102/Region: complementarity-determining 3

F:103-112/Region: framework 4

Query Match

Best Local Similarity 70.4%; Score 57; DB 2; Length 112;

Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 KSSQSVFPSSSQKNYLA 17
|||||:|:|||||
Db 24 KSSQSVLNSGNQKNYLA 40

RESULT 40

C30535

Ig kappa chain V region (2B2) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 23-Feb-1989 #sequence_revision 23-Feb-1989 #text_change 21-Jan-2000

C:Accession: C30535

R:Clafilin, J.L.; Berry, J.; Flaherty, D.; Dunnick, W.

J. Immunol. 138, 3060-3068, 1987

A:Title: Somatic evolution of diversity among anti-phosphocholine antibodies induced with

A:Reference number: A30556; MUID:87196439; PMID:3106498

A:Accession: C30535

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-105 <CLA>

A:Cross-references: UNIPARC:UPI0000176AF4

A:Note: the sequence was determined from the differentiated gene

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 69.1%; Score 56; DB 2; Length 105;
Best Local Similarity 70.6%; Pred. No. 0.0098;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 KSSQSVFPSSSQKNYLA 17
|||||:|:|||||
Db 24 KSSQSVLNSGNQKNYLA 40

RESULT 41

F30535

Ig kappa chain V region (5G4) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 23-Feb-1989 #sequence_revision 23-Feb-1989 #text_change 21-Jan-2000

C:Accession: F30535

R:Clafilin, J.L.; Berry, J.; Flaherty, D.; Dunnick, W.

J. Immunol. 138, 3060-3068, 1987

A:Title: Somatic evolution of diversity among anti-phosphocholine antibodies induced with

A:Reference number: A30556; MUID:87196439; PMID:3106498

A:Accession: F30535

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-107 <CLA>

A:Cross-references: UNIPARC:UPI0000176AF4

A:Note: the sequence was determined from the differentiated gene

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 69.1%; Score 56; DB 2; Length 107;
Best Local Similarity 70.6%; Pred. No. 0.01;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 KSSQSVFPSSSQKNYLA 17
|||||:|:|||||
Db 24 KSSQSVLNSGNQKNYLA 40

RESULT 42

D30535

Ig kappa chain V region (7C9) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 23-Feb-1989 #sequence_revision 23-Feb-1989 #text_change 16-Aug-1996

C:Accession: D30535

R:Clafilin, J.L.; Berry, J.; Flaherty, D.; Dunnick, W.

J. Immunol. 138, 3060-3068, 1987

A:Title: Somatic evolution of diversity among anti-phosphocholine antibodies induced with

A:Reference number: A30556; MUID:87196439; PMID:3106498

A:Accession: D30535

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-107 <CLA>

A:Cross-references: UNIPARC:UPI0000176AF9

A:Note: the sequence was determined from the differentiated gene

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 69.1%; Score 56; DB 2; Length 107;
Best Local Similarity 70.6%; Pred. No. 0.01;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 KSSQSVFPSSSQKNYLA 17
|||||:|:|||||
Db 24 KSSQSVLNSGNQKNYLA 40

RESULT 43

G30535

Ig kappa chain V region (2G6) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 23-Feb-1989 #sequence_revision 23-Feb-1989 #text_change 21-Jan-2000

C:Accession: G30535

R:Clafilin, J.L.; Berry, J.; Flaherty, D.; Dunnick, W.

J. Immunol. 138, 3060-3068, 1987

A:Title: Somatic evolution of diversity among anti-phosphocholine antibodies induced with

A:Reference number: A30556; MUID:87196439; PMID:3106498

A:Accession: G30535

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-107 <CLA>

A:Cross-references: UNIPARC:UPI0000176AF6

A:Note: the sequence was determined from the differentiated gene

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 69.1%; Score 56; DB 2; Length 107;
Best Local Similarity 70.6%; Pred. No. 0.01;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 KSSQSVFSSSQKNTLA 17
|||||:|:|||||
DB 24 KSSQSLNSGNQKNTLA 40

RESULT 44

E30538

Ig kappa chain V region (6D10) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 23-Feb-1989 #sequence_revision 23-Feb-1989 #text_change 21-Jan-2000

C:Accession: E30538

R:Clafin, J.L.; Berry, J.; Flaherty, D.; Dunnick, W.

J:Immunol. 138, 3060-3068, 1987

A:Title: Somatic evolution of diversity among anti-phosphocholine antibodies induced with

A:Reference number: A30556; MUID:87196439; PMID:3106498

A:Accession: E30535

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-108 <CLA>

A:Cross-references: UNIPARC:UPI0000176AED

A:Note: the sequence was determined from the differentiated gene

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-96/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 70.6%; Pred. No. 0.01;

Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 KSSQSVFSSSQKNTLA 17
|||||:|:|||||
DB 24 KSSQSLNSGNQKNTLA 40

RESULT 45

F30538

Ig kappa chain V region (253.15D10) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 10-Feb-1989 #sequence_revision 10-Feb-1989 #text_change 21-Jan-2000

C:Accession: F30538

R:Clafin, J.L.; Berry, J.

J:Immunol. 141, 4012-4019, 1988

A:Title: Genetics of the phosphocholine-specific antibody response to Streptococcus pneu

A:Reference number: A30534; MUID:89035545; PMID:3141511

A:Accession: F30538

A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra

A:Molecule type: mRNA

A:Residues: 1-112 <CLA>

A:Cross-references: UNIPARC:UPI0000176CD5

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-96/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 70.6%; Pred. No. 0.01;

Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 KSSQSVFSSSQKNTLA 17
|||||:|:|||||
DB 24 KSSQSLNSGNQKNTLA 40

RESULT 46

E30538

Ig kappa chain V region (253.12D3) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 10-Feb-1989 #sequence_revision 10-Feb-1989 #text_change 21-Jan-2000

C:Accession: E30538

R:Clafin, J.L.; Berry, J.

J:Immunol. 141, 4012-4019, 1988

A:Title: Genetics of the phosphocholine-specific antibody response to Streptococcus pneu

A:Reference number: A30534; MUID:89035545; PMID:3141511

A:Accession: E30538

A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra

A:Molecule type: mRNA

A:Residues: 1-112 <CLA>

A:Cross-references: UNIPARC:UPI0000176CD4

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-96/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 70.6%; Pred. No. 0.01;

Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 KSSQSVFSSSQKNTLA 17
|||||:|:|||||
DB 24 KSSQSLNSGNQKNTLA 40

RESULT 47

S40364

Ig kappa chain - human

C:Species: Homo sapiens (man)

C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C:Accession: S40364

R:Klein, R.; Jaenichen, R.; Zachau, H.G.

J:Immunol. 23, 3248-3271, 1993

A:Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8256341

A:Accession: S40364

A:Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-124 <KLB>

A:Cross-references: UNIPARC:UPI0000176CB0; EMBL:X72474; NID:G441416; PID:G441417

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:26-106/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 58.8%; Pred. No. 0.012;

Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 KSSQSVFSSSQKNTLA 17
|||||:|:|||||
DB 34 KSSRSILVTSNNKNTLA 50

RESULT 48

S37531

Ig kappa chain V region (V-kappa 4) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C:Accession: S37531

R:Klein, U.; Kuipers, R.; Rajewsky, K.

submitted to the EMBL Data Library, September 1993

A:Description: Human IGM(+)19D(+) cells, the major B cell subset in the peripheral blood

A:Reference number: S37501

A:Accession: S37531

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-92 <KLB>

A:Cross-references: UNIPARC:UPI000011658D; EMBL:Z26629; NID:G405704; PIDN:CAAB1382.1; PI

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match

Best Local Similarity 64.7%; Pred. No. 0.013;

Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 KSSQSVFPSSSQKNYLA 17
 |||:|:|:|:|:|
 Db 2 KSSRSVLYSPNNKNYLA 18

RESULT 49

S20648
 Ig heavy chain V region - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
 C:Accession: S20648
 R:osman, M.; Fasy, T.M.; Novick, K.E.; Monestier, M.
 Submitted to the EMBL Data Library, February 1992
 A:Description: Relationships among antinuclear antibodies from autoimmune MRL mice react
 A:Reference number: S20639
 A:Accession: S20648
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-94 <LOS>
 A:Cross-references: UNIPARC:UPI0000116028; EMBL:X65011; NID:g52641; PIDN:CAA46144.1; PID
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

Query Match 67.9%; Score 55; DB 2; Length 94;
 Best Local Similarity 70.6%; Pred. No. 0.013;
 Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 KSSQSVFPSSSQKNYLA 17
 |||:|:|:|:|:|
 Db 24 KSSQSLNRSNQKNYLA 40

RESULT 50

S26336
 Ig light chain V region - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 21-Jan-2000
 C:Accession: S26336
 R:Stark, S.E.; Caton, A.J.
 J. Exp. Med. 174, 613-624, 1991
 A:Title: Antibodies that are specific for a single amino acid interchange in a protein e
 A:Reference number: S26309; WUID:91341421; PMID:1908510
 A:Accession: S26336
 A:Molecule type: mRNA
 A:Residues: 1-109 <STA>
 A:Cross-references: UNIPARC:UPI00001769AF; EMBL:X59201
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-95/Domain: immunoglobulin homology <IMM>

Query Match 67.9%; Score 55; DB 2; Length 109;
 Best Local Similarity 70.6%; Pred. No. 0.015;
 Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 KSSQSVFPSSSQKNYLA 17
 |||:|:|:|:|:|
 Db 23 KSSQSLNRSNQKNYLA 39

Search completed: May 4, 2006, 13:09:15
 Job time : 40.2857 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 4, 2006, 12:46:39 ; Search time 159.206 Seconds
(without alignments)
75.336 Million cell updates/sec

Title: US-10-700-632-4

Perfect score: 81

Sequence: 1 KSSQSVFFSSSQKNYIA 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : UniProt_05.80:*\n1: uniprot_sprot:*\n2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	64	79.0	114	1	KV4A_HUMAN
2	64	79.0	121	1	KV4O_HUMAN
3	64	79.0	133	1	KV4B_HUMAN
4	62	76.5	134	1	KV4C_HUMAN
5	61	75.3	109	1	KV4D_HUMAN
6	60	74.1	240	2	Q52L64_MOUSE
7	58	71.6	130	2	Q9NP29_HUMAN
8	55	67.9	255	2	Q6K805_MOUSE
9	45	55.6	516	2	Q54VY2_DICDI
10	44	54.3	446	2	Q17913_CABEL
11	44	54.3	606	2	Q4YZ19_PLABE
12	44	54.3	674	2	Q9H917_HUMAN
13	44	54.3	674	2	Q6P1W4_HUMAN
14	44	54.3	674	2	Q86V18_HUMAN
15	43	53.1	431	2	Q72RE7_LEPIC
16	43	53.1	431	2	Q8R4C1_LEPIN
17	43	53.1	470	2	Q4Y717_PLACH
18	43	53.1	870	2	Q81JX7_PLAF7
19	42	51.9	286	2	Q54KN1_DICDI
20	42	51.9	295	2	Q94475_DICDI
21	42	51.9	377	2	Q6F092_BACAN
22	42	51.9	378	2	Q81LRF_BACAN
23	42	51.9	379	2	Q6HSW3_BACAN
24	42	51.9	379	2	Q6HD94_BACHK
25	42	51.9	379	2	Q730A1_BACCI
26	42	51.9	380	2	Q4MS37_BACCB
27	42	51.9	380	2	Q634B2_BACCB
28	42	51.9	380	2	Q817V5_BACCR
29	42	51.9	499	2	Q51KX5_MAGGR
30	42	51.9	607	2	Q65ZJ1_CABEL
31	42	51.9	619	2	Q83182_TREPA

32	42	51.9	621	2	Q18897_CABEL	Q18897 caenorhabdi
33	42	51.9	694	2	Q9VL25_DROME	Q9VL25 drosophila
34	42	51.9	3933	2	Q97239_PLAF7	Q97239 plasmodium
35	41	50.6	232	2	Q97MX3_CIOAB	Q97MX3 clostridium
36	41	50.6	290	2	Q5P012_XENPA	Q5P012 xenopus lae
37	41	50.6	296	2	Q9LS30_PHYPA	Q9LS30 physcomitre
38	41	50.6	313	2	Q5DCCO_SCHJA	Q5DCCO schistosoma
39	41	50.6	396	2	Q75H81_ORYSA	Q75H81 oryza sativ
40	41	50.6	463	2	Q59S58_CANAL	Q59S58 candida alb
41	41	50.6	509	1	MATK_AUSVS	Q9560 austrococyl
42	41	50.6	510	2	Q5LEB8_BACFN	Q5LEB8 bacteroides
43	41	50.6	521	1	DBP45_DROME	Q07886 drosophila
44	41	50.6	542	2	Q86132_DICDI	Q86132 dictyosteli
45	41	50.6	543	2	Q64VD1_BACFR	Q64VD1 bacteroides
46	41	50.6	653	2	Q75HM8_ORYSA	Q75HM8 oryza sativ
47	41	50.6	745	2	Q7QC68_AMOGA	Q7QC68 anopheles g
48	41	50.6	752	2	Q4YW61_PLABE	Q4YW61 plasmodium
49	41	50.6	944	2	Q7R3J8_PLAYO	Q7R3J8 plasmodium
50	41	50.6	1047	2	Q7RM00_PLAYO	Q7RM00 plasmodium
51	41	50.6	1223	1	SRE9_SCHPO	Q9HE02 schizosacch
52	41	50.6	3650	2	Q6RKL4_GIBMO	Q6RKL4 gibberella
53	41	50.6	5229	2	Q7RTF4_PLAYO	Q7RTF4 plasmodium
54	40.5	50.0	294	2	Q9XVP3_CABEL	Q9XVP3 caenorhabdi
55	40.5	50.0	400	2	Q58NA3_CHLYR	Q58NA3 chlamydia t
56	40.5	50.0	400	2	Q84642_CHLYR	Q84642 chlamydia t
57	40.5	50.0	523	2	Q9X112_ARATH	Q9X112 arabidopsis
58	40.5	50.0	57	2	Q71111_LACDL	Q71111 lactobacill
59	40.4	49.4	70	2	Q4X103_PLACH	Q4X103 plasmodium
60	40.4	49.4	137	2	Q4X8X1_PLACH	Q4X8X1 plasmodium
61	40.4	49.4	174	2	Q4XZD4_PLACH	Q4XZD4 plasmodium
62	40.4	49.4	175	2	Q4X119_PLACH	Q4X119 plasmodium
63	40.4	49.4	207	1	ERP4_YEAST	Q1450 saccharomyc
64	40.4	49.4	273	2	Q517F9_ENTHI	Q517F9 entamoeba h
65	40.4	49.4	281	2	Q4YPO2_PLABE	Q4YPO2 plasmodium
66	40.4	49.4	292	2	P95854_SULSO	P95854 sulfolobus
67	40.4	49.4	298	2	Q4X338_PLACH	Q4X338 plasmodium
68	40.4	49.4	347	1	RUVB_BORBU	Q70828 borrella bu
69	40.4	49.4	369	1	DHAX_BUCBP	Q893ab8 buchnera ap
70	40.4	49.4	380	2	Q4YPC5_PLABE	Q4YPC5 plasmodium
71	40.4	49.4	380	2	Q9BB91_USED0	Q9BB91 phedimus hy
72	40.4	49.4	399	2	Q5CGW2_CRYUD	Q5CGW2 cryptospori
73	40.4	49.4	425	2	Q5GSD8_PLABE	Q5GSD8 plasmodium
74	40.4	49.4	483	2	Q6FAU9_ACTIAD	Q6FAU9 actinobact
75	40.4	49.4	511	2	Q4HG77_CAMCO	Q4HG77 campylobact
76	40.4	49.4	627	2	Q5MW44_BACSK	Q5MW44 bacillus cl
77	40.4	49.4	676	2	Q7RDE6_PLAYO	Q7RDE6 plasmodium
78	40.4	49.4	710	2	Q5B0R3_EMENT	Q5B0R3 aspergillus
79	40.4	49.4	738	2	Q50112_XENTR	Q50112 xenopus tro
80	40.4	49.4	754	2	Q4XVL8_PLACH	Q4XVL8 plasmodium
81	40.4	49.4	1661	2	Q7QX84_GIADLA	Q7QX84 giardia lam
82	40.4	49.4	1665	2	Q52B02_MAGGR	Q52B02 magnaporthe
83	40.4	49.4	1726	2	Q4XRS9_PLACH	Q4XRS9 plasmodium
84	40.4	49.4	1800	2	Q5CQZ7_CRYPV	Q5CQZ7 cryptospori
85	40.4	49.4	1819	2	Q7R3J5_PLAYO	Q7R3J5 plasmodium
86	40.4	49.4	4015	2	Q4YV66_PLABE	Q4YV66 plasmodium
87	40.4	49.4	1054	2	Q54KX3_DICDI	Q54KX3 dictyosteli
88	39.5	48.8	38	2	Q4XN85_PLACH	Q4XN85 plasmodium
89	39.5	48.1	43	2	Q8N0T1_HUMAN	Q8N0T1 homo sapien
90	39.5	48.1	99	2	Q5B484_EMENT	Q5B484 aspergillus
91	39.5	48.1	136	1	NRDI_ECOS7	P08773 escherichia
92	39.5	48.1	136	1	NRDI_ECOLI	P08773 escherichia
93	39.5	48.1	136	1	NRDI_ECOLI	P08773 escherichia
94	39.5	48.1	136	1	NRDI_SHIRL	P08775 shigella fl
95	39.5	48.1	139	2	Q5HV45_CAMJR	Q5HV45 campylobact
96	39.5	48.1	140	2	Q5HUN2_ARATH	Q5HUN2 arabidopsi
97	39.5	48.1	158	2	Q73ON4_TREDE	Q73ON4 trepionema d
98	39.5	48.1	184	2	Q6IVS0_PGAMM	Q6IVS0 uncultured
99	39.5	48.1	210	2	Q5BFU0_EMENT	Q5BFU0 aspergillus
100	39.5	48.1	212	2	Q5D922_SCHJA	Q5D922 schistosoma
101	39.5	48.1	322	2	Q58MW3_GCAUD	Q58MW3 cyanophage
102	39.5	48.1	337	1	Y1076_MERTU	Q58476 methanococc
103	39.5	48.1	339	2	Q54A03_DICDI	Q54A03 dictyosteli
104	39.5	48.1	347	2	Q4KZ34_ECOLI	Q4KZ34 escherichia

105	39	48.1	372	2	05CKN3_CRYHO	05ckn3 cryptospori	178	38	46.9	416	2	090G3_9NIDO	090g3 human torov
106	39	48.1	373	2	06FUN3_CANEA	06fun3 candida gia	179	38	46.9	450	2	04TGO_6IBZE	04tgo gibberella
107	39	48.1	418	2	04ZXB1_PSEBY	04zxb1 pseudomonas	180	38	46.9	451	2	07Z1P3_CABEL	07z1p3 caenorhabdi
108	39	48.1	443	2	09LJG2_ARATH	09ljg2 arabidopsis	181	38	46.9	452	2	050YV9_ENTHI	050yv9 entamoeba h
109	39	48.1	445	2	04546 STAHJ	04546 staphylococ	182	38	46.9	453	2	065624_ARATH	065624 arabidopsis
110	39	48.1	458	2	067P6_ORYSA	067p6 oryza sativ	183	38	46.9	459	1	ARLY_BUCAP	08KAS9 buchnera lae
111	39	48.1	468	2	07RGT1_PLAYO	07rgt1 plasmodium	184	38	46.9	466	2	06NRG3_XENIA	06nrng3 xenopus lae
112	39	48.1	468	2	08LF37_ARATH	08lf37 arabidopsis	185	38	46.9	467	2	0949P1_ARATH	0949p1 arabidopsis
113	39	48.1	510	2	06ZDE3_ORYSA	06zde3 oryza sativ	186	38	46.9	469	2	07Y187_ORYSA	07y187 oryza sativ
114	39	48.1	514	1	MATK_DROLU	023637 ARATH	187	38	46.9	494	2	07RP4_PLAYO	07rp4 plasmodium
115	39	48.1	517	2	023637_ARATH	023637 arabidopsis	188	38	46.9	503	2	08WKM3_9NMGJ	08wkm3 hyalotrichi
116	39	48.1	517	2	09AR1_ARATH	09ard1 arabidopsis	189	38	46.9	514	2	09ZMS4_RHIME	09zms4 rhizobium m
117	39	48.1	517	2	09LEU8_ARATH	09leu8 arabidopsis	190	38	46.9	522	2	060AT1_METCA	060at1 methylococc
118	39	48.1	553	2	09ZJUS_HELPU	09zjjs hellicobacte	191	38	46.9	523	2	05LE91_BACFN	05le91 bacteroides
119	39	48.1	566	2	09FMJ3_ARATH	09fmj3 arabidopsis	192	38	46.9	533	2	064VD4_BACFR	064vd4 bacteroides
120	39	48.1	607	2	054FR3_DICDI	054fr3 dicystostei	193	38	46.9	533	2	08L7Y9_ARATH	08l7y9 arabidopsis
121	39	48.1	728	2	04Z055_PLABE	04z055 plasmodium	194	38	46.9	533	2	09JML5_ARATH	09jml5 arabidopsis
122	39	48.1	752	2	059T53_CANAL	059t53 candida alb	195	38	46.9	612	2	05GSMO_WOLTR	05gsmo wolbachia s
123	39	48.1	773	2	0725U3_DESVA	0725j3 desulfovibr	196	38	46.9	612	2	04HKW3_CAMLA	04hkws campylobact
124	39	48.1	817	2	088K06_PSEBP	088k06 pseudomonas	197	38	46.9	640	2	093AP2_STPAM	093ap2 strephyloccc
125	39	48.1	828	2	04KBX3_PSEBP	04kbx3 pseudomonas	198	38	46.9	640	2	08C0E3_STIAP	08c0e3 strephyloccc
126	39	48.1	897	2	04IAYS_GIBZE	04iays gibberella	199	38	46.9	675	2	09FNM5_ARYTH	09fnm5 arabidopsis
127	39	48.1	972	2	09ZJW1_HELPU	09zjw1 helicobacte	200	38	46.9	681	2	08RWP3_ARATH	08rwp3 arabidopsis
128	39	48.1	1049	2	045572_CABEL	045572 caenorhabdi	201	38	46.9	722	2	06GNB3_XENIA	06gnb3 xenopus lae
129	39	48.1	1140	2	04I3D7_GIBZE	04i3d7 gibberella	202	38	46.9	722	2	054FZ9_DICDI	054fz9 dicystostei
130	39	48.1	1171	2	08EC38_SHEON	08ec38 shewanella	203	38	46.9	757	2	021407_CABEL	021407 caenorhabdi
131	39	48.1	1216	2	06L2C5_PICTO	06l2c5 picrophilus	204	38	46.9	775	2	04K536_PLACH	04k536 plasmodium
132	39	48.1	1317	2	07RDR7_PLAYO	07rd77 plasmodium	205	38	46.9	778	2	06CP63_KULIA	06cp63 kluyveromyc
133	39	48.1	1322	2	07X7E9_ORYSA	07x7e9 oryza sativ	206	38	46.9	779	1	PURL_PROMP	07V315 pichlorotoxo
134	39	48.1	1510	2	07RDA0_PLAYO	07rda0 plasmodium	207	38	46.9	810	2	0814Y6_PLAF7	0814y6 plasmodium
135	39	48.1	1511	2	05BHE7_EWENT	05bhe7 aspergillus	208	38	46.9	866	2	05KMG9_CRYNE	05kmg9 cryptococcu
136	39	48.1	2117	2	05BK90_MAGGR	05bk90 magnaporthe	209	38	46.9	866	2	05ZBR4_CRYNE	05zbr4 cryptococcu
137	39	48.1	4133	2	06JN13_BURMA	06jn13 burkholderi	210	38	46.9	919	2	054RG2_DICDI	054rg2 dicystostei
138	39	48.1	4580	2	04VFE5_BURMA	04vfe5 burkholderi	211	38	46.9	933	2	04XY01_PLACH	04xy01 plasmodium
139	39	48.1	6858	2	07OW11_GIALA	07ow11 giardia lam	212	38	46.9	930	2	0811I6_PLAF7	0811i6 plasmodium
38.5	38	47.5	304	1	HTPX_LISMO	09y8e1 listeria mo	213	38	46.9	937	2	07R790_PLAYO	07r790 plasmodium
140	38	46.9	72	2	08B601_VYIRU	08b601 tobacco mos	214	38	46.9	996	2	08VNS4_YANSP	08vns4 yarrowia li
141	38	46.9	83	2	07R43_LEPIC	07r43 leptospira	215	38	46.9	1011	2	06CR27_YARLI	06cr27 yarrowia li
142	38	46.9	88	2	08F4P0_LEPIC	08f4p0 leptospira	216	38	46.9	1028	2	09V3C4_DROME	09v3c4 drosophila
143	38	46.9	91	2	04Y749_PLACH	04y749 plasmodium	217	38	46.9	1088	2	059P41_CANAL	059p41 candida alb
144	38	46.9	91	2	04XKG8_PLACH	04xkg8 plasmodium	218	38	46.9	1125	2	055BQ3_DICDI	055bq3 dicystostei
145	38	46.9	116	2	04XKG8_PLACH	04xkg8 schistosoma	219	38	46.9	1241	2	09SH75_ARATH	09sh75 arabidopsis
146	38	46.9	158	2	06X900_SCHUA	06x900 bacillus th	220	38	46.9	1267	2	09NGM0_STRPU	09ngm0 strongyloce
147	38	46.9	167	2	06X3W7_VYIRU	06x3w7 bacillus th	221	38	46.9	1378	2	04N1P0_THERA	04n1p0 thelairaia p
148	38	46.9	167	2	07WSG7_BACTU	07wsg7 bacillus th	222	38	46.9	1535	2	06K9S9_ORYSA	06k9s9 oryza sativ
149	38	46.9	168	2	054JN4_DICDI	054j4 dicystostei	223	38	46.9	1589	2	08KA02_DICDI	08ka02 dicystostei
150	38	46.9	183	2	07SEKO_ASHGO	07seko ashbya goss	224	38	46.9	1589	2	08WTP4_DICDI	08wtp4 dicystostei
151	38	46.9	224	2	0531L0_ORYSA	0531l0 oryza sativ	225	38	46.9	2077	1	NIPB_DROME	081q7 plasmodium
152	38	46.9	239	2	09NGJ8_STRPU	09ngj8 strongyloce	226	38	46.9	4832	2	081I07_PLAF7	081i07 plasmodium
153	38	46.9	244	2	07R7T3_PLAYO	07r7t3 plasmodium	227	38	46.9	9271	2	08IS87_PLAF7	08is87 plasmodium
154	38	46.9	244	2	05OU02_ENTHI	05ou02 entamoeba h	228	38	46.9	400	2	09PUL0_CHLNU	09pul0 chlamydia m
155	38	46.9	249	2	097H88_CIOAB	097h88 clostridium	229	38	46.9	43	2	05NPN3_ZYMMO	05npn3 zymomonas m
156	38	46.9	270	2	051H11_ENTHI	051h11 entamoeba h	230	38	46.9	51	2	09J210_SHEPC	09j210 heparitis c
157	38	46.9	271	2	07Z1P2_CABEL	07z1p2 caenorhabdi	231	38	46.9	72	2	04GYT3_GTRYP	04gyt3 trypanosoma
158	38	46.9	273	2	065HRT_BACLD	065hrt bacillus li	232	38	46.9	75	2	04XYV1_PLABE	04xyv1 plasmodium
159	38	46.9	282	2	069LG4_ORYSA	069lg4 oryza sativ	233	38	46.9	75	2	08R0I8_BACCE	08r0i8 bacillus ce
160	38	46.9	295	2	09NGJ9_STRPU	09ngj9 strongyloce	234	38	46.9	88	2	06SF08_BACCH	06sf08 uncultured
161	38	46.9	322	2	09ZQ36_ARATH	09zq36 arabidopsis	235	38	46.9	95	2	09KFE8_BACT	09kfe8 bacillus na
162	38	46.9	322	2	08HIM6_ARATH	08him6 arabidopsis	236	38	46.9	103	1	04T2D4_TETNG	04t2d4 tetraodon n
163	38	46.9	333	2	054C63_DICDI	054c63 dicystostei	237	38	46.9	110	2	07Q7Z8_ANOCA	07q7z8 anopheles g
164	38	46.9	334	2	09GGP4_9ASTR	09ggp4 thegadiolus	238	38	46.9	153	2	073BE4_BACCI	073be4 bacillus ce
165	38	46.9	336	1	Y6Z5_METPA	098042 methanococ	239	38	46.9	155	2	081ZF2_BACCI	081zf2 bacillus an
166	38	46.9	354	2	06B0T5_DEBVA	06b0t5 debaryomyce	240	38	46.9	156	2	064WV6_BACFR	064wv6 bacteroides
167	38	46.9	360	2	07WPL5_VIBVY	07wpl5 vibrio vuln	241	38	46.9	165	2	08T9C6_DROME	08t9c6 drosophila
168	38	46.9	366	1	FLGI_LEPIC	08f2s8 leptospira	242	38	46.9	170	2	09ZKL3_HELPU	09zkl3 hellicobacte
169	38	46.9	366	1	FLGI_LEPIC	08f2s9 leptospira	243	38	46.9	173	2	04M1A2_BACE	04m1a2 bacillus ce
170	38	46.9	368	1	P91449_CABEL	p91449 caenorhabdi	244	38	46.9	182	2	073FC7_BACCI	073fc7 bacillus ce
171	38	46.9	371	2	06LIMV5_CABER	06limv5 caenorhabdi	245	38	46.9	182	2	081WV1_BACKN	081wv1 bacillus na
172	38	46.9	377	2	05TID0_MOUSE	05tid0 mus musculi	246	38	46.9	182	2	06HPT8_BACKN	06hpt8 bacillus th
173	38	46.9	386	2	09LSB2_ARATH	09lsb2 arabidopsis	247	38	46.9	182	2	063HC0_BACCE	063hc0 bacillus ce
174	38	46.9	401	1	Y1002_CHICV	09p5m3 chlamydophi	248	38	46.9	182	2	063HC0_BACCE	063hc0 bacillus ce
175	38	46.9	409	1	04P5M3_USTMA	04p5m3 ustilago ma	249	38	46.9	183	2	081J68_BACCR	081j68 bacillus ce
176	38	46.9	412	2	04S301_CABEL	04s301 caenorhabdi	250	38	46.9	202	2	05K743_URCC	05k743 dolium na
177	38	46.9	413	2	080F55_TTICI	08f55 titlurus ca	250	38	46.9	202	2	05K743_URCC	05k743 dolium na

[illegible]

251	37	45.7	222	2	O54UJ2_DICDI	O54J2 dictyosteli	324	37	45.7	959	1	DP01_AERPE	O93745 aeropyrum f	
252	37	45.7	241	1	PLFG_RHIL0	O98e3 rhizobium l	325	37	45.7	979	2	O4T5V1_TETNG	O4T5V1 theleria f	
253	37	45.7	244	2	O5L3A6_GEOXA	O5L3a6 geobacillus	326	37	45.7	1001	2	O4UC45_THEAN	O4UC45 theileria a	
254	37	45.7	245	2	O02665_PODAN	O02665 podospora a	327	37	45.7	1031	1	YDG9_SCHPO	P10496 schizosacche	
255	37	45.7	247	2	O5L670_CHLAB	O5L670 chlamydomo	328	37	45.7	1071	1	UBP7_YEAST	O14053 saccharomy	
256	37	45.7	266	2	O98S40_GUTTH	O98S40 guttallia	329	37	45.7	1109	2	O8RYQ0_BACAN	O8RYQ0 bacillus ar	
257	37	45.7	267	2	O4X628_PLACH	O4X628 plasmodium	330	37	45.7	1109	2	O4MKK5_BACAN	O4MKK5 bacillus ac	
258	37	45.7	268	2	O4Y0M6_PLABE	O4Y0M6 plasmodium	331	37	45.7	1109	2	O6EZV3_BACAN	O6EZV3 bacillus ac	
259	37	45.7	270	2	O89NH9_BRAJA	O89nh9 bradyrhizob	332	37	45.7	1111	1	KIPI_YEAST	P28742 saccharomy	
260	37	45.7	279	2	O36506_PEPPO	O36506 pepercopia p	333	37	45.7	1132	1	CT106_HUMAN	O6P010 homo sapien	
261	37	45.7	280	2	O20954_PEPBO	O20954 pepercopia o	334	37	45.7	1166	2	O74P21_BACCL	O74P21 bacillus ce	
262	37	45.7	280	2	O20956_PMAPN	O20956 pepercopia c	335	37	45.7	1261	2	O5KGT3_CRYNE	O5KGT3 cryptococcu	
263	37	45.7	283	2	O20953_PEPGR	O20953 pepercopia g	336	37	45.7	1264	2	O5LEU1_BNTHI	O5LEU1 entamoeba h	
264	37	45.7	301	2	O4UDK1_THEAN	O4UDK1 theileria a	337	37	45.7	1287	2	O7PDW0_PLAYO	O7PDW0 plasmodium	
265	37	45.7	304	1	HTPX_LISIN	O92458 listeria in	338	37	45.7	1298	2	O4YV32_PLABE	O4YV32 plasmodium	
266	37	45.7	304	2	O4XVR7_PLACH	O4XVR7 plasmodium	339	37	45.7	1302	2	O5SSD9_CRYNE	O5SSD9 cryne	
267	37	45.7	305	2	O59A94_PLAL0	O59A94 ornithobact	340	37	45.7	1378	2	O8EW21_MYCPE	O8EW21 mycoplasma	
268	37	45.7	322	2	O6UNK7_GOSHI	O6UNK7 goessyptium h	341	37	45.7	1538	2	O72OP6_LEPIC	O72OP6 leptospira	
269	37	45.7	334	2	O5CJH5_CRYHO	O5CJH5 cryptospori	342	37	45.7	1780	2	O6FTH3_CANGA	O6FTH3 candida gla	
270	37	45.7	345	2	O4T0U1_TETNG	O4T0U1 tetraodon n	343	37	45.7	1898	2	O6ZPI4_MOUSE	O6ZPI4 mus musculi	
271	37	45.7	383	2	O5LJ40_BACFN	O5LJ40 bacteroides	344	37	45.7	1941	2	O54JF1_DICDI	O54JF1 dictyosteli	
272	37	45.7	398	2	O40066_HORVU	O40066 hordeum vul	345	37	45.7	2026	2	O81S65_PLAP7	O81S65 plasmodium	
273	37	45.7	399	1	PRYZ_HORVU	P06Z93 hordeum vul	346	37	45.7	2124	2	O6FXG1_CANGA	O6FXG1 candida gla	
274	37	45.7	400	2	O40076_HORVU	O40076 hordeum vul	347	37	45.7	2218	2	O8RYJ1_SITAU	O8RYJ1 sitmaetella	
275	37	45.7	400	2	O64Q28_BACFR	O64Q28 bacteroides	348	37	45.7	2271	2	O4YC54_PLABE	O4YC54 plasmodium	
276	37	45.7	402	2	O9ZIT8_ECOLI	O9ZIT8 escherichia	349	37	45.7	2732	2	O8G341_BRUBU	O8G341 bruceella su	
277	37	45.7	402	2	O7DB96_ECO57	O7DB96 escherichia	350	37	45.7	2773	2	O8IBF4_PLAP7	O8IBF4 plasmodium	
278	37	45.7	408	2	O83BP1_SHIFL	O83BP1 shigella fl	351	37	45.7	2789	2	O9BXT5_HUMAN	O9BXT5 homo sapien	
279	37	45.7	408	2	O4XRX0_PLACH	O4XRX0 plasmodium	352	37	45.7	2831	2	O8S166_BRUBA	O8S166 bruceella ab	
280	37	45.7	409	2	O8B194_STRAS	O8B194 streptococc	353	37	45.7	2867	2	O57FR0_BRUBA	O57FR0 bruceella ab	
281	37	45.7	409	2	O8B6P9_STRAS	O8B6P9 streptococc	354	37	45.7	2867	2	O8YEP1_BRUME	O8YEP1 bruceella me	
282	37	45.7	413	2	O4XYM3_PLACH	O4XYM3 plasmodium	355	37	45.7	3005	1	ZFH2_DROME	ZFH2 drosophila	
283	37	45.7	417	2	O9V6O3_DROME	O9V6O3 drosophila	356	37	45.7	3663	2	O7RTC2_PLAYO	O7RTC2 plasmodium	
284	37	45.7	417	2	O9V6O4_DROME	O9V64 drosophila	357	37	45.7	5052	2	O5MP00_BACT	O5MP00 symbiont ba	
285	37	45.7	442	2	O7SH78_ORYSA	O7SH78 oryza sativ	358	37	45.7	1122	1	RL18E_PICTO	O61295 picrophilus	
286	37	45.7	446	2	O5SRN8_PONPY	O5SRN8 pongo pygma	359	37	45.7	212	2	O7NAV4_MYCGA	O7NAV4 mycoplasma	
287	37	45.7	450	2	O6OT00_CABBR	O6OT00 caenorhabdi	360	37	45.7	396	2	O7VAK6_PROMA	O7VAK6 prochloroc	
288	37	45.7	453	2	O8YNO7_ANASP	O8YNO7 anabaena sp	361	37	45.7	45.1	689	2	O5CPQ0_CRYPV	O5CPQ0 cryptospori
289	37	45.7	459	2	O5SD89_DICDI	O5SD89 dictyosteli	362	37	45.7	45.1	1377	2	O9VJ42_DROME	O9VJ42 drosophila
290	37	45.7	460	2	O54V83_DICDI	O54V83 dictyosteli	363	37	45.7	45.1	33	2	O5BZ45_SCHJA	O5BZ45 schistosoma
291	37	45.7	464	2	O8TY63_METKA	O8TY63 methanopyru	364	37	45.7	44.4	43	2	O888U5_PESBM	O888U5 pseudomonas
292	37	45.7	470	2	O617V7_CABBR	O617V7 caenorhabdi	365	37	45.7	44.4	53	2	O4XTY6_PLACH	O4XTY6 plasmodium
293	37	45.7	478	1	VINC_HUMAN	P04004 homo sapien	366	37	45.7	44.4	56	2	O5BXE7_SCHJA	O5BXE7 schistosoma
294	37	45.7	478	2	O5NV55_PONPY	O5NV55 pongo pygma	367	37	45.7	44.4	61	2	O4X8M6_PLACH	O4X8M6 plasmodium
295	37	45.7	487	2	O5UJF8_ORYSA	O5UJF8 oryza sativ	368	37	45.7	44.4	62	2	O72SW7_LEPIC	O72SW7 leptospira
296	37	45.7	488	2	O5BP07_EMENT	O5BP07 aspergillus	369	37	45.7	44.4	73	2	O9XSW9_PANGI	O9XSW9 pantocoea cit
297	37	45.7	490	2	O84680_CHLTR	O84680 chlamydia t	370	37	45.7	44.4	93	2	O4ZT21_PESBY	O4ZT21 pseudomonas
298	37	45.7	509	2	O8YV35_PLACH	O8YV35 plasmodium	371	37	45.7	44.4	102	2	O87HL6_VIBPA	O87HL6 vibrio para
299	37	45.7	516	2	O8BVV2_MOUSE	O8BVV2 mus musculi	372	37	45.7	44.4	109	2	O8CA19_MOUSE	O8CA19 mus musculi
300	37	45.7	524	2	O5TMZ6_ANOGA	O5TMZ6 anopheles g	373	37	45.7	44.4	114	2	O8Y521_LISMO	O8Y521 listeria mo
301	37	45.7	567	2	O6ETW1_ORYSA	O6ETW1 oryza sativ	374	37	45.7	44.4	134	2	O7OV62_GITALA	O7OV62 giardia lam
302	37	45.7	569	2	O7R8P0_PLAYO	O7R8P0 plasmodium	375	37	45.7	44.4	134	2	O6SV08_GNUCL	O6SV08 antheraea p
303	37	45.7	574	2	O4MYX7_THEPA	O4MYX7 theileria p	376	37	45.7	44.4	140	2	O4SLB8_TETNG	O4SLB8 tetraodon n
304	37	45.7	609	2	O5Z2L1_MYCHY	O5Z2L1 mycoplasma	377	37	45.7	44.4	145	1	LIRP_LOCMI	P41818 locusta mig
305	37	45.7	612	1	GIDA_MYCCE	P47619 mycoplasma	378	37	45.7	44.4	146	2	O6SUZ3_GNUCL	O6SUZ3 trichoplusi
306	37	45.7	612	2	O7RFM5_PLAYO	O7RFM5 plasmodium	379	37	45.7	44.4	146	2	O6SV03_NPVEM	O6SV03 bombyx mori
307	37	45.7	612	2	O6M1J2_BDEBA	O6M1J2 bdellovibri	380	37	45.7	44.4	152	2	O8EP25_SCHJA	O8EP25 schistosoma
308	37	45.7	616	1	EYA4_MOUSE	O91191 mus musculi	381	37	45.7	44.4	152	2	O01918_PHYIN	O01918 phytothor
309	37	45.7	616	2	O8BY78_MOUSE	O8BY78 mus musculi	382	37	45.7	44.4	157	2	O5QLC1_ORYSA	O5QLC1 oryza sativ
310	37	45.7	625	2	O5DGS2_SCHJA	O5DGS2 schistosoma	383	37	45.7	44.4	158	2	O5B109_EMENT	O5B109 aspergillus
311	37	45.7	636	2	O4RR13_TETNG	O4RR13 tetraodon n	384	37	45.7	44.4	165	2	O7RDU9_PLAYO	O7RDU9 plasmodium
312	37	45.7	680	2	O91GK9_NPVER	O91GK9 ephypae po	385	37	45.7	44.4	166	2	O9ZNX8_TOBAC	O9ZNX8 nicotiana t
313	37	45.7	765	2	O7RC10_PLAYO	O7RC10 plasmodium	386	37	45.7	44.4	167	2	O8EYV0_MYCPE	O8EYV0 mycoplasma
314	37	45.7	793	2	O7RDY3_PLAYO	O7RDY3 plasmodium	387	37	45.7	44.4	171	2	O5UPF9_MIMTY	O5UPF9 mimivirus
315	37	45.7	821	2	O54V08_DICDI	O54V08 dictyosteli	388	37	45.7	44.4	173	2	O7RCQ9_PLAYO	O7RCQ9 plasmodium
316	37	45.7	839	2	O7XDO4_ORYSA	O7XDO4 oryza sativ	389	37	45.7	44.4	188	2	O72MS8_LEPIC	O72MS8 leptospira
317	37	45.7	851	2	O4Z1N7_PLABE	O4Z1N7 plasmodium	390	37	45.7	44.4	188	2	O8EYV6_LEPIC	O8EYV6 leptospira
318	37	45.7	881	2	O8EM44_MYCPE	O8EM44 mycoplasma	391	37	45.7	44.4	190	2	O9ALO2_ENTPA	O9ALO2 enterococcu
319	37	45.7	885	2	O6KHN7_MYCMO	O6KHN7 mycoplasma	392	37	45.7	44.4	192	2	O812P8_PLAP7	O812P8 plasmodium
320	37	45.7	885	2	O91615_XENLA	O91615 xenopus lae	393	37	45.7	44.4	205	2	O4HHC1_CAMCO	O4HHC1 campylobact
321	37	45.7	923	2	O7RHB7_PLAYO	O7RHB7 plasmodium	394	37	45.7	44.4	207	2	O5MBL6_XENTR	O5MBL6 xenopus tro
322	37	45.7	931	2	O8IDU4_PLAF7	O8IDU4 plasmodium	395	37	45.7	44.4	231	2	O4XRC8_PLACH	O4XRC8 plasmodium
323	37	45.7	936	2	O8IBS9_PLAF7	O8IBS9 plasmodium	396	37	45.7	44.4	233	2	O5LSN7_CHLAB	O5LSN7 chlamydomo

397	36	44.4	240	2	05GSB6	WOLTR	05gs66 wolbachia s	470	36	44.4	535	2	04Z3Z1	PIABE	04z3z1 plasmodium
398	36	44.4	240	2	073GK1	WOLPM	073gk1 wolbachia p	471	36	44.4	538	1	YOK4	CABEL	099288 caenorhabdi
399	36	44.4	258	2	004209	ARATH	004209 arabidopsis	472	36	44.4	543	2	09CH21	IACAL	09ch21 laccococcus
400	36	44.4	258	2	0819R8	ARATH	0819r8 arabidopsis	473	36	44.4	545	2	06CD74	YARLI	06cd74 yarrowia li
401	36	44.4	258	2	07MP97	VIBVY	07mf97 vibrio vuln	474	36	44.4	555	2	04KEF3	PSEB5	04kef3 pseudomonas
402	36	44.4	260	2	0710U2	TRIST	071qj2 trimeresuru	475	36	44.4	558	2	05CG40	CRYHO	05cg40 c espi prom
403	36	44.4	260	2	0710I4	TRIST	071qj2 trimeresuru	476	36	44.4	568	2	06DWM5	9CRUS	06dwm5 triops long
404	36	44.4	270	2	05AH30	CANAL	05ah30 candida alb	477	36	44.4	572	1	K2C1B	HOUSE	06tf66 mus musculu
405	36	44.4	274	2	04XGM2	PLACH	04xgm2 plasmodium	478	36	44.4	577	2	07NAZ0	MYCGA	07naz0 mycoplasma
406	36	44.4	276	1	DLX2B	BRARE	098876 brachydanio	479	36	44.4	584	2	072U41	LEPIC	072u41 leptospira
407	36	44.4	277	2	079543	CATRO	079543 catharanthu	480	36	44.4	595	2	054HP5	DICDI	054hp5 medicago tr
408	36	44.4	290	2	05SDN1	DICDI	05sdn1 dictyosteli	481	36	44.4	601	2	08IDP3	PIAF7	08idp3 plasmodium
409	36	44.4	291	2	05NFD5	FRATY	05nfd5 francisella	482	36	44.4	613	2	05HT02	CAMR	05ht02 campylobact
410	36	44.4	298	2	04YOR7	PIABE	04yq77 piabeb	483	36	44.4	639	2	08D341	WIGBR	08d341 wigglewort
411	36	44.4	301	2	04NSZ6	THEPA	04nsz6 theileria p	484	36	44.4	654	2	06YVY2	GLILI	06yv22 hangana ma
412	36	44.4	305	2	073NE4	TREDE	073ne4 treponema d	485	36	44.4	673	2	091HA3	ARATH	091ha3 arabidopsis
413	36	44.4	317	2	04QEH6	LEIMA	04qeh6 leishmania	486	36	44.4	687	2	04YVA2	PIABE	04yva2 plasmodium
414	36	44.4	320	2	087T08	PESBM	087t08 pseudomonas	487	36	44.4	688	2	091X99	CAEBR	091x99 caenorhabdi
415	36	44.4	322	2	07RHX0	PLAYO	07rhx0 plasmodium	488	36	44.4	689	2	095AX2	GLILI	095ax2 hangana ma
416	36	44.4	323	2	09GGM3	9ASTR	09gsm3 utrospermum	489	36	44.4	699	2	003620	PLANI	003620 caryopteris
417	36	44.4	325	2	08BV78	METMA	08bv78 methanosarc	490	36	44.4	720	2	03YCU7	PIABE	03ycul7 piabeb
418	36	44.4	325	2	08D539	VIBVU	08d539 vibrio vuln	491	36	44.4	746	2	033080	9ASTR	033080 yarrowia li
419	36	44.4	331	2	07WBX6	VIBVY	07wbx6 vibrio vuln	492	36	44.4	748	2	05AUD1	DICDI	05aud1 dictyosteli
420	36	44.4	331	2	SRALI1	CABEL	020411 caenorhabdi	493	36	44.4	762	2	05FKS4	IACAC	05fks4 lactobacilli
421	36	44.4	335	2	0869U0	DICDI	0869u0 dictyosteli	494	36	44.4	763	2	09R6V7	ANASP	09r6v7 anabaena sp
422	36	44.4	338	2	017167	BRUMA	017167 briglia mala	495	36	44.4	779	2	07RLD7	PIAYO	07rld7 plasmodium
423	36	44.4	340	2	05RJX9	XENIA	05rjx9 xenopus lae	496	36	44.4	784	2	04HL52	CANLA	04hl52 campylobact
424	36	44.4	342	2	06MDY6	PARUM	06mdy6 paracramyid	497	36	44.4	793	2	04Q3S1	LEIMA	04q3s1 leishmania
425	36	44.4	343	1	Y3526	METUA	060856 methanococc	498	36	44.4	797	2	08V4R1	MONPV	08v4r1 monkeypox v
426	36	44.4	346	1	OST5	HUMAN	0812t8 homo sapien	499	36	44.4	795	2	07R178	PIAYO	07r178 plasmodium
427	36	44.4	346	1	OST5	HOUSE	08bd14 mus musculu	500	36	44.4	805	1	PIE1	SCHPO	09ua2 schizosacch
428	36	44.4	346	2	06BWM4	DEBHA	06bwm4 debaryomyce	501	36	44.4	816	2	06LUT4	9ASPA	06lut4 x mokara cv
429	36	44.4	346	2	060151	WATSC	060151 watasenia s	502	36	44.4	821	2	07RCG2	PIAYO	07rcg2 plasmodium
430	36	44.4	362	2	04YXG5	PLABE	04yxg5 plasmodium	503	36	44.4	823	2	09PLI0	CHIMU	09pli0 chlamydia m
431	36	44.4	369	2	06ARRJ	PARTI	06arfj7 paramedium	504	36	44.4	839	2	06G315	BARHE	06g315 bartonella
432	36	44.4	372	2	05OCN8	CENAS	05cgn8 centibacteri	505	36	44.4	855	2	08ZVP9	PYRAB	08zvp9 pyrobaculum
433	36	44.4	373	2	082M15	NITEU	082m15 nitrosomona	506	36	44.4	855	2	0869V0	DICDI	0869v0 dictyosteli
434	36	44.4	378	2	09NAX7	CABEL	09nax7 caenorhabdi	507	36	44.4	872	2	04I678	GIBZE	04i678 gibberella
435	36	44.4	380	2	06LO98	PHOPR	06l998 photobacter	508	36	44.4	876	2	07ORG1	GIATA	07org1 giardia lam
436	36	44.4	388	2	05AJA2	DICDI	05aja2 dictyosteli	509	36	44.4	876	1	ROB9	NPVRC	08b9k0 neopvrc
437	36	44.4	395	2	07RER3	PIAYO	07rer3 plasmodium	510	36	44.4	892	2	08B9K0	NPVRC	08b9k0 neopvrc
438	36	44.4	396	2	0812X3	PIAF7	081x3 plasmodium	511	36	44.4	897	2	055596	NEPVM	055596 neopvrc
439	36	44.4	397	2	043492	HOREV	043492 hotetum vul	512	36	44.4	899	2	08CGY0	HERGA	08cgy0 heterocypia
440	36	44.4	405	2	09PMZ4	CAMJE	09pmz4 campylobact	513	36	44.4	912	2	05SYHO	CRYNB	05syho cryptococcu
441	36	44.4	405	2	04HHC2	CAMCO	04hhc2 campylobact	514	36	44.4	912	2	05KLE0	CRYNB	05kle0 cryptococcu
442	36	44.4	408	2	09PMW2	CAMJE	09pmw2 campylobact	515	36	44.4	915	2	06BLP9	DEBHA	06blp9 debaryomyce
443	36	44.4	408	2	09PMW2	CAMJE	09pmw2 campylobact	516	36	44.4	915	2	06BLP9	DEBHA	06blp9 debaryomyce
444	36	44.4	412	1	CCA	BUCAP	08ka53 buchnera ap	517	36	44.4	936	2	097272	PIAF7	097272 piabeb
445	36	44.4	414	2	07MM80	VIBVY	07mm80 vibrio vuln	518	36	44.4	1016	2	0688J1	ORYSA	0688j1 oryza sativ
446	36	44.4	426	2	06BTT8	DEBHA	06btt8 debaryomyce	519	36	44.4	1030	2	TPR2B	HUMAN	081a76 caenorhabdi
447	36	44.4	432	2	073064	TREDE	073064 treponema d	520	36	44.4	1039	1	081A76	CABEL	081a76 caenorhabdi
448	36	44.4	436	2	09W4R9	DROME	09w4r9 drosophila	521	36	44.4	1068	2	081A76	CABEL	081a76 caenorhabdi
449	36	44.4	455	2	05OKB2	PHACH	05okb2 phanerochaet	522	36	44.4	1075	2	081A76	CABEL	081a76 caenorhabdi
450	36	44.4	455	1	MUPR	BICAI	09yuj3 buchnera ap	523	36	44.4	1082	1	SEC73	SCHPO	081a76 caenorhabdi
451	36	44.4	468	1	09UTU3	PYRAB	09yuj3 pyrococcus	524	36	44.4	1089	2	06C318	YARLI	06c318 yarrowia li
452	36	44.4	468	2	06M048	METMP	06m048 methanococc	525	36	44.4	1092	2	0815E0	PIAF7	0815e0 plasmodium
453	36	44.4	469	2	08BVT7	MOUSE	08bvt7 mus musculu	526	36	44.4	1115	2	017267	CABEL	017267 caenorhabdi
454	36	44.4	471	2	027141	EUPCR	027141 euplotes cr	527	36	44.4	1130	2	081T78	CABEL	081t78 candida gla
455	36	44.4	472	2	073981	PYRHO	073981 pyrococcus	528	36	44.4	1154	2	06FTT6	CANGA	06ftt6 candida gla
456	36	44.4	472	2	05S841	YMACN	05s841 guaterlia o	529	36	44.4	1178	2	07RKE3	PIAYO	07rke3 plasmodium
457	36	44.4	477	2	05UGQ5	TYRKO	05jgq5 pyrococcus	530	36	44.4	1189	2	04Z5J5	PLABE	04z5j5 plasmodium
458	36	44.4	485	2	073MW7	TREDE	073mw7 treponema d	531	36	44.4	1191	2	04U9F4	THEAN	04u9f4 theileria a
459	36	44.4	486	2	04XXH6	PLACH	04xxh6 plasmodium	532	36	44.4	1238	2	054G96	DICDI	054g96 dictyosteli
460	36	44.4	486	2	072008	LEPIC	072008 leptospira	533	36	44.4	1272	2	081M24	PIAF7	081m24 plasmodium
461	36	44.4	486	2	08F665	LEPIN	08f665 leptospira	534	36	44.4	1277	2	LICAM	FUGRU	081m24 plasmodium
462	36	44.4	493	1	FUT3	ARATH	09c471 arabidopsis	535	36	44.4	1277	2	06FG00	CIOIN	06fg00 ciona intes
463	36	44.4	493	1	056TH9	ARATH	056th9 arabidopsis	536	36	44.4	1361	2	06FRS2	CANGA	06frs2 candida gla
464	36	44.4	507	2	095BX5	9GROA	095bx5 hemiptelea	537	36	44.4	1379	1	PARD3	CABEL	017153 caenorhabdi
465	36	44.4	516	1	ROAA	EUGGR	0956h9 arabidopsis	538	36	44.4	1401	2	06CS85	KUTIA	06cs85 kluyveromyc
466	36	44.4	518	2	0709N8	ANOGA	0709n8 anopheles g	539	36	44.4	1418	2	070B22	ANOGA	070b22 anopheles g
467	36	44.4	521	2	067XV8	ARATH	067xv8 arabidopsis	540	36	44.4	1429	2	081HP1	PIAF7	081hp1 plasmodium
468	36	44.4	525	2	081663	PIAF7	081663 plasmodium	541	36	44.4	1435	2	09DSO0	9PROV	09dso0 colostrado ti
469	36	44.4	529	2	050UD4	ENTHI	050uj4 entamoeba h	542	36	44.4	1473	2	054TV0	DICDI	054tv0 dictyosteli

689	35	43.2	357	2	Q57Z62_9TRYP	057Z62	trypanosoma
690	35	43.2	364	1	TDP22_MOUSE	Q717B2	mus_musculus
691	35	43.2	366	2	OSLHJ2_ARATH	Q9S1I2	arabidopsis
692	35	43.2	367	2	OSMCW7_BACSK	05mcw7	bacillus_c1
693	35	43.2	367	2	098OG5_MYCPU	098og5	mycoplasma
694	35	43.2	372	2	06CX96_YARLI	06cx96	varicorbia_l1
695	35	43.2	372	2	06OXK4_CABER	06oxk4	caenorhabdi
696	35	43.2	374	2	Q4J6U0_SULAC	Q4j6u0	sulfolobus
697	35	43.2	375	2	05M4T5_STRT2	05m4t5	streptococc
698	35	43.2	377	2	07RLI5_PLAYO	Q7rli5	plasmodium
700	35	43.2	383	2	07OT54_GIALA	Q7ot54	giardia_lam
701	35	43.2	393	2	Q5Y2C3_TETTH	05y2c3	tetrahymena
702	35	43.2	394	1	Q5PQA3_UREPA	05ppqa	ureaplasma
703	35	43.2	394	1	Q9HEZ3_PENJA	P399z3	saccharomye
704	35	43.2	399	1	HM39_CABEL	Q9he23	penicillium
705	35	43.2	399	2	Q7N1S9_PHOIL	Q22812	caenorhabdi
706	35	43.2	402	2	06SXHB_ORYSA	Q7n159	photographu
707	35	43.2	408	2	Q59SC6_CANAL	06sxhb	oryza_sativ
708	35	43.2	411	2	Q9N448_CABEL	059sc6	candida_alb
709	35	43.2	414	2	Q9LR52_ARATH	Q9n448	caenorhabdi
710	35	43.2	418	2	O4E329_9FLOP	Q9lr52	arabidopsis
711	35	43.2	420	2	06IHV1_CABBR	O4e329	gracilariops
712	35	43.2	421	1	GSA_THIEAC	06ihv1	caenorhabdi
713	35	43.2	429	1	WDR50_CABEL	06htk6	thermoplasma
714	35	43.2	431	2	Q9M0H6_ARATH	P42000	caenorhabdi
715	35	43.2	435	2	Q5HJH3_STPAC	Q9m0h6	arabidopsis
716	35	43.2	435	2	06GCR9_STPAS	05hj33	staphylococ
717	35	43.2	435	2	06GKA8_STPAR	06gcr9	staphylococ
718	35	43.2	437	2	Q9XX97_CABEL	06gka8	staphylococ
719	35	43.2	439	2	Q5CNRO_CRYHO	Q9xx97	caenorhabdi
720	35	43.2	443	1	PREA_BACTU	Q5cnro	cryptospori
721	35	43.2	445	2	08GLD7_BACTU	Q9c722	arabidopsis
722	35	43.2	445	2	Q7AIX3_STPAM	P10025	bacillus_th
723	35	43.2	445	2	Q99QS6_STRAM	Q8glf7	bacillus_th
724	35	43.2	448	2	Q9ERW1_HUMAN	Q7aix3	staphylococ
725	35	43.2	449	2	Q4YNFI_PLABA	Q9erw1	homio_sapien
726	35	43.2	452	2	Q6BTN2_DEBHA	Q4ynfi	plasmodium
727	35	43.2	455	2	Q9HG32_DEBHA	Q6bt22	depariomyce
728	35	43.2	455	2	08RX03_ARATH	Q9hg32	depariomyce
729	35	43.2	455	2	08HIF5_ARATH	08rx03	arabidopsis
730	35	43.2	455	2	Q6LUQ7_PHOPR	08hif5	arabidopsis
731	35	43.2	459	2	Q7MXI2_PORGI	Q6luq7	photobacter
732	35	43.2	460	2	Q5S876_SYNY3	Q7mx12	porphyromon
733	35	43.2	462	1	APG4D_XENLA	Q5s876	synechocyst
734	35	43.2	469	1	05IA80_ENTHI	Q6sfj9	xenopus_lae
735	35	43.2	471	2	Q4STI8_TETNG	05ia80	tetradodon_h
736	35	43.2	474	2	08LUV2_9ROSI	Q4st18	tetradodon_n
737	35	43.2	480	2	Y009_CHLTE	08luy2	dipentodon
738	35	43.2	483	1	Q7OCRI_ANOGA	08kgf9	chlorobidum
739	35	43.2	486	2	Q7RAM1_GIALA	Q7ocr1	anopheles_g
740	35	43.2	489	2	05IA78_ENTHI	Q7ram1	giardia_lam
741	35	43.2	490	2	Q4TWM7_TETNG	05ia78	entamoeba_h
742	35	43.2	494	1	PAC1_YEAST	Q4twm7	tetradodon_n
743	35	43.2	495	1	Q5OAVD2_IDILO	P399z6	saccharomye
744	35	43.2	496	2	09G8R4_NIEGR	P32622	saccharomye
745	35	43.2	497	2			

981 34 42.0 104 2 Q6BGC6 PARTS Q6bgd6 paramacium
 982 34 42.0 107 2 Q5C4M5_SCHJA Q5C4m5 schistosoma
 983 34 42.0 107 2 Q8BPM7_MOUSE Q8Bpm7 mus musculu
 984 34 42.0 116 1 YUG7_YEAST P40365 saccharomyc
 985 34 42.0 116 2 Q4N8B7_THEPA Q4n8b7 theileria p
 986 34 42.0 118 2 Q9Y9X0_AERPE Q9y9x0 aeropyrum p
 987 34 42.0 122 2 Q40822_PHYCS Q40822 physalis cr
 988 34 42.0 123 2 Q8Q0D6_METWA Q8q0d6 methanosarc
 989 34 42.0 123 2 Q5L184_GEOKA Q5l184 geobacillus
 990 34 42.0 123 2 Q5N142_FRATY Q5n142 francisella
 991 34 42.0 124 2 Q8U5C8_AGRF5 Q8u5c8 agrobacteri
 992 34 42.0 130 2 Q977D6_SUFTO Q977d6 sulfolobus
 993 34 42.0 136 1 TVB4_MOUSE P04212 mus musculu
 994 34 42.0 139 2 Q5A776_CANAL Q5a776 candida alb
 995 34 42.0 142 2 Q7ZX08_XENIA Q7zx08 xenopus lae
 996 34 42.0 145 2 Q72TD1_LEPIC Q72td1 leptospira
 997 34 42.0 145 2 Q8F206_LEBPIA Q8f206 leptospira
 998 34 42.0 146 2 Q6IKN7_DROME Q6ikn7 drosophila
 999 34 42.0 147 2 Q9CVD9_MOUSE Q9cvd9 m mus muscu
 1000 34 42.0 153 2 Q55C11_DICDI Q55c11 dictyostell

ALIGNMENTS

RESULT 1

KV4A_HUMAN STANDARD; PRT; 114 AA.
 ID KV4A_HUMAN P01625;

DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE IG kappa chain V-IV region len.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 OX [1]
 RN PROTEIN SEQUENCE.
 RP MEDLINE=76004342; PubMed=50995;
 RA Schneider M., Hilschmann N.;
 RT "The primary structure of a monoclonic immunoglobulin-L-chain of
 subGroup IV of the kappa type (Bence-Jones protein len).";
 RL Hoppe-Seyler's Z. Physiol. Chem. 356:507-557(1975).
 RP [12]
 RN SEQUENCE REVISION TO 9.
 RA Salomon A.;
 RL Submitted (AUG-1996) to Swiss-Prot.
 CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
 CC
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC
 CC PDB; 1EBQ; X-ray; A/B=1-114.
 DR PDB; 1EBQ; X-ray; A/B=1-114.
 DR PDB; 1ERQ; X-ray; A=1-114.
 DR PDB; 1EK3; X-ray; A/B=1-114.
 DR PDB; 1LVE; X-ray; @=1-114.
 DR PDB; 2LVE; X-ray; @=1-114.
 DR PDB; 3LVE; X-ray; @=1-114.
 DR PDB; 4LVE; X-ray; A/B=1-114.
 DR PDB; 5LVE; X-ray; A=1-114.
 DR GO; GO:0005576; C:extracellular region; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR SMART; SM00406; IGV, 1.

DR PROSITE: PS50835; IG LIKE; 1.

KM 3D-structure; Bence-Jones protein; Direct protein sequencing;
 KM Immunoglobulin domain; Immunoglobulin V region.

FT REGION 1 23 Framework-1.
 FT REGION 21 40 Complementarity-determining-1.
 FT REGION 24 55 Framework-2.
 FT REGION 56 62 Complementarity-determining-2.
 FT REGION 63 94 Framework-3.
 FT REGION 95 101 Complementarity-determining-3.
 FT REGION 102 113 Framework-4.
 FT DISULFID 23 94 By similarity.

FT NON TER 114 114
 FT STRAND 4 7
 FT STRAND 10 13
 FT TURN 15 16
 FT TURN 19 25
 FT STRAND 30 31
 FT TURN 32 35
 FT STRAND 36 37
 FT STRAND 39 44
 FT TURN 46 47
 FT STRAND 51 55
 FT TURN 56 58
 FT STRAND 59 60
 FT TURN 62 63
 FT TURN 66 67
 FT STRAND 68 73
 FT TURN 74 75
 FT STRAND 76 81
 FT HELIX 86 88
 FT STRAND 90 96
 FT STRAND 103 104
 FT STRAND 108 112
 SQ SEQUENCE 114 AA, 12640 MW, 0647FD17P235485 CRC64;

Query Match 79.0%; Score 64; DB 1; Length 114;
 Best Local Similarity 76.5%; Pred. No. 0.0027;
 Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KSSQSYFFSSQKNTLA 17
 ||||| :|||
 Db 24 KSSQSYLYSSNSKNYLA 40

RESULT 2
 ID KV40_HUMAN STANDARD; PRT; 121 AA.

AC P06312;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE IG kappa chain V-IV region precursor (Fragment).
 GN Name=IGKV4-1; (human).
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 OX [1]
 RN NUCLEOTIDE SEQUENCE.
 RP MEDLINE=86041853; PubMed=2997712;
 RA Klobock H.G., Bornkamm G.W., Combriato G., Mochkat R., Pohlentz H.D.,
 RA Zechau H.G.;
 RT "Subgroup IV of human immunoglobulin K light chains is encoded by a
 RT single germline gene.";
 RL Nucleic Acids Res. 13:6515-6529(1985).
 CC -1- MISCELLANEOUS: There is only one IG kappa V-IV gene.
 CC
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use as long as its content is in no way modified and this statement is not
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CC -----
DR EMBL; Z00023; CAA77318.1; -, Genomic_DNA.
DR PIR; A01902; KAHU.
DR HSSP; P01625; 1LVE.
DR SMR; P06313; 21-121.
DR Ensembl; ENSG00000153586; Homo sapiens.
DR HGNC; HGNC:5834; IGKV-1.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR003596; Ig-like.
DR InterPro; IPR007110; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 >121 Ig kappa chain V-IV region.
FT REGION 21 43 Framework-1.
FT REGION 44 60 Complementarity-determining-1.
FT REGION 61 75 Framework-2.
FT REGION 76 82 Complementarity-determining-2.
FT REGION 83 114 Framework-3.
FT REGION 115 121 Complementarity-determining-3.
FT DISULFID 43 114 By similarity.
FT NON_TER 121
SQ SEQUENCE 121 AA; 13380 MW; 9586AD4188D33974 CRC64;

```

```

Query Match
Best Local Similarity 79.0%; Score 64; DB 1; Length 121;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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```

QY 1 KSSQVFPSSSQNYLA 17
    |||||:|||||
Db 44 KSSQVLYSSNNKYLA 60

```

RESULT 3

```

KV4B_HUMAN STANDARD; PRT; 133 AA.
ID P06313;
AC 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DE 10-MAY-2005 (Rel. 47, Last annotation update)
DI Ig kappa chain V-IV region JI precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86041853; PubMed=2997712;
RA Klobbeck H.G., Bornkamm G.W., Combrat G., Mocikat R., Pohlentz H.D.,
RA Zachau H.G.;
RT "Subgroup IV of human immunoglobulin K light chains is encoded by a
RT single germline gene.";
RL Nucleic Acids Res. 13:6515-6529 (1985).
CC -----
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC EMBL; Z00022; CAA77317.1; -, Genomic_DNA.
DR PIR; A01904; KAHU1.
DR HSSP; P01625; 1LVE.
DR SMR; P06313; 21-133.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.

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DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 133 Ig kappa chain V-IV region JI.
FT REGION 21 43 Framework-1.
FT REGION 44 60 Complementarity-determining-1.
FT REGION 61 75 Framework-2.
FT REGION 76 82 Complementarity-determining-2.
FT REGION 83 114 Framework-3.
FT REGION 115 122 Complementarity-determining-3.
FT REGION 123 132 Framework-4.
FT DISULFID 43 114 By similarity.
FT NON_TER 133
SQ SEQUENCE 133 AA; 14633 MW; 5FB3953066744AF4 CRC64;

```

```

Query Match
Best Local Similarity 79.0%; Score 64; DB 1; Length 133;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 1 KSSQVFPSSSQNYLA 17
    |||||:|||||
Db 44 KSSQVLYSSNNKYLA 60

```

RESULT 4

```

KV4C_HUMAN STANDARD; PRT; 134 AA.
ID P06314;
AC 01-JAN-1988 (Rel. 06, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DE 10-MAY-2005 (Rel. 47, Last annotation update)
DI Ig kappa chain V-IV region B17 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86041854; PubMed=2997713;
RA Marsh P., Mills F., Gould H.;
RT "Detection of a unique human V kappa IV germline gene by a cloned cDNA
RT probe.";
RL Nucleic Acids Res. 13:6531-6544 (1985).
RN [2]
RP SEQUENCE REVISION TO 76.
RA Marsh P.;
RL Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC EMBL; X02990; CAA26733.1; -, mRNA.
DR HSSP; P01625; 1LVE.
DR SMR; P06314; 21-134.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 134 Ig kappa chain V-IV region B17.
FT REGION 21 43 Framework-1.
FT REGION 44 60 Complementarity-determining-1.
FT REGION 61 75 Framework-2.
FT REGION 76 82 Complementarity-determining-2.

```

FT REGION 83 114 Framework-3.
FT REGION 115 121 Complementarity-determining-3.
FT REGION 122 133 Framework-4.
FT DISULFID 43 114 By similarity.
FT NON TER 134 134
SQ SEQUENCE 134 AA; 14966 MW; 6413A22FDD738832 CRC64;

Query Match 76.5%; Score 62; DB 1; Length 134;
Best Local Similarity 70.6%; Pred. No. 0.0073;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KSSQSVFFSSQKNYLA 17
Db 44 KSSQSLVSSDKNYLA 60

RESULT 5

KV4D_HUMAN STANDARD; PRT; 109 AA.
AC P83593;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-IV region STH (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Abdominal adipose tissue;
RX MEDLINE=98249779; PubMed=9588180; DOI=10.1006/bbrc.1998.8515;
RA Olsen K.E., Sletten K., Westernmark P.;
RT "Extended analysis of Al-amyloid protein from abdominal wall
subcutaneous fat biopsy: kappa IV immunoglobulin light chain.";
RL Biochem. Biophys. Res. Commun. 245:713-716(1998).
CC -!- FUNCTION: May play an important role in fibrillogenesis.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
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DR SMR; P83593; 1-109.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23 Framework-1.
FT REGION 24 40 Complementarity-determining-1.
FT REGION 41 55 Framework-2.
FT REGION 56 62 Complementarity-determining-2.
FT REGION 63 94 Framework-3.
FT REGION 95 101 Complementarity-determining-3.
FT REGION 102 109 Framework-4.
FT DISULFID 23 94 By similarity.
FT UNSURE 23 23
FT UNSURE 94 94
FT NON TER 109 109
SQ SEQUENCE 109 AA; 12060 MW; 0C4F31EA11E12A0B CRC64;

Query Match 75.3%; Score 61; DB 1; Length 109;
Best Local Similarity 70.6%; Pred. No. 0.0087;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KSSQSVFFSSQKNYLA 17
Db 24 KSSQSVLYSSDKNYLA 40

RESULT 6
O52L64_MOUSE PRELIMINARY; PRT; 240 AA.
ID O52L64_MOUSE
AC O52L64;
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE Hypothetical protein.
OC Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.

RC STRAIN=Mix FVB/N;
RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshynski S., Carrinci P., Prange C.,
RA Rana S.S., Loggiano N.A., Peters G.J., Abramson R.D., Mulian S.J.,
RA Bosak S.A., McKernan F.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriquez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield J.S.N., Krzyzanski M.I., Skalska J., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Mix FVB/N;
RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
RG NIH MGC Project;
Submitted (Apr-2005) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC094049; AAH94049.1; -, mRNA.
DR SMR; O52L64; 21-240.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; C1-se; 1.
DR SMART; SM00409; IGV; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR Hypothetical protein.
SQ SEQUENCE 240 AA; 26609 MW; CF8630CC002B52C CRC64;

Query Match 74.1%; Score 60; DB 2; Length 240;
Best Local Similarity 70.6%; Pred. No. 0.032;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KSSQSVFFSSQKNYLA 17
Db 44 KSSQSLVSSDKNYLA 60

RESULT 7
Q9NP29_HUMAN PRELIMINARY; PRT; 130 AA.
ID Q9NP29_HUMAN

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AC Q9NP29;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Microfibrillar protein 2 (Fragment).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96354815; PubMed=8753791; DOI=10.1006/jbrc.1996.1202;
RA Ozsvath K.J., Xia S., Hirose H., Tilson M.D.;
RT "Two hypothetical proteins of human aortic adventitia, with Ig kappa,
RT collagenous, and aromatic-rich motifs."
RL Biochem. Biophys. Res. Commun. 225:500-504(1996).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=9224393; PubMed=9224393; DOI=10.1006/jbre.1997.5030;
RA Ozsvath K.J., Hirose H., Xia S., Chew D., Knoetgen J. III,
RA Tilson M.D.;
RT "Expression of two novel recombinant proteins from aortic adventitia
RT (kappaIbs) sharing amino acid sequences with cytomagalovirus."
RL J. Surg. Res. 69:277-282(1997).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Ozsvath K.J., Xia S., Hirose H., Tilson M.D.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF206020; AAF62402.1; -; mRNA.
DR HSSP; P01625; 1LVE.
DR SMR; Q9NP29; 21-84.
DR Ensemble; ENSG00000153586; Homo sapiens.
FT NON TER 130 130
SQ SEQUENCE 130 AA; 14128 MW; 51275185ACC6FA1E CRC64;

Query Match 71.6%; Score 58; DB 2; Length 130;
Best Local Similarity 64.7%; Pred. No. 0.036;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 KSSQSVFSSSQKNYLA 17
Db 44 KSSQRLFFGSSKNYLA 60

RESULT 8
OCRB05_MOUSE PRELIMINARY; PRT; 255 AA.
AC Q6KB05;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE ScFv BBES protein (Fragment).
GN Name=ScFv BBES;
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Balb/c;
RA Peter J.C., Wallukat G., Tugler J., Maurice D., Roegel J.C.,
RA Briand J.P., Hoebeke J.;
RT "Modulation of the M2 muscarinic acetylcholine receptor activity with
RT monoclonal anti-M2 receptor antibody fragments."
RL J. Biol. Chem. 279:55697-55706(2004).
DR EMBL; AJ746180; CAG34081.1; -; Other_DNA.
DR HSSP; P01837; 1KCR.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00409; IG; 2.

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DR SMART; SM00406; IGV; 2.
DR PROSITE; PSS0835; IG_LIKE; 2.
DR NON TER 1
SQ SEQUENCE 255 AA; 27445 MW; B68BD38395DP713B CRC64;

Query Match 67.9%; Score 55; DB 2; Length 255;
Best Local Similarity 70.6%; Pred. No. 0.27;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 KSSQSVFSSSQKNYLA 17
Db 160 KSSQSLNSRNQKNYLA 176

RESULT 9
OC54VY2_DICDI
ID Q54VY2;
AC Q54VY2;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=DD80206356;
OS Dictyostelium discoideum (slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
RA Sungang R., Bertram M., Song J., Olsen R., Szafrenski K., Xu Q.,
RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
RA Bahlter A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA Plicher K., Chen G., Saunders D., Sodetgren E., Davis P.,
RA Kernornu A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
RA Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,
RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
RA Wardrop A., Felder M., Thangavelu M., Johnson D., Knights A.,
RA Loussegod H., Mungall K., Oliver K., Price C., Quail M.A.,
RA Unishihara H., Hernandez J., Rabinowitsch E., Steffen D., Sanders M.,
RA Ma J., Kohara Y., Sharp S., Simmonds M., Slegler S., Tivey A.,
RA Sugano S., White B., Walker D., Woodward J., Winkler T., Tanaka Y.,
RA Shaulsky G., Schleicher M., Weinstock G., Rosenthal A., Cox E.C.,
RA Chisholm R.L., Gibbs R., Loomis W.F., Platzer M., Kay R.R.,
RA Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.;
RT "The genome of the social amoeba Dictyostelium discoideum."
RL Nature 0:0-0(2005).
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAF0100066; EAL67260.1; -; Genomic_DNA.
DR KW Hypothetical protein.
SQ SEQUENCE 516 AA; 56738 MW; 1A8753F32C19C6A9 CRC64;

Query Match 55.6%; Score 45; DB 2; Length 516;
Best Local Similarity 71.4%; Pred. No. 36;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 KSSQSVFSSSQKN 14
Db 17 KSSNSVLKSSQKN 30

RESULT 10
ID1913_CAEEL
ID1913_CAEEL PRELIMINARY; PRT; 446 AA.
AC Q1913;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein H36L18.1.

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GN ORENAMES=H36L18.1;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RC MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology."
RL Science 282:2012-2018(1998).
RL EMBL; Z95309; CAB08559.2; -; Genomic_DNA.
DR PIR; T23132; T23132.
DR HSSP; P39900; 101Z.
DR Ensembl; H36L18.1; Caenorhabditis elegans.
DR WormBase; WBGene00010423; H36L18.1.
DR WormPep; H36L18.1; CE28576.
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO; GO:0004223; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR001818; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR006026; Peptidase_M.
DR Pfam; PF00045; Hemopexin; 3.
DR Pfam; PF00413; Peptidase_M10; 1.
DR PRINTS; PR00138; MATRIXIN.
DR SMART; SM00120; HX; 3.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKOWN_1.
DR Complete proteome; Hypothetical protein.
SQ SEQUENCE 446 AA; 52177 MW; 832238CC545B2F7F CRC64;

Query Match 54.3%; Score 44; DB 2; Length 446;
Best Local Similarity 53.3%; Pred. No. 46;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 KSSQVFFSSSQNY 15
DB 369 KSEKNIFFSQYNY 383

RESULT 11
Q4YZ19_PLABE PRELIMINARY; PRT; 606 AA.
ID Q4YZ19;
AC Q4YZ19;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORENAMES=PB103734.00.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5821;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kool J.T.W.A.,
RA Bertram M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutheford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrett B., Turner C.M.R., Waters A.P., Sinden R.S.;
RA "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses."
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CA01001508; CA96553.1; -; Genomic_DNA.
DR Hypothetical protein.
FT NON_TER 606 606

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SQ SEQUENCE 606 AA; 70235 MW; 48C14FA36D498DC CRC64;
Query Match 54.3%; Score 44; DB 2; Length 606;
Best Local Similarity 46.7%; Pred. No. 64;
Matches 7; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 1 KSSQVFFSSSQNY 15
DB 196 KANSFFFSNMNF 210

RESULT 12
Q9H917_HUMAN PRELIMINARY; PRT; 674 AA.
ID Q9H917_HUMAN;
AC Q9H917;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein FLJ13080.
GN Name=FIG1L;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obaishi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto T.-I., Saito K., Kawai Y., Isoh Y., Nakamura Y.,
RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Fujimori K., Tanai H., Kimata M., Watanabe S., Yosida M., Hociuta T.,
RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hociuta T.,
RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
RA Nomura Y., Togashi S., Komai F., Hara R., Takeuchi K., Arita M.,
RA Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotauka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shihara N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Teraehima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hiro M., Ohmori Y.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano Y., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi N., Masuno Y., Yamashita K.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isegaki T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs."
RL Nat. Genet. 36:40-45(2004).
CC -!- SIMILARITY: Belongs to the AAA ATPase family.
CC EMBL; AK023142; BAB14426.1; -; mRNA.
DR HSSP; 001853; 1R7R.
DR Ensembl; ENSG00000132436; Homo sapiens.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0005224; F:ATP binding; IEA.
DR GO; GO:0017111; F:nucleoside-triphosphatase activity; IEA.
DR GO; GO:0000166; F:nucleoside binding; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003959; AAA_ATPase_cent.
DR Pfam; PF00004; AAA; 1.
DR SMART; SM00382; AAA; 1.

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RA Eddy S.R., McPherson J.D., Olson M.V., Eichler E.E., Green E.D.,
RA Waterston R.H., Wilson R.K.;
RT "The DNA sequence of human chromosome 7.";
RL Nature 424:157-164(2003).
RN
RN NUCLEOTIDE SEQUENCE.
RA Waterston R.;
RP Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN
RN NUCLEOTIDE SEQUENCE.
RA Waterston R.;
RP Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
RN
RN NUCLEOTIDE SEQUENCE.
RA Wilson R.;
RP Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC -1 SIMILARITY: Belongs to the AAA ATPase family.
DR EMBL; BC051867; AAH51867.1; -; mRNA.
DR EMBL; AC018705; AAS0196.1; -; Genomic_DNA.
DR HSSP; Q01853; 1R7R.
DR Ensembl; ENSG00000132436; Homo sapiens.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0017111; F:nucleoside-triphosphatase activity; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003959; AAA_ATPase_cent.
DR Pfam; PF000004; AAA; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00674; AAA; 1.
KW ATP-binding; Hypothetical protein; Nucleotide-binding; Transmembrane.
SQ SEQUENCE 674 AA; 74077 MW; 2EB812B407495BF2 CRC64;

Query Match 54.3%; Score 44; DB 2; Length 674;
Best Local Similarity 54.5%; Pred. No. 72;
Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 SSQSVPFSSSQKNYLA 17
Db 5 SRSRVHLEWQKNYFA 20

RESULT 15
Q72RE7_LEPIC 54.3%; Score 44; DB 2; Length 674;
ID Q72RE7_LEPIC PRELIMINARY; PRT; 431 AA.
AC Q72RE7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=LI11798;
OS Leptospira interrogans (serogroup Icterohaemorrhagiae / serovar
OS Copenhagen).
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OK NCBI_Taxid=44275;

RN
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=Fiocruz LI-130;
PUBMED=15028702; DOI=10.1126/JB.186.7.2164-2172.2004;
RA Nascimento A.L.T.O., Ko A.I., Martins E.A.L., Monteiro-Vitorello C.B.,
RA Ho P.L., Haake D.A., Verjovski-Almeida S., Hartkeetel R.A.,
RA Marques M.V., Oliveira M.C., Menck C.F.M., Leite L.C.C., Carrier H.,
RA Coutinho L.L., Degraive W.M., Dellagostin O.A., El-Dorri H.,
RA Ferro E.S., Ferro M.I.T., Furlan L.R., Gamberini M., Gigliotti E.A.,
RA Goes-Neto A., Goldman G.H., Goldman M.H.S., Harakava R.,
RA Jeronimo S.M.B., Junqueira-de-Azevedo J.L.M., Kimura E.T.,
RA Kuramae E.E., Lemos E.G.M., Lemos M.V.F., Marino C.L., Nunes L.R.,
RA de Oliveira R.C., Pereira G.G., Reis M.S., Schriefer A.,
RA Siqueira W.J., Sommer P., Teal S.M., Simpson A.D.G., Ferro J.A.,
RA Camargo L.E.A., Kitajima J.P., Setubal J.C., Van Sluys M.A.;
RT "Comparative genomics of two Leptospira interrogans serovars reveals
RT novel insights into physiology and pathogenesis.";
RL J. Bacteriol. 186:2164-2172(2004).

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DR EMBL; AB017294; AAS70387.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 431 AA; 50636 MW; 817863881A2403D CRC64;

Query Match 53.1%; Score 43; DB 2; Length 431;
Best Local Similarity 43.8%; Pred. No. 66;
Matches 7; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KSSQGVFPSSSQKNYL 16
Db 170 KKIESLYFNAXKXSYL 185

RESULT 16
Q8F4C1_LEPIN 53.1%; Score 43; DB 2; Length 431;
ID Q8F4C1_LEPIN PRELIMINARY; PRT; 431 AA.
AC Q8F4C1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Flagellar motor switch protein flig.
GN Name=flig3; OrderedLocustNames=LA2120;
OS Leptospira interrogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OK NCBI_Taxid=173;

RN
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
RX MEDLINE=22598143; PubMed=12712204; DOI=10.1038/nature01597;
RA Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,
RA Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,
RA Jiang Y.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,
RA Zhang Y., Zhu G.-F., Wan M., Huang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,
RA Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,
RA Saint Girons I., Somerville R.L., Wen Y.-M., Shi W.-H., Chen Z.,
RA Xu J.-G., Zhao G.-P.;
RT "Unique physiological and pathogenic features of Leptospira
RT interrogans revealed by whole-genome sequencing.";
RL Nature 422:888-893(2003).
DR EMBL; AB011383; AAN9319.1; -; Genomic_DNA.
KW Complete proteome.
SQ SEQUENCE 431 AA; 50664 MW; 97090A4E3598103D CRC64;

Query Match 53.1%; Score 43; DB 2; Length 431;
Best Local Similarity 43.8%; Pred. No. 66;
Matches 7; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KSSQGVFPSSSQKNYL 16
Db 170 KKIESLYFNAXKXSYL 185

RESULT 17
Q4Y717_PLACH 53.1%; Score 43; DB 2; Length 431;
ID Q4Y717_PLACH PRELIMINARY; PRT; 470 AA.
AC Q4Y717;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PC000384.00.0;
OS Plasmidococcus albae.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
OK NCBI_Taxid=5825;

RN
RN NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kool J.T.W.A.,
RA Bertram M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carnocet D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,

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transcriptomic, and proteomic analyses.";
 RL Science 307:82-86(2005).
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL/CAJ01000408/CAH74871.1; -; Genomic_DNA.
 KW Hypothetical protein.
 FT NON TER 470
 SQ SEQUENCE 470 AA; 54884 MW; DBAFA6829A6D97 CRC64;

Query Match 53.1%; Score 43; DB 2; Length 470;
 Best Local Similarity 66.7%; Pred. No. 73;
 Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

1 KSSQSVFPSSQKNY 15
 ||:|||||
 Db 327 KSNLSPFSSQKNY 341

RESULT 18
 081UX7_PLAF7 PRELIMINARY; PRT; 870 AA.
 AC 081UX7;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=PF10_0064;
 OS Plasmodium falciparum (isolate 3D7).
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=36329;
 OX (1)
 RN NUCLEOTIDE SEQUENCE.
 RP MEDLINE=22255705; PubMed=12368864; DOI=10.1038/nature01097;
 RA Gardner M.J., Hall N., Fung B., White O., Berriman M., Hyman R.W.,
 RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
 RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyse S.,
 RA Chan M.-S., Nene V., Shallow S.J., Sub B., Peterson J., Angiuoli S.,
 RA Pereira M., Allen J., Selengut J., Haft D., Mather M.W., Valdivia A.B.,
 RA Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
 RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
 RA Venter J.C., Carucci D.J., Hoffman S.V., Newbold C., Davis R.W.,
 RA Fraser C.M., Barrell B.G.;
 RT "Genome sequence of the human malaria parasite Plasmodium
 RT falciparum.";
 RL Nature 419:498-511 (2002).
 DR EMBL/AE014830/AAH35262.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 870 AA; 103334 MW; FE3FD8EA035BADE6 CRC64;

Query Match 53.1%; Score 43; DB 2; Length 870;
 Best Local Similarity 53.8%; Pred. No. 15e+02;
 Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

4 OSVFPSSQKNYL 16
 :::|||:|
 Db 744 EBYYSSEKYNL 756

RESULT 19
 054KN1_DICDI PRELIMINARY; PRT; 286 AA.
 AC 054KN1;
 DT 13-SEP-2005 (TREMBlrel. 31, Created)
 DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
 DE 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
 DE Random cDNA clone veg110.
 GN Name=rcdJf; ORFNames=DD0216186;
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
 OX NCBI_TaxID=44689;
 OX (1)
 RN NUCLEOTIDE SEQUENCE.

RC STRAIN=AX4;
 RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
 RA Sugang R., Berriman M., Song J., Olesl R., Szafarski K., Xu Q.,
 RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
 RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
 RA Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
 RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
 RA Fairbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.,
 RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
 RA Muzny D., Moutier T., Pain A., Lu M., Harper D., Lindsay I.,
 RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
 RA Wardrop A., Felder M., Thangavelu M., Johnson D., Knights A.,
 RA Louised H., Mungall K., Oliver K., Price C., Quail M.A.,
 RA Urushihara H., Hernandez J., Rabinowitsch E., Steffen D., Sanders M.,
 RA Ma J., Kohara Y., Sharp S., Simmonds M., Speigler S., Tivey A.,
 RA Sugano S., White B., Walker D., Woodward J., Winkler T., Tanaka Y.,
 RA Shaulsky G., Schleicher M., Weinstein G., Rosenthal A., Cox E.C.,
 RA Chisholm R.L., Gibbs R., Loomis W.F., Platzer M., Kay R.R.,
 RA Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.;
 RT "The genome of the social amoeba Dictyostelium discoideum.";
 RL Nature 0:0-0(2005).
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL/AAFI01000149; FAL63808.1; -; Genomic DNA.
 SQ SEQUENCE 286 AA; 33391 MW; 6FB19E2CDE17BBCA CRC64;

Query Match 51.9%; Score 42; DB 2; Length 286;
 Best Local Similarity 57.1%; Pred. No. 63;
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

1 KSSQSVFPSSQKN 14
 ||:|||||
 Db 33 KSNQLFPSSNNKN 46

RESULT 20
 094475_DICDI PRELIMINARY; PRT; 295 AA.
 AC 094475;
 DT 01-FEB-1997 (TREMBlrel. 02, Created)
 DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE ORFvegl10 (Fragment).
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
 OX NCBI_TaxID=44689;
 OX (1)
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=AX4;
 RC Loomis W.F.;
 RL Submitted (AUC-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL/U66370/AB06762.1; -; mRNA.
 DR DictyBase; DDB0216186; rcdJf.
 FT NON TER 1
 SQ SEQUENCE 295 AA; 34592 MW; FA5252A855840E0C CRC64;

Query Match 51.9%; Score 42; DB 2; Length 295;
 Best Local Similarity 57.1%; Pred. No. 65;
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

1 KSSQSVFPSSQKN 14
 ||:|||||
 Db 36 KSNQLFPSSNNKN 49

RESULT 21
 06F092_BACAN PRELIMINARY; PRT; 377 AA.
 AC 06F092;
 DT 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)

DE AminoTransferrase, class V.
 GN OrderedLocustNames=GBAA4663;
 OS Bacillus anthracis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
 CC Bacillus cereus group.
 OK NCBI_TaxID=1392;
 RN (1)
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Ames / isolate 0581;
 RA Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
 RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
 RA Fraser C.M.;
 RT "Bacillus anthracis comparative genomics."
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
 CC -1 SIMILARITY: Belongs to the class-V pyridoxal-phosphate-dependent
 CC aminoTransferrase family.
 DR EMBL: AE017334; AT70154.1; -; Genomic_DNA.
 DR TIGR: GBA4663; -;
 DR GO: GO:0008483; F:transaminase activity; IEA.
 DR GO: GO:0016740; F:transferrase activity; IEA.
 DR GO: GO:0008152; P:metabolism; IEA.
 DR InterPro: IPR000192; AminoTrans_V.
 DR Pfam: PF00266; AminoTrans_5; 1.
 KW AminoTransferrase; Complete proteome; Transferrase.
 SQ SEQUENCE 377 AA; 41579 MW; 93148263FDB6AD CRC64;
 QY Query Match 51.9%; Score 42; DB 2; Length 377;
 Best Local Similarity 62.5%; Pred. No. 86;
 Matches 10; Conservative 2; Mismatches 2; Indels 2; Gaps 1;
 Db 4 QSVFSS--SQNYLA 17
 60 QGVFTSGSESNTYA 75
 RESULT 22
 ID Q81LF8_BACAN PRELIMINARY; PRT; 378 AA.
 AC Q81LF8;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE AminoTransferrase, class V.
 GN OrderedLocustNames=BA4663;
 OS Bacillus anthracis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
 CC Bacillus cereus group.
 OK NCBI_TaxID=1392;
 RN (1)
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Ames / isolate Porton;
 RC MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;
 RA Read T.D., Peterson S.N., Tourasse N.J., Bailly L.W., Paulsen I.T.,
 RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
 RA Holtzapple E.K., Ostad O.A., Helgeson E., Ristone J., Wu M.,
 RA Kolonay J.F., Beaman M.J., Dodson R.J., Brinkac L.M., Giam M.L.,
 RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
 RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
 RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
 RA Berry K.J., Platt R.D., Wolf A.M., Watkins K.L., Nieman W.C.,
 RA Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,
 RA Salzberg S.L., Thomson B., Friedlander A.M., Koehler T.M.,
 RA Hanna P.C., Kolstoe A.-B., Fraser C.M.;
 RT "The genome sequence of Bacillus anthracis Ames and comparison to
 RT closely related bacteria."
 RL Nature 423:81-86 (2003)
 CC -1 SIMILARITY: Belongs to the class-V pyridoxal-phosphate-dependent
 CC aminoTransferrase family.
 DR EMBL: AE017038; AAP28364.1; -; Genomic_DNA.
 DR HSSP: P39171; 1P3W.
 DR TIGR: BA4663; -;
 DR GO: GO:0008483; F:transaminase activity; IEA.
 DR GO: GO:0016740; F:transferrase activity; IEA.

DR GO: GO:0008152; P:metabolism; IEA.
 DR InterPro: IPR000192; AminoTrans_V.
 DR Pfam: PF00266; AminoTrans_5; 1.
 KW AminoTransferrase; Transferrase.
 SQ SEQUENCE 378 AA; 41692 MW; 2B91F2FDCBBD50E0 CRC64;
 QY Query Match 51.9%; Score 42; DB 2; Length 378;
 Best Local Similarity 62.5%; Pred. No. 86;
 Matches 10; Conservative 2; Mismatches 2; Indels 2; Gaps 1;
 Db 4 QSVFSS--SQNYLA 17
 61 QGVFTSGSESNTYA 76
 RESULT 23
 ID Q6HSW3_BACAN PRELIMINARY; PRT; 379 AA.
 AC Q6HSW3;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE AminoTransferrase, class V.
 GN OrderedLocustNames=BA54328;
 OS Bacillus anthracis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
 CC Bacillus cereus group.
 OK NCBI_TaxID=1392;
 RN (1)
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Sterne;
 RA Bretin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
 RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
 RA Richardson P., Rubin E., Rice H.;
 RT "Complete genome sequence of Bacillus anthracis Sterne."
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 CC -1 SIMILARITY: Belongs to the class-V pyridoxal-phosphate-dependent
 CC aminoTransferrase family.
 DR EMBL: AE017225; AAT56626.1; -; Genomic_DNA.
 DR GO: GO:0008483; F:transaminase activity; IEA.
 DR GO: GO:0016740; F:transferrase activity; IEA.
 DR GO: GO:0008152; P:metabolism; IEA.
 DR InterPro: IPR000192; AminoTrans_V.
 DR Pfam: PF00266; AminoTrans_5; 1.
 KW AminoTransferrase; Transferrase.
 SQ SEQUENCE 379 AA; 41823 MW; 0A19C885D54D42D9 CRC64;
 QY Query Match 51.9%; Score 42; DB 2; Length 379;
 Best Local Similarity 62.5%; Pred. No. 86;
 Matches 10; Conservative 2; Mismatches 2; Indels 2; Gaps 1;
 Db 4 QSVFSS--SQNYLA 17
 62 QGVFTSGSESNTYA 77
 RESULT 24
 ID Q6HD94_BACHK PRELIMINARY; PRT; 379 AA.
 AC Q6HD94;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Cystathionine gamma-lyase (cysteine desulfhydrase) (EC 4.4.1.1).
 GN Name=nlts; OrderedLocustNames=B19727_4165;
 OS Bacillus thuringiensis (subsp. konkukian).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
 CC Bacillus cereus group.
 OK NCBI_TaxID=180856;
 RN (1)
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=97-27;
 RA Bretin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,

RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
 RA Richardson P., Rubin E., Tice H.;
 RT "Complete genome sequence of *Bacillus thuringiensis* 97-27.";
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Belongs to the class-V pyridoxal-phosphate-dependent
 aminotransferase family.
 CC EMBL: AE017355; AF62325.1; -; Genomic DNA.
 DR GO: GO:0004123; F:cystathionine gamma-lyase activity; IEA.
 DR GO: GO:0016829; F:lyase activity; IEA.
 DR GO: GO:0008483; F:transaminase activity; IEA.
 DR GO: GO:0008152; P:metabolism; IEA.
 DR InterPro: IPR000192; AminoTrans_V.
 DR Pfam: PF00266; AminoTrans_5; 1.
 KW Complete proteome; Lyase.
 SQ SEQUENCE 379 AA; 41737 MW; 64212B09605D4503 CRC64;

Query Match 51.9%; Score 42; DB 2; Length 379;
 Best Local Similarity 62.5%; Pred. No. 86;
 Matches 10; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

Oy 4 QSVFSS--SOKNYLA 17
 |||||:|:|:|:|:|:|
 Db 62 QGVFTSGSGSESNYLA 77

RESULT 25

0730A1_BACCI PRELIMINARY; PRT; 379 AA.

AC 0730A1; 05-JUL-2004 (TREMBlrel. 27, Created)

DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)

DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)

GN OrderedAccessionNames=BCE4516;

OS *Bacillus cereus* (strain ATCC 10987).

OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; *Bacillus*;

OC *Bacillus cereus* group.

OX NCBI_TaxID=222523;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA PubMed:14960714; DOI=10.1093/nar/gkh258;

RA Raabso D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,

RA Shores K.A., Fouts D.E., Tourasse N.J., Anguilo J.F.,

RA Nelson W.C., Kolts E.A.-B., Fraser C.M., Read T.D.;
 "The genome sequence of *Bacillus cereus* ATCC 10987 reveals metabolic
 adaptations and a large plasmid related to *Bacillus anthracis* pXO1.";
 Nucleic Acids Res. 32:977-988(2004).

CC -!- SIMILARITY: Belongs to the class-V pyridoxal-phosphate-dependent
 aminotransferase family.

CC EMBL: AE017278; AAS43417.1; -; Genomic DNA.

DR TIGR: BCE4516; -; F:transaminase activity; IEA.

DR GO: GO:0008483; F:transaminase activity; IEA.

DR InterPro: IPR000192; AminoTrans_V.

DR Pfam: PF00266; AminoTrans_5; 1.

DR Complete proteome.

KW SEQUENCE 379 AA; 41711 MW; 2B752F3396B7B468 CRC64;

Oy 4 QSVFSS--SOKNYLA 17
 |||||:|:|:|:|:|:|
 Db 61 QGVFTSGSGSESNYLA 76

Query Match 51.9%; Score 42; DB 2; Length 379;
 Best Local Similarity 62.5%; Pred. No. 86;
 Matches 10; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

RESULT 26

04MS37_BACCE PRELIMINARY; PRT; 380 AA.

DT 13-SEP-2005 (TREMBlrel. 31, Created)

DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)

DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)

DE Aminotransferase, class V, putative.

GN ORFNames=BCE G9241.4488;

OS *Bacillus cereus* G9241.

OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; *Bacillus*;

OC *Bacillus cereus* group.

OX NCBI_TaxID=269801;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA PubMed:15155910; DOI=10.1073/pnas.0402414101;

RA Hoffmaster A.R., Ravel J., Raabso D.A., Chapman G.D., Chute M.D.,

RA Maister C.K., De B.K., Sacchi C.T., Fitzgerald C., Mayer L.W.,

RA Maiden M.C.J., Priest F.G., Barker M., Jiang L., Cer R.Z.,

RA Riltstone J., Peterson S.N., Weyant R.S., Galloway D.R., Read T.D.,

RA Popovic T., Fraser C.M.;
 "Identification of anthrax toxin genes in a *Bacillus cereus* associated
 with an illness resembling inhalation anthrax.";
 Proc. Natl. Acad. Sci. U.S.A. 101:8449-8454(2004).

CC -!- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.

CC EMBL: AE0100010; EAL14984.1; -; Genomic DNA.

DR Aminotransferase; Transferase.

KW SEQUENCE 380 AA; 41922 MW; 694F885C2DC5880C CRC64;

Oy 4 QSVFSS--SOKNYLA 17
 |||||:|:|:|:|:|:|
 Db 62 QGVFTSGSGSESNYLA 77

Query Match 51.9%; Score 42; DB 2; Length 380;
 Best Local Similarity 62.5%; Pred. No. 87;
 Matches 10; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

RESULT 27

0634B2_BACCE PRELIMINARY; PRT; 380 AA.

DT 25-OCT-2004 (TREMBlrel. 28, Created)

DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)

DE 25-OCT-2004 (TREMBlrel. 28, Last annotation update)

GN Cystathionine gamma-lyase (Cysteine desulfhydrase) (EC 4.4.1.1).

OS *Bacillus cereus* (strain ZK).

OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; *Bacillus*;

OC *Bacillus cereus* group.

OX NCBI_TaxID=288681;

RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RA Brettn T.S., Bruce D., Chalacombe J.P., Gilna P., Han C., Hill K.,

RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,

RA Richardson P., Rubin E., Tice H.;
 "Complete genome sequence of *Bacillus cereus* ZK.";
 Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.

CC -!- SIMILARITY: Belongs to the class-V pyridoxal-phosphate-dependent
 aminotransferase family.

CC EMBL: CP000001; AAU16093.1; -; Genomic DNA.

DR GO: GO:0004123; F:cystathionine gamma-lyase activity; IEA.

DR GO: GO:0016829; F:lyase activity; IEA.

DR GO: GO:0008483; F:transaminase activity; IEA.

DR InterPro: IPR000192; AminoTrans_V.

DR Pfam: PF00266; AminoTrans_5; 1.

DR Complete proteome; Lyase.

KW SEQUENCE 380 AA; 41826 MW; 57FB1BA5B1BD980 CRC64;

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Db      62 QGVFFSGSGSESNLYA 77

RESULT 28
ID      081V75_BACCR PRELIMINARY; PRT; 380 AA.
AC      081V75;
DT      01-JUN-2003 (TREMBlrel. 24, Created)
DT      01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT      01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE      Cysteine desulphydase (EC 4.4.1.-).
GN      OrderedLocusNames=BC4442;
OS      Bacillus cereus (strain ATCC 14579 / DSM 31).
OC      Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC      Bacillus cereus group.
OC      NCBI_TaxID=226900;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RX      MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
RA      Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
RA      Kapetral V., Bhattacharya A., Reznik G., Mikhailova N., Lapidus A.,
RA      Chu L., Mazur M., Goldman E., Larsen N., D'Souza M., Malunas T.,
RA      Grechkin Y., Pusch G., Haselkorn R., Fomstein M., Ehrlich S.D.,
RA      Overbeek R., Kyriides N.C.;
RT      "Genome sequence of Bacillus cereus and comparative analysis with
RT      Bacillus anthracis."
RL      Nature 423:87-91(2003).
CC      -1 SIMILARITY: Belongs to the class-V pyridoxal-phosphate-dependent
CC      aminotransferase family.
CC      EMBL, AE017012; AAP1337.1; -; Genomic_DNA.
DR      HSSP; P39171; 1P3W.
DR      GO; GO:0016829; F:lyase activity; IEA.
DR      GO; GO:0008483; P:transaminase activity; IEA.
DR      GO; GO:0008152; P:metabolism; IEA.
DR      InterPro: IPR00192; Aminoctrans_V.
DR      Pfam; PF00266; Aminoctran_5; 1.
DR      Complete proteome; Lyase.
KW      SEQUENCE 380 AA; 41971 MW; 702BDA4345N3C86C CRC64;

Query Match      51.9%; Score 42; DB 2; Length 380;
Best Local Similarity 62.5%; Pred. No. 87;
Matches 10; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

QY      4 QGVFFSS--SQKNYLA 17
Db      62 QGVFFSGSGSESNLYA 77

RESULT 29
ID      051KX5_MAGGR PRELIMINARY; PRT; 499 AA.
AC      051KX5;
DT      13-SEP-2005 (TREMBlrel. 31, Created)
DT      13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT      13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE      Hypothetical protein.
GN      ORFNames=MG09003.4;
OS      Magnaporthe grisea 70-15.
OC      Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC      Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.
OC      NCBI_TaxID=42507;
OX      [1]
RN      NUCLEOTIDE SEQUENCE.
RN      STRAIN=70-15;
RC      Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,
RC      Alt-Zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,
RC      Atchachi H., Armbruster J., Bachantang P., Baldwin J., Barry A.,
RC      Bayul T., Blitshteyn B., Bloom T., Biye J., Boguslavsky L.,
RC      Borowsky M., Boukhalter B., Brumache A., Butler J., Calixte N.,
RC      Calvo S., Camarata J., Campo K., Chang J., Cheshtasang Y., Citroen M.,
RC      Collymore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
RC      David R., Dawoe T., Degray S., Dodge S., Doolley K., Dorje P.,
RC      Dorjee K., Dorris L., Dufley N., Dupes A., Elkins T., Engels R.,

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RA      Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
RA      Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Gierre S.,
RA      Glinka A., Goyette A., Graham J., Grahbois E., Gyllen K., Hafez N.,
RA      Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
RA      Honan T., Horn A., Houde N., Hughes L., Hulme W., Hubby E., Iliev I.,
RA      Jaffe D., Jones C., Kamal M., Kamat A., Kamysseilis M., Karlsson E.,
RA      Kells C., Kieu A., Kistner P., Kodira C., Kulbokas E., Labutti K.,
RA      Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,
RA      Lindblad-toh K., Liu X., Lokitsang T., Lokitsang Y., Lucien O.,
RA      Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,
RA      Manning U., Marbella R., Maru K., Matthews C., Mauceli E.,
RA      McArthur M., McDonough S., Mcghee T., Meldrim J., Meus L.,
RA      Meitrov J., Mihalev A., Mihova T., Mikelsen T., Mlenga V., Moru K.,
RA      Mores J., Mullrain L., Munson G., Naylor J., News C., Nguyen C.,
RA      Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,
RA      Norbu N., O'donnell P., Okoawo O., O'leary S., Onotombo B.,
RA      O'Neill K., Osman S., Parker S., Perrin D., Phunkhang P., Pigant B.,
RA      Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,
RA      Rector R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,
RA      Rucman M., Schuppach R., Seaman C., Settipalli S., Sharpe T.,
RA      Sheridan J., Sherpa N., Shi J., Smitrov S., Smirnov S., Sougnuez C.,
RA      Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,
RA      Stetson K., Stone C., Stone S., Stubbs M., Talamas J., Tchuinga P.,
RA      Tenzing P., Tesfaye S., Theodore J., Thoultsang Y., Topham K.,
RA      Towey S., Tsamla T., Tsomo N., Vallee D., Vassiliev H.,
RA      Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,
RA      Wangdi T., Whitaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,
RA      Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,
RA      Zimmer A., Zody M., Lander E.;
RT      "The genome sequence of Magnaporthe grisea."
RL      Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
RN      [2]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=70-15;
RC      Dean R., Mitchell T., Brown D., Pan H., Thon M.;
RL      Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
RN      [3]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=70-15;
RC      Zhu H., Blackmon B.;
RL      Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
CC      -1 CAUTION: The sequence shown here is derived from an
CC      EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC      preliminary data.
DR      EMBL, AACU01001606; EAA47873.1; -; Genomic_DNA.
KW      Hypothetical protein.
KW      SEQUENCE 499 AA; 55992 MW; 52972747CEBDDA0 CRC64;

Query Match      51.9%; Score 42; DB 2; Length 499;
Best Local Similarity 60.0%; Pred. No. 1,2e+02;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      1 KSGQVFFSSSQKNY 15
Db      75 KASQSSIFSSSQKNH 89

RESULT 30
ID      Q65ZJ1_CAEBL PRELIMINARY; PRT; 607 AA.
AC      Q65ZJ1;
DT      25-OCT-2004 (TREMBlrel. 28, Created)
DT      25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT      25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE      Hypothetical protein C56E6.3.
GN      ORFNames=C56E6.3;
OS      Caenorhabditis elegans.
OC      Eukaryota; Metazoa; Nemacoda; Chromadorea; Rhabditida; Rhabditoidae;
OC      Rhabditidae; Peloderinae; Caenorhabditis.
OX      [1]
RN      NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RN      STRAIN=Bristol N2;

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RX MEDLINE=99069613; PubMed=9851916; DOI=10.1126/science.282.5396.2012;
 RG The C. elegans sequencing consortium;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology".
 RL Science 282:2012-2018(1998).
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 DR EMBL; U39996; AAU20848.1; -; Genomic DNA.
 DR Ensembl; C56E6.3; Caenorhabditis elegans.
 DR WormBase; WBGene00016971; C56E6.3.
 DR WormPeP; C56E6.3b; CR35261.
 DR InterPro; IPR011991; Wing_hlx_DNA_bd.
 KM Complete proteome; DNA-binding; Hypothetical protein; Nuclear protein;
 KW Transcription.
 SQ SEQUENCE 607 AA; 69516 MW; A43795C8A3A4A17A CRC64;

Query Match 51.9%; Score 42; DB 2; Length 607;
 Best Local Similarity 64.3%; Pred. No. 1.5e+02;
 Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 KSSQSVFFSSSQKN 14
 ||:|:|:|:|:|
 DB 232 KSTWSLFSSSSSEKN 245

RESULT 31
 ID 083182 TREPA PRELIMINARY; PRT; 619 AA.
 AC 083182;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Alpha-amylase 1, putative.
 GN OrderedLocustNames=TP0147;
 OS Treponema pallidum.
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
 OX NCBI_TaxID=160;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Nichols;
 RX MEDLINE=98332770; PubMed=9665876; DOI=10.1126/science.281.5375.375;
 RA Fraser C.M., Norris S.J., Weinstein G.M., White O., Sutton G.G.,
 RA Dodson R.J., Winn M.L., Hickey E.K., Clayton R.A., Ketchum K.A.,
 RA Sodergren E., Hardam J.M., McLeod M.P., Salzberg S.L., Peterson J.D.,
 RA Khalak H.G., Richardson D.L., Howell J.K., Chidambaram M.,
 RA Uetrebeck T.R., McDonald L.A., Artach P., Bowman C., Cotton M.D.,
 RA Fujii C., Garland S.A., Hatch B., Horst K., Roberts K.M., Sandusky M.,
 RA Weidman J.F., Smith H.O., Venter J.C.;
 RT "Complete genome sequence of Treponema pallidum, the syphilis
 RT spirochete".
 RL Science 281:375-388(1998).
 DR EMBL; AE001199; AAC65134.1; -; Genomic DNA.
 DR PIR; D71361; D71361.
 DR TIGR; TP0147; -;
 DR GO; GO:0003824; F:catalytic activity; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR004300; Glyco_hydro_57.
 DR Pfam; PF03065; Glyco_hydro_57; 1.
 KW Complete proteome.
 SQ SEQUENCE 619 AA; 70405 MW; 1FDAF4D80379894B CRC64;

Query Match 51.9%; Score 42; DB 2; Length 619;
 Best Local Similarity 53.3%; Pred. No. 1.5e+02;
 Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 KSSQSVFFSSSQKN 15
 ||:|:|:|:|:|
 DB 320 KAEQGVFPISSDRGY 334

RESULT 32
 ID 018897 CAEEL PRELIMINARY; PRT; 621 AA.
 AC 018897;

DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Hypothetical protein C56E6.3.
 GN ORFNames=C56E6.3;
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916; DOI=10.1126/science.282.5396.2012;
 RG The C. elegans sequencing consortium;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology".
 RL Science 282:2012-2018(1998).
 CC -1- INTERACTION:
 CC 017915; ran-1; NDExp=1; InAct=EBI-319539, EBI-324099;
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 DR EMBL; U39996; AAA81089.1; -; Genomic DNA.
 DR PIR; T15859; T15859.
 DR InAct; 018897; -;
 DR Ensembl; C56E6.3; Caenorhabditis elegans.
 DR WormBase; WBGene00016971; C56E6.3.
 DR WormPeP; C56E6.3a; CE04275.
 DR InterPro; IPR011991; Wing_hlx_DNA_bd.
 KM Complete proteome; DNA-binding; Hypothetical protein; Nuclear protein;
 KW Transcription.
 SQ SEQUENCE 621 AA; 71355 MW; CF76019BBE1E71F1 CRC64;

Query Match 51.9%; Score 42; DB 2; Length 621;
 Best Local Similarity 64.3%; Pred. No. 1.5e+02;
 Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 KSSQSVFFSSSQKN 14
 ||:|:|:|:|:|
 DB 232 KSTWSLFSSSSSEKN 245

RESULT 33
 ID 03VL25 DROME PRELIMINARY; PRT; 694 AA.
 AC 03VL25; 08MY2;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2005 (TREMBLrel. 30, Last annotation update)
 DE CG4901-PA (R848269p).
 GN ORFNames=CG4901;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Chame M., Pfeiffer G.L.G.,
 RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolintinas S.,
 RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brotter P.,
 RA Burdick K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunn B.C., Dunn P.,
 RA Durbin J.K., Evangelista C.C., Ferraz C., Fertiret S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegun C.,
RA Jatali M., Kalush F., Karpen G.H., Ke Z., Kemison J.A., Kechum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laiko P., Lei Y., Lavitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Matzel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mekulov G., Milhina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert C., Remington K., Saunders R.D.C., Schaefer F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svrtskas R., Teocor C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang X., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).
[12]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=22426065; PubMed=12537568;
RX Celinker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodeggen E.J.,
RA Svrtskas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*
melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
[13]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=22426070; PubMed=12537573;
RX Kaminker J.S., Bergman C.M., Krommiller B., Carlson J.W., Svrtskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celinker S.E.;
RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
a genomic perspective.";
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
[14]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=22426069; PubMed=12537572;
RX Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
RA Smith C.D., Tudy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Betencourt B.R., Celinker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
[15]
RN NUCLEOTIDE SEQUENCE.
RP Berkeley *Drosophila* Genome Project;
RA Celinker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton M., Pacleb J., Park S., Svrtskas R., Smith E.,
RA Yu C., Rubin G.;
RT "Drosophila melanogaster release 4 sequence.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[16]
RN NUCLEOTIDE SEQUENCE.
RP FlyBase;
RG Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
RN [7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Berkeley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorese V., Dresnek D., Partan D., Frise E.,

RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Munro J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celinker S.;
RT Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL: AE003627; AAF52873.2; -; Genomic_DNA.
DR EMBL: AY113491; AAF29496.1; -; mRNA.
DR FlyBase: FBgn0032194; CG4901.
DR GO: GO:0005634; C:nucleus; IEA.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0008026; F:ATP-dependent helicase activity; IEA.
DR GO: GO:0016787; F:hydrolyase activity; IEA.
DR GO: GO:0003676; F:nucleic acid binding; IEA.
DR InterPro: IPR001410; DEAD.
DR InterPro: IPR011545; DEAD/DEAH_N.
DR InterPro: IPR002464; DEAH_box.
DR InterPro: IPR011709; DUF1605.
DR InterPro: IPR001650; Helicase_C.
DR InterPro: IPR007502; Helicase_dom.
DR Pfam: PF00270; DEAD.1.
DR Pfam: PF07717; DUF1605; 1.
DR Pfam: PF04408; HA2; 1.
DR Pfam: PF00271; Helicase_C; 1.
DR SMART: SM00487; DEXDC; 1.
DR SMART: SM00490; HELIC; 1.
DR PROSITE: PS00690; DEAH_ATP_HELICASE; 1.
KW ATP-binding; Helicase; Hydrolyase; Nuclear protein.
SQ SEQUENCE 694 AA; 78319 MW; C363A4C0B8D608DE CRC64;

Query Match 51.9%; Score 42; DB 2; Length 694;
Best Local Similarity 56.2%; Pred. No. 1.7e+02;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 2 SSQSVFSSQKRYIA 17
DB 521 SSDHVFVSNSEKEMWA 536

RESULT 34
ID O97239_P1AF7 PRELIMINARY; PRT; 3933 AA.
AC O97239;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein MAL3P2.18.
GN Name=MAL3P2.18; Synonyms=PF0245c;
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=99376085; PubMed=10448855; DOI=10.1038/22964;
RX Bowman S., Lawson D., Baeham D., Brown D., Chillingworth T.,
RA Churcher C.M., Craig A., Davies R.M., Devlin K., Fellwell T.,
RA Gentles S., Gwilliam R., Hamlin N., Harris D., Holroyd S., Hornsby T.,
RA Horrocks P., Jagsels K., Jassal B., Kyles S., McLean J., Moule S.,
RA Mungall K., Murphy L., Oliver K., Quail M.A., Rajandream M.-A.,
RA Rutter S., Skelton J., Squares S., Squares S., Sulston J.E.,
RA Whitehead S., Woodward J.R., Newbold C., Barrett B.G.;
RT "The complete nucleotide sequence of chromosome 3 of *Plasmodium*
falciparum.";
RL Nature 400:532-538(1999).
[2]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=22255708; PubMed=12368867; DOI=10.1038/nature01095;
RX Hall N., Pain A., Berriman M., Churcher C., Harris B., Harris D.,
RA Mungall K., Bowman S., Atkin R., Baker S., Barton A., Brooks K.,
RA Buckee C.O., Burrows C., Cherevach I., Chillingworth C.,
RA Chillingworth T., Christodoulou Z., Clark L., Clark R., Cotton C.,
RA Cronin A., Davies R., Davis P., Dear P., Dearden F., Doggett J.,
RA Feltwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,

RA Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,
 RA Humphray S., Jørgensen K., James K.D., Johnson D., Kermorou A.,
 RA Knights A., Kontorov B., Kyes S., Larke N., Lawson D., Lennard N.,
 RA Line A., Maddison M., McLean J., Mooney P., Moul S., Murphy L.,
 RA Oliver K., Ormond D., Price C., Quail M.A., Rabbittsch E.,
 RA Rajandrem M.A., Rutter S., Rutherford K.W., Sanders M., Simmons M.,
 RA Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens K.,
 RA Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,
 RA Sulston J.E., Craig A., Newbold C., Barrett B.G.;
 RT "Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13.";
 RL Nature 419:527-531(2002)
 DR EMBL: AL034558; CAB39005.1; -; Genomic_DNA.
 DR InterPro: IPR012351; Cytokine_4_hlx.
 DR InterPro: IPR002048; EF_hand_Ca_bd.
 DR Pfam: PF04118; Dopey N; 1.
 DR PROSITE: PS00018; EF_HAND; UNKNOWN_1.
 KW Cytokine; Hypothetical protein.
 SQ SEQUENCE 3933 AA; 467882 MW; 51444604EE36933 CRC64;

Query Match 51.9%; Score 42; DB 2; Length 3933;
 Best Local Similarity 50.0%; Pred. No. 1.2e+03;
 Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 SSQSVFSSSQKNYLA 17
 Db 654 SSSSIFSPSTKSLIA 669

RESULT 35
 Q97MX3_CLOAB PRELIMINARY; PRT; 232 AA.
 AC Q97MX3;
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-UN-2003 (TrEMBLrel. 24, Last annotation update)
 DE (FS) similar to ABC transporter (Permease), YXDM B. subtilis
 DE ortholog.
 GN OrderedLocusNames=CAC0067;
 OS Clostridium acetobutylicum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1488;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN-ATCC 824 / DSM 792 / VKM B-1787;
 RX MEDLINE=21359325; PubMed=11466286;
 DOI=10.1128/JB.183.16.4823-4838.2001;
 RA Noelling J., Breton G., Omeichenko M.V., Makarova K.S., Zeng Q.,
 RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
 RA Tatusov R.L., Sabathe F., Doucette-Stamm L.A., Soucaille P.,
 RA Daly M.J., Bennett G.N., Koonin E.V., Smith D.R.;
 RT "Genome sequence and comparative analysis of the solvent-producing
 RT bacterium Clostridium acetobutylicum";
 RL J. Bacteriol. 183:4823-4838(2001).
 DR EMBL: AE007519; AAK78053.1; -; Genomic_DNA.
 DR PIR: B96908; B96908.
 DR GO: GO:0016020; C:membrane; IEA.
 DR InterPro: IPR003838; DUF214.
 DR Pfam: PF02687; FtsX; 1.
 KW Complete proteome.
 SQ SEQUENCE 232 AA; 26046 MW; 52AD4DA27B694EAF CRC64;

Query Match 50.6%; Score 41; DB 2; Length 232;
 Best Local Similarity 61.5%; Pred. No. 75;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 SSQSVFSSSQKNY 15
 Db 76 SSQSVFMKARQXDY 88

RESULT 36

Q5P012_XENIA
 ID Q5P012_XENIA PRELIMINARY; PRT; 290 AA.
 AC Q5P012;
 DT 01-FEB-2005 (TrEMBLrel. 29, Created)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE LOC496017 protein.
 GN Name=LOC496017;
 OS Xenopus laevis (African clawed frog).
 OC Baktarya; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
 OC Xenopodinae; Xenopus; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Testis;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT Initiative.";
 RL Dev. Dyn. 225:384-391(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Testis;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg H., Buetow K.H., Scheffer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Hong L.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loughell N.A., Peters G.J., Abramson R.D., Millihy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A.C., Shevchenko Y., Bouffard G.G.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield V.S.N., Krzywinski M.I., Skalska D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Testis;
 RA Klein S., Gerhard D.S.;
 RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC087408; AA07408.1; -; mRNA.
 SQ SEQUENCE 290 AA; 32593 MW; CC3B46D21F5942AC CRC64;

Query Match 50.6%; Score 41; DB 2; Length 290;
 Best Local Similarity 53.3%; Pred. No. 96;
 Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 SSQSVFSSSQKNYL 16
 Db 165 SPQKTFLLSKRSKSYL 179

RESULT 37
 Q9LS30_PHYPA
 ID Q9LS30_PHYPA PRELIMINARY; PRT; 296 AA.
 AC Q9LS30;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Homeobox protein Pbh8.
 DE Name=Pbh8;
 GN Physcomitrella patens (Moss).

```
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
OX NCBL_TaxID=3218;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21165321; PubMed=11264400;
RA Sakakibara K., Nishiyama T., Kato M., Hasebe M.;
RT "Isolation of homeodomain-leucine zipper genes from the moss
RT Physcomitrella patens and the evolution of homeodomain-leucine zipper
RT genes in land plants.";
RL Mol. Biol. Evol. 18:491-502(2001).
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL; AB028079; BAA93467.1; -, mRNA.
DR HSSP; P01367; IAKI.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007275; P:development; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR01287; Homeodomain-rel.
DR InterPro; IPR002197; HTH_Fis.
DR InterPro; IPR000047; HTH_Lambdaressr.
DR InterPro; IPR003106; Leu_zip_homeo.
DR Pfam; PF02183; HALZ; 1.
DR Pfam; PF00046; Homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR PRINTS; PR01590; HTHFIS.
DR PRINTS; PR00031; HTHREPRESSR.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS50071; HOMEBOX_2; 1.
DR DNA-binding; Homeobox; Nuclear protein.
KW SEQUENCE 296 AA; 32838 MW; 808B6045089B4650 CRC64;

Query Match 50.6%; Score 41; DB 2; Length 296;
Best Local Similarity 64.3%; Pred. No. 99;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 KSSQSVFFSSSQKN 14
DB 163 KSSQSVFFSSSQKN 176

RESULT 38
OSDCO SCHUA PRELIMINARY; PRT; 313 AA.
AC OSDCCO;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeiida;
OC Schistosomatoidea; Schistosomatidae; Schistosoma.
OX NCBL_TaxID=6182;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Han Z.;
RT "The full-length cDNA sequences of Schistosoma japonicum genes.";
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY814804; AAN26536.1; -, mRNA.
KW Hypothetical protein.
SQ SEQUENCE 313 AA; 35083 MW; SDE000D131CBF5E0 CRC64;

Query Match 50.6%; Score 41; DB 2; Length 313;
Best Local Similarity 60.0%; Pred. No. 1e+02;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 KSSQSVFFSSSQKN 15
DB 159 KSSQSVFFSSSQKN 173
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RESULT 39
OS5H81_ORYSA PRELIMINARY; PRT; 396 AA.
AC 075H81_ORYSA
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative serpin.
GN Name=OSUNB0007E22.7;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhacridae; Oryzeae; Oryza.
OX NCBL_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
RA Overton II L.L., Tsaltrin T., Kim M.M., Bera J.J., Jin S.S.;
RA Padrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S.,
RA Vanden S.S., Riedmuller S.B., Uterback T.T., Feldblyum T.V.,
RA Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
RA White O., Salzberg S.L., Fraser C.M.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Buell R.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the serpin family.
DR EMBL; AC136972; AAR00595.1; -, Genomic_DNA.
DR HSSP; P01008; IATH.
DR Gramene; 075H81; -.
DR GO; GO:004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR000215; Prot_inh_serpin.
DR Pfam; PF00079; Serpin; 1.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; 1.
KW Serpin.
KW SEQUENCE 396 AA; 42140 MW; 33EA5971B713175D CRC64;

Query Match 50.6%; Score 41; DB 2; Length 396;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 1 KSSQSVFFSSSQKN 16
DB 204 KSSQSVFFSSSQKN 219

RESULT 40
OS9S58_CANAL PRELIMINARY; PRT; 463 AA.
AC 059S58;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein NP1;
GN Name=NP1; ORFNames=CA019.10986, CA019.3482;
OS Candida albicans SC5314.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBL_TaxID=37561;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=SC5314;
RX PubMed=15123810; DOI=10.1073/pnas.0401648101;
RA Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S.,
RA Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,
RA Davis R.W., Scherer S.;
RL "The diploid genome sequence of Candida albicans.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
```


Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablos B., Delcher A., Deng Z., Maye A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferrelle S., Fleischmann W., Fowler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howard T.J., Wei M.-H., Ibegwam C., Jaiswal M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Mlehnina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusken D.R., Pacle J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Venter E., Wang X., Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhao X., Zhu S., Zhu X., Smith H.O., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

"The genome sequence of *Drosophila melanogaster*." Science 287:2185-2193(2000).

[3]

GENOME REANNOTATION.

RA MEDLINE=22426069; PubMed=12537572;

RA Miura S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitefield E.J., Bayraktaroglu L., Berman B.P., Betencourt B.R., Celisner S.E., de Grey A.D.N.J., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M., Lewis S.E.;

RA "Annotation of the *Drosophila melanogaster* euchromatic genome: a systematic review." Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).

RT [4]

NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

RA STRAIN=Berkeley; TISSUE=Embryo;

RA MEDLINE=22426066; PubMed=12537569;

RA Scapleton M., Carlson J.W., Brostelein P., Yu C., Champe M., George R.A., Garin H., Krommiller B., Pacle J.M., Park S., Wan K.H., Rubin G.M., Celisner S.E.;

RA "A *Drosophila* full-length cDNA resource." Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).

RT - FUNCTION: Probable ATP-binding RNA helicase.

CC - SIMILARITY: Belongs to the DEAD box helicase family.

CC -----

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CC -----

CC EMBL: L13612; AAA16339.1; -; Unassigned DNA.

CC EMBL: 223266; CAAB0804.1; -; Genomic DNA.

CC EMBL: AE003834; AAF58994.1; -; Genomic DNA.

CC EMBL: AY058728; AAL13957.1; -; mRNA.

CC EMBL: S38329; S38329.

CC PIR: S38329; S38329.

CC HSSP: P10081; 10DE.

CC DR Ensembl: CG12759; *Drosophila melanogaster*.

CC DR FlyBase: FBGN0010220; Dbp45A.

CC DR InterPro: IPR001410; DEAD.

CC DR InterPro: IPR011545; DEAD/DEAH_N.

CC DR InterPro: IPR000629; DEAD box_C.

CC DR InterPro: IPR001650; Helicase_C.

CC DR Pfam: PF00270; DEAD; 1.

CC DR Pfam: PF00271; Helicase_C; 1.

CC SMART: SM00487; DEXDC; 1.

DR SMART: SM00490; HELIC; 1.

DR PROSITE: PS00039; DEAD_ATP_HELICASE; 1.

KW ATP-binding; Helicase; Hydrolyase; Nucleotide-binding; RNA-binding.

FT NP_BIND 51 58 ATP (potential).

FT MOTIF 157 160 DEAD box.

FT CONFLICT 161 161 R -> P (in Ref. 1).

FT CONFLICT 211 217 SODSVA -> CASANR (in Ref. 1).

FT CONFLICT 224 225 OR -> HG (in Ref. 1).

FT CONFLICT 228 229 LC -> VS (in Ref. 1).

FT CONFLICT 234 234 R -> P (in Ref. 1).

FT CONFLICT 327 327 M -> I (in Ref. 1).

FT CONFLICT 407 407 P -> C (in Ref. 1).

FT CONFLICT 456 456 P -> S (in Ref. 1).

FT CONFLICT 493 493 D -> Y (in Ref. 1).

FT CONFLICT 517 521 KDKRA -> NKSKGKRDV (in Ref. 1).

FT CONFLICT 521 AA; 59678 MW; 89C68C43CD947913 CRC64;

SO SEQUENCE

Query Match 50.6%; Score 41; DB 1; Length 521;

Best local similarity 37.5%; Pred. No. 1.9e+02;

Matches 6; Conservative 8; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KSSQVFFSSQKXNYL 16

Db 180 KTRQNLFFSATMKDFI 195

RESULT 44

086132 DICI1 PRELIMINARY; PRT; 542 AA.

ID 086132 DICI1 PRELIMINARY; PRT; 542 AA.

AC 086132-

DT 01-JUN-2003 (TRENBLrel. 24, Created)

DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)

DT 10-MAY-2005 (TRENBLrel. 30, Last annotation update)

DE Hypothetical protein.

GN ORFNames=DD80217617;

OS *Dictyostelium discoideum* (Slime mold).

OC Dictyosteliales; Dictyosteliales; Dictyostelium.

OC NCBI_taxid=44689;

OK NCBI_taxid=44689;

RT [1]

NUCLEOTIDE SEQUENCE.

RA STRAIN=AX4;

RA MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847;

RA Gloeckner G., Eichinger L., Szatranski K., Pachebat J.A., Bankier A.T., Dear P.H., Lehmann R., Baugart C., Parra G., Abri J.F., Gaigo R., Kumpf K., Tunggal B., Cox E., Quail M.A., Platzter M., Rosenthal A., Noegel A.A.;

RA "Sequence and analysis of chromosome 2 of *Dictyostelium discoideum*." Nature 418:79-85(2002).

RT [2]

NUCLEOTIDE SEQUENCE.

RA STRAIN=AX4;

RA Baugart C.;

RA Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.

RT [3]

NUCLEOTIDE SEQUENCE.

RA STRAIN=AX4;

RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A., Sungang R., Bettman M., Song J., Olsen R., Szatranski K., Xu Q., Tunggal B., Kummerfeld S., Madera M., Kontorov B.A., Rivero F., Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P., Pilcher K., Chen G., Saunders D., Sodergren E., Davis P., Kethornou A., Nie X., Hall N., Anjard C., Hemphill L., Bacon N., Fairbrother P., Deasny B., Just E., Morio T., Rost R., Churcher C., Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I., Muzny D., Moutier T., Pain A., Lu M., Harper D., Lindsey R., Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchliesser C., Wardrop A., Felder M., Thangavelu M., Johnson D., Knights A., Louisse H., Mungall K., Oliver K., Price C., Quail M.A., Trushkova H., Hernandez J., Rabinowitsch E., Steffen D., Sanders M., Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A., Sugano S., White B., Walker D., Woodward J., Winkler T., Tanaka Y., Shaulsky G., Schleicher M., Weinstein G., Rosenthal A., Cox E.C., Chisholm R.L., Gibbs R., Loomis W.F., Platzter M., Kay R.R.;

RA Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.;
 RT "The genome of the social amoeba *Dictyostelium discoideum*."
 RL Nature 0:0-0(2005).
 DR EMBL; AC116305; AAC52318.1; -; Genomic_DNA.
 DR EMBL; AAF101000028; EAL6918.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 542 AA; 59715 MW; CD4D773B2B53765 CRC64;

Query Match 50.6%; Score 41; DB 2; Length 542;
 Best Local Similarity 60.0%; Pred. No. 1.9e+02;
 Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 2 SSGSVFFSSSQKNTL 16
 ||:|||||:|:
 Db 374 SRSRYFNSSNNQYL 388

RESULT 45
 ID Q64VD1_BACFR PRELIMINARY; PRT; 543 AA.
 AC Q64VD1;
 DT 25-OCT-2004 (TReMBLrel. 28, Created)
 DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
 DE Hypothetical protein.
 GN Ordered locus names=BFL800;
 OS Bacteroides fragilis.
 OC Bacteroidetes; Bacteroidales; Bacteroidia; Bacteroidaceae; Bacteroides.
 OC NCBI_taxid=817;
 RN (1)
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=YCH46;
 RX PubMed=15466707; DOI=10.1073/pnas.0404172101;
 RA Kuwahara T., Yamashita A., Hirakawa H., Nakayama H., Toh H., Okada N.,
 RA Kuhara S., Hattori M., Hayashi T., Ohnishi Y.,
 RT "Genomic analysis of Bacteroides fragilis reveals extensive DNA
 RT Inversions regulating cell surface adaptation."
 RL Proc. Natl. Acad. Sci. U.S.A. 101:14919-14924(2004).
 DR EMBL; AP006841; BAD48547.1; -; Genomic DNA.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 543 AA; 58176 MW; 035B51B913C4A956 CRC64;

Query Match 50.6%; Score 41; DB 2; Length 543;
 Best Local Similarity 46.7%; Pred. No. 1.9e+02;
 Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 1 KSSQSVFFSSSQKNT 15
 ||:|||||:
 Db 384 KSGNFYFASQSNY 398

RESULT 46
 ID Q75HM8_ORYSA PRELIMINARY; PRT; 653 AA.
 AC Q75HM8;
 DT 05-JUL-2004 (TReMBLrel. 27, Created)
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
 DE Putative serine protease inhibitor.
 GN ORFNames=OSJNBa0034004.19;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaeae; Oryza.
 OC NCBI_taxid=399477;
 RN (1)
 RP NUCLEOTIDE SEQUENCE.

RA Buell C., Yuan Q., Ouyang S., Liu J., Wang A., Maiti R., Lin H.,
 RA Zhu W., Hamilton J., Jones K., Tallon L., Feldblum T., Tselirin T.,
 RA Bera J., Kim M., Jin S., Padrosh D., Vuong H., Overton II L.,
 RA Reardon M., Weaver B., Johni S., Lewis M., Uteirback T., Van Aken S.,
 RA Wortman J., Haas B., Koo H., Zismann V., Hsiao J., Tobst S.,

RA de Vazelles A., White O., Salzberg S., Fraser C.;
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 RN (2)
 RP NUCLEOTIDE SEQUENCE.

RA Buell R.;
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the serpin family.
 DR EMBL; AC135500; AAR87358.1; -; Genomic_DNA.
 DR HSP; P01008; IATH.
 DR Gramene; 075HM8; -;
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
 DR InterPro; IPR000215; Prot_inh_serpin.
 DR Pfam; PF00079; Serpin; 2.
 DR SMART; SM00093; SERPIN; 2.
 DR PROSITE; PS00284; SERPIN; 2.
 KW Protease; Serpin.
 SQ SEQUENCE 653 AA; 70791 MW; FA6D9A06AE67B0BB CRC64;

Query Match 50.6%; Score 41; DB 2; Length 653;
 Best Local Similarity 50.0%; Pred. No. 2.4e+02;
 Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 1 KSSQSVFFSSSQKNTL 16
 ||:|||||:
 Db 204 KSVQAPFMTSKQYI 219

RESULT 47
 ID Q7QC68_ANOGA PRELIMINARY; PRT; 745 AA.
 AC Q7QC68;
 DT 01-MAR-2004 (TReMBLrel. 26, Created)
 DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE ENSANGP0000021939.
 GN ORFNames=ENSANGG00000019450;
 OS Anopheles gambiae str. PEST.
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Preygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Culicidae;
 OC Anophelinae; Anopheles.
 OC NCBI_taxid=180454;
 RN (1)
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=PEST;
 RG The Anopheles gambiae Sequence Committee;
 RT Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 RN (2)
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PEST;
 RG The Anopheles gambiae Sequence Committee;
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AAB01008859; EAA08192.2; -; Genomic_DNA.
 DR InterPro; IPR011108; RMBL.
 DR Pfam; PF07521; RMBL; 1.
 SQ SEQUENCE 745 AA; 84650 MW; SB77CEB685C17938 CRC64;

Query Match 50.6%; Score 41; DB 2; Length 745;
 Best Local Similarity 61.5%; Pred. No. 2.8e+02;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 3 SSGSVFFSSSQKNT 15
 ||:|||||:
 Db 443 SHTGFFRSKKNY 455

RESULT 48
 ID Q4YW61_PLABE PRELIMINARY; PRT; 752 AA.

```
AC 04Y61;
DT 13-SEP-2005 (TReMBLrel. 31, Created)
DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
DE GRP-binding protein, putative.
OS ORFNames=PB000500.02.0;
GN Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5621;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Beriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Omond D., Doggett J., Trueman H.E., Mendoza J.,
RA Biwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
DR EMBL; CAI01002147; CAH97745.1; -; Genomic_DNA.
SQ SEQUENCE 752 AA; 87211 MW; 6D7F775590AE259 CRC64;

Query Match 50.6%; Score 41; DB 2; Length 752;
Best Local Similarity 37.5%; Pred. No. 2.8e+02;
Matches 6; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

OY 1 KSSQSVFFSSSQKNTL 16
Db |::|::|::|:
221 KKKQKIYFINSKKSYY 236

RESULT 49
O7RJ38 PLAYO PRELIMINARY; PRT; 944 AA.
ID O7RJ38_
AC O7RJ38_
DT 01-MAR-2004 (TReMBLrel. 26, Created)
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Elongation factor Tu family, putative.
GN Name=PY033426;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=73239;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=17XNL;
RX MEDLINE=22255706; PubMed=1236865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perce M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoaihi A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Valdivia A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.O.;
RT "Genome sequence and comparative analysis of the model rodent malaria
parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
DR EMBL; AABL01000982; EAA22995.1; -; Genomic_DNA.
DR HSSP; P13551; 1DAR.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0003746; F:translation elongation factor activity; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR GO; GO:0007264; P:small GTPase mediated signal transduction; IEA.
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```
DR GO; GO:0006414; P:translational elongation; IEA.
DR InterPro; IPR000640; EFG_C.
DR InterPro; IPR004161; EFTU_D2.
DR InterPro; IPR006297; LepA.
DR InterPro; IPR000795; ProtSyn GRPbind.
DR InterPro; IPR001806; Ras transfrmng.
DR InterPro; IPR005225; Small_GTP.
DR Pfam; PF00679; EFG_C_1.
DR Pfam; PF00009; GTP_EFTU_1.
DR Pfam; PF03144; GTP_EFTU_D2_1.
DR Pfam; PF06421; LepA_C_1.
DR PRINTS; PR00315; ELONGATINFCT.
DR PRINTS; PR00449; RASTRSTRFMNG.
DR TIGRFAMs; TIGR00231; small_GTP_1.
SQ SEQUENCE 944 AA; 110561 MW; C6592F72D2AFAB2 CRC64;

Query Match 50.6%; Score 41; DB 2; Length 944;
Best Local Similarity 37.5%; Pred. No. 3.6e+02;
Matches 6; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

OY 1 KSSQSVFFSSSQKNTL 16
Db |::|::|::|:
412 KKKQKIYFINSKKSYY 427

RESULT 50
O7RM00 PLAYO PRELIMINARY; PRT; 1047 AA.
ID O7RM00_
AC O7RM00_
DT 01-MAR-2004 (TReMBLrel. 26, Created)
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Similar to sentrin/SUMO-specific protease.
GN Name=PY02338;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=73239;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=17XNL;
RX MEDLINE=22255706; PubMed=1236865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perce M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoaihi A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Valdivia A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.O.;
RT "Genome sequence and comparative analysis of the model rodent malaria
parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
DR EMBL; AABL01000655; EAA21830.1; -; Genomic_DNA.
DR HSSP; Q02724; 1EUV.
DR GO; GO:0008234; F:cysteine-type peptidase activity; IEA.
DR GO; GO:0005508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR003653; Peptidase_C48.
DR Pfam; PF02902; Peptidase_C48_1.
DR PROSITE; PS50600; ULP_PROTEASE; 1.
KM PROTEASE.
SQ SEQUENCE 1047 AA; 123328 MW; 31BA7C91EBEC50AA CRC64;

Query Match 50.6%; Score 41; DB 2; Length 1047;
Best Local Similarity 46.7%; Pred. No. 4.1e+02;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 1 KSSQSVFFSSSQKNTL 15
```

Db 807 KIDKNIEFKKONY 821

Search completed: May 4, 2006, 13:09:44
Job time : 206.206 Secs

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Tue May 9 08:59:43 2006

us-10-700-632-4.rat

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 4, 2006, 13:09:53 ; Search time 38.3175 Seconds

(without alignments)
36.680 Million cell updates/sec

Title: US-10-700-632-4

Perfect score: 81

Sequence: 1 KSSQSVFFSSQKNYLA 17

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Issued Patents AA:*

1: /cgn2_6/ptodata/1/1aa/5 COMB.pep:*

2: /cgn2_6/ptodata/1/1aa/6 COMB.pep:*

3: /cgn2_6/ptodata/1/1aa/H COMB.pep:*

4: /cgn2_6/ptodata/1/1aa/PTTUS COMB.pep:*

5: /cgn2_6/ptodata/1/1aa/RE COMB.pep:*

6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	69	85.2	112	2	US-08-435-516-4	Sequence 4, Appli
2	69	85.2	112	2	US-08-435-516-28	Sequence 28, Appli
3	69	85.2	301	1	US-08-661-052-14	Sequence 14, Appli
4	69	85.2	301	2	US-09-188-082-14	Sequence 14, Appli
5	69	85.2	301	2	US-09-364-088-14	Sequence 14, Appli
6	69	85.2	301	2	US-09-102-716-14	Sequence 14, Appli
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20	66	81.5	259	2	US-09-419-788-115	Sequence 11, Appli
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96	62	76.5	113	2	US-09-998-817-28	Sequence 28, Appli
97	62	76.5	113	2	US-09-998-817-29	Sequence 29, Appli
98	62	76.5	113	2	US-09-998-817-30	Sequence 30, Appli
99	62	76.5	113	2	US-09-998-817-31	Sequence 31, Appli
100	62	76.5	113	2	US-09-998-817-32	Sequence 32, Appli

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988 31 18.3 371 1 US-08-894-236-6 Sequence 6, Appli
989 31 18.3 371 1 US-08-919-624-4 Sequence 4, Appli
990 31 18.3 372 4 PCT-US96-01444-6 Sequence 4, Appli
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995 31 18.3 375 2 US-09-328-352-8084 Sequence 8084, Ap
996 31 18.3 376 2 US-09-134-000C-4846 Sequence 4846, Ap
997 31 18.3 379 2 US-09-303-518D-708 Sequence 708, App
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ALIGNMENTS

RESULT 1
US-08-435-516-4
; Sequence 4, Application US/08435516
; Patent No. 6500931
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANIZED ANTIBODIES TO FC RECEPTORS FOR
; TITLE OF INVENTION: IMMUNOBLOBLIN G ON HUMAN MONONUCLEAR PHAGOCYTES
; NUMBER OF SEQUENCES: 28
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,516
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: UK 92 23377.4; PCT/US93/10384
; FILING DATE: 04-NOV-1992; -02-NOV-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-013
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-435-516-4

Query Match 85.2%; Score 69; DB 2; Length 112;
Best Local Similarity 82.4%; Pred. No. 0.00011;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

1 KSSQSVFFSSQKNYLA 17
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Db 24 KSSQSVLYSSNQKNYLA 40

RESULT 2
US-08-435-516-28
; Sequence 28, Application US/08435516
; Patent No. 6500931
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANIZED ANTIBODIES TO FC RECEPTORS FOR
; TITLE OF INVENTION: IMMUNOBLOBLIN G ON HUMAN MONONUCLEAR PHAGOCYTES
; NUMBER OF SEQUENCES: 28
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,516
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: UK 92 23377.4; PCT/US93/10384
; FILING DATE: 04-NOV-1992; -02-NOV-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-013
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-435-516-28

Query Match 85.2%; Score 69; DB 2; Length 112;
Best Local Similarity 82.4%; Pred. No. 0.00011;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSSQSVFFSSQKNYLA 17
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Db 24 KSSQSVLYSSNQKNYLA 40

RESULT 3
US-08-661-052-14
; Sequence 14, Application US/08661052
; Patent No. 5837243
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo
; APPLICANT: Joel Goldstein
; APPLICANT: Robert Graziano
; APPLICANT: Chezian Somasundaram
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISD
; TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/661,052
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/484,172
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MXI-043CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 301 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-661-052-14

Query Match 85.2%; Score 69; DB 1; Length 301;
Best Local Similarity 82.4%; Pred. No. 0.00034;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSSQSVFSSQKNYLA 17
| | | | | : | | | | |
Db 178 KSSQSVLYSSNQKNYLA 194

RESULT 4
US-09-188-082-14
Sequence 14, Application US/09188082
Patent No. 6270765
GENERAL INFORMATION:
APPLICANT: Yashwant M. Deo
APPLICANT: Joel Goldstein
APPLICANT: Robert Graziano
APPLICANT: Chezia Somsundaram
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/188,082
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/661,052
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MXI-043CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 301 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-09-188-082-14

Query Match 85.2%; Score 69; DB 2; Length 301;
Best Local Similarity 82.4%; Pred. No. 0.00034;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSSQSVFSSQKNYLA 17
| | | | | : | | | | |
Db 178 KSSQSVLYSSNQKNYLA 194

RESULT 5
US-09-364-088-14
Sequence 14, Application US/09364088
Patent No. 6365161

GENERAL INFORMATION:
APPLICANT: Yashwant M. Deo, et al.
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street, 24th Floor
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/364,088
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/188,082
FILING DATE: 07-JUNE-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/484,172
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Remillard, Jane E.
REGISTRATION NUMBER: 38,872
REFERENCE/DOCKET NUMBER: MXI-043CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)742-7414
TELEFAX: (617)742-7414
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 301 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-364-088-14

Query Match 85.2%; Score 69; DB 2; Length 301;
Best Local Similarity 82.4%; Pred. No. 0.00034;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSSQSVFSSQKNYLA 17
| | | | | : | | | | |
Db 178 KSSQSVLYSSNQKNYLA 194

RESULT 6
US-09-102-716-14

Sequence 14, Application US/09102716
Patent No. 6395272
GENERAL INFORMATION:
APPLICANT: Yashwant M. Deo
APPLICANT: Joel Goldstein

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Robert Graziano
Chezian Somasundaram
TITLE OF INVENTION: OF ANTI-PC RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSER: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/102,716
FILING DATE: 22-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/661,052
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MXI-043CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 301 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-102-716-14

Query Match      85.2%; Score 69; DB 2; Length 301;
Best Local Similarity 82.4%; Pred. No. 0.00034;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KSSQSVFPSSQKNYLA 17
      |||||:|||||
      178 KSSQSVLYSSNQKNYLA 194

Db

RESULT 7
US-09-203-958A-2
; Sequence 2, Application US/09203958A
; Patent No. 6682928
; GENERAL INFORMATION:
; APPLICANT: KELER, Tibor
; APPLICANT: GOLDSTEIN, Joel
; APPLICANT: GRAZIANO, Robert
; APPLICANT: DEO, Yashwant M.
; TITLE OF INVENTION: CELLS EXPRESSING ANTI-PC RECEPTOR
; TITLE OF INVENTION: BINDING COMPONENTS
; FILE REFERENCE: MXI-099CPA
; CURRENT APPLICATION NUMBER: US/09/203,958A
; CURRENT FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 60/067232
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; US-09-203-958A-2
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Query Match      85.2%; Score 69; DB 2; Length 352;
Best Local Similarity 82.4%; Pred. No. 0.0004;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KSSQSVFPSSQKNYLA 17
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      61 KSSQSVLYSSNQKNYLA 77

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RESULT 8
US-08-661-052-16
; Sequence 16, Application US/08661052
; Patent No. 5837243
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo
; APPLICANT: Joel Goldstein
; APPLICANT: Robert Graziano
; APPLICANT: Chezian Somasundaram
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
; TITLE OF INVENTION: OF ANTI-PC RECEPTOR ANTIBODIES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSER: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/661,052
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,172
; FILING DATE: 07-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-043CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-661-052-16

Query Match      85.2%; Score 69; DB 1; Length 553;
Best Local Similarity 82.4%; Pred. No. 0.00067;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KSSQSVFPSSQKNYLA 17
      |||||:|||||
      178 KSSQSVLYSSNQKNYLA 194

Db

RESULT 9
US-09-188-082-16
; Sequence 16, Application US/09188082
; Patent No. 6270765
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo
; APPLICANT: Joel Goldstein
; APPLICANT: Robert Graziano
; APPLICANT: Chezian Somasundaram
```

TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRIS
TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/188,082
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/661,052
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MXI-043CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-188-082-16
Query Match 85.2%; Score 69; DB 2; Length 553;
Best Local Similarity 82.4%; Pred. No. 0.00067;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 KSSQSVFSSSQKNYLA 17
Db 178 KSSQSVLYSSNQKNYLA 194
RESULT 10
US-09-364-088-16
Sequence 16, Application US/09364088
Patent No. 6365161
GENERAL INFORMATION:
APPLICANT: Yashwant M. Deo, et al.
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISD
TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street, 24th Floor
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/364,088
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/188,082
FILING DATE: 07-JUNE-1996
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/484,172
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Remillard, Jane E.
REGISTRATION NUMBER: 38,872
REFERENCE/DOCKET NUMBER: MXI-043CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-7414
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-364-088-16
Query Match 85.2%; Score 69; DB 2; Length 553;
Best Local Similarity 82.4%; Pred. No. 0.00067;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 KSSQSVFSSSQKNYLA 17
Db 178 KSSQSVLYSSNQKNYLA 194
RESULT 11
US-09-102-716-16
Sequence 16, Application US/09102716
Patent No. 6395272
GENERAL INFORMATION:
APPLICANT: Yashwant M. Deo
Joel Goldstein
Robert Graziano
Chezian Somasundaram
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISD
TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/102,716
FILING DATE: 22-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/661,052
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MXI-043CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-102-716-16
Query Match 85.2%; Score 69; DB 2; Length 553;

Best Local Similarity 82.4%; Pred. No. 0.00067;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSSQSVFSSSQKNYLA 17
|||:|:|:|:|:|
Db 178 KSSQSVLYSSNQKNYLA 194

RESULT 12

PCT-US93-08435-22
; Sequence 22, Application PC/TUS9308435
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham, Corporation
; APPLICANT: U. S. Government, Secretary of
; APPLICANT: the Navy
; APPLICANT: U. S. Government, Secretary of
; TITLE OF INVENTION: Novel Antibodies for Confering Passive
; TITLE OF INVENTION: Immunity Against Infection by a Pathogen in Man
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Box 457, 321 Norristown Road
; CITY: Spring House
; STATE: PA
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08435
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/941,654
; FILING DATE: 09-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: SBC P50107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 540-9200
; TELEFAX: (215) 540-5818
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
PCT-US93-08435-22

Query Match 81.5%; Score 66; DB 4; Length 17;
Best Local Similarity 76.5%; Pred. No. 4.4e-05;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSSQSVFSSSQKNYLA 17
|||:|:|:|:|:|
Db 1 KSSQSVLYSSNQKNYLA 17

RESULT 13

PCT-US93-08435-35
; Sequence 35, Application PC/TUS9308435
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham, Corporation
; APPLICANT: U. S. Government, Secretary of
; APPLICANT: the Navy
; APPLICANT: U. S. Government, Secretary of
; APPLICANT: the Army
; TITLE OF INVENTION: Novel Antibodies for Confering Passive

TITLE OF INVENTION: Immunity Against Infection by a Pathogen in Man
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Box 457, 321 Norristown Road
; CITY: Spring House
; STATE: PA
; COUNTRY: USA
; ZIP: 19477

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08435
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/941,654
; FILING DATE: 09-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: SBC P50107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 540-9200
; TELEFAX: (215) 540-5818
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
PCT-US93-08435-35

Query Match 81.5%; Score 66; DB 4; Length 17;
Best Local Similarity 76.5%; Pred. No. 4.4e-05;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSSQSVFSSSQKNYLA 17
|||:|:~:|:|:|:|
Db 1 KSSQSVLYSSNQKNYLA 17

RESULT 14

US-08-483-749A-16
; Sequence 16, Application US/08483749A
; Patent No. 6054561
; GENERAL INFORMATION:
; APPLICANT: RING, DAVID B.
; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: INTELLECTUAL PROPERTY - R440, PO BOX 8097
; CITY: EMERYVILLE
; STATE: CA
; COUNTRY: USA
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,749A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: SAVERIDE, PAUL B.
; REGISTRATION NUMBER: 36,914

REFERENCE/DOCKET NUMBER: 0508.008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2585
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-483-749A-16

Query Match 81.5%; Score 66; DB 2; Length 113;
Best Local Similarity 76.5%; Pred. No. 0.00037;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KSSQSVFSSSQKNYLA 17
|||||:|||||
Db 24 KSSQSLYSSNQKNYLA 40

RESULT 15
PCT-US93-08435-4:
Sequence 4, Application PC/TUS9308435
GENERAL INFORMATION:
APPLICANT: SmithKline Beecham, Corporation
APPLICANT: U. S. Government, Secretary of
APPLICANT: the Navy
APPLICANT: U. S. Government, Secretary of
APPLICANT: the Army
TITLE OF INVENTION: Novel Antibodies for Confering Passive
TITLE OF INVENTION: Immunity Against Infection by a Pathogen in Man
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Box 457, 321 Norristown Road
CITY: Spring House
STATE: PA
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08435
CLASSIFICATION:
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,654
FILING DATE: 09-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: SBC P50107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 540-9200
TELEFAX: (215) 540-5818
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-08435-4

Query Match 81.5%; Score 66; DB 4; Length 113;
Best Local Similarity 76.5%; Pred. No. 0.00037;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Qy 1 KSSQSVFSSSQKNYLA 17
|||||:|||||

Db 24 KSSQSLYSSNQKNYLA 40

RESULT 16
PCT-US93-08435-6
Sequence 6, Application PC/TUS9308435
GENERAL INFORMATION:
APPLICANT: SmithKline Beecham, Corporation
APPLICANT: U. S. Government, Secretary of
APPLICANT: the Navy
APPLICANT: U. S. Government, Secretary of
APPLICANT: the Army
TITLE OF INVENTION: Novel Antibodies for Confering Passive
TITLE OF INVENTION: Immunity Against Infection by a Pathogen in Man
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Box 457, 321 Norristown Road
CITY: Spring House
STATE: PA
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08435
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,654
FILING DATE: 09-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: SBC P50107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 540-9200
TELEFAX: (215) 540-5818
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-08435-6

Query Match 81.5%; Score 66; DB 4; Length 113;
Best Local Similarity 76.5%; Pred. No. 0.00037;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KSSQSVFSSSQKNYLA 17
|||||:|||||
Db 24 KSSQSLYSSNQKNYLA 40

RESULT 17
PCT-US93-08435-8
Sequence 8, Application PC/TUS9308435
GENERAL INFORMATION:
APPLICANT: SmithKline Beecham, Corporation
APPLICANT: U. S. Government, Secretary of
APPLICANT: the Navy
APPLICANT: U. S. Government, Secretary of
APPLICANT: the Army
TITLE OF INVENTION: Novel Antibodies for Confering Passive
TITLE OF INVENTION: Immunity Against Infection by a Pathogen in Man
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Box 457, 321 Norristown Road

CITY: Spring House
STATE: PA USA
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08435
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,654
FILING DATE: 09-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 540-9200
TELEFAX: (215) 540-5818
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-08435-8

Query Match 81.5%; Score 66; DB 4; Length 113;
Best Local Similarity 76.5%; Pred. No. 0.00037;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSSQSVFFSSQKNYLA 17
|||:|:|:|:|:|:|
DB 24 KSSQSLVYSSQKNYLA 40

RESULT 18
US-08-952-235-1
Sequence 1, Application US/08952235
Patent No. 6207152
GENERAL INFORMATION:
APPLICANT: Schwall, Ralph H.
APPLICANT: Tabor, Kelly H.
TITLE OF INVENTION: Hepatocyte Growth Factor Receptor
TITLE OF INVENTION: Antagonists and Uses Thereof
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/952,235
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/460368
FILING DATE: 02-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P0938P1

TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 220 amino acids
TYPE: Amino Acid
TOPOLOGY: linear
US-08-952-235-1

Query Match 81.5%; Score 66; DB 2; Length 220;
Best Local Similarity 76.5%; Pred. No. 0.00079;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSSQSVFFSSQKNYLA 17
|||:|:|:|:|:|:|
DB 24 KSSQSLVYSSQKNYLA 40

RESULT 19
US-09-669-971-1
Sequence 1, Application US/09669971
Patent No. 6468529
GENERAL INFORMATION:
APPLICANT: Schwall, Ralph H.
APPLICANT: Tabor, Kelly H.
TITLE OF INVENTION: Hepatocyte Growth Factor Receptor
TITLE OF INVENTION: Antagonists and Uses Thereof
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/669,971
FILING DATE: 05-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/952,235
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/460368
FILING DATE: 02-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P0938P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 220 amino acids
TYPE: Amino Acid
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-669-971-1

Query Match 81.5%; Score 66; DB 2; Length 220;
Best Local Similarity 76.5%; Pred. No. 0.00079;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSSQSVFFSSQKNYLA 17
|||:|:~|:~|:~|:~|:~|
DB 24 KSSQSLVYSSQKNYLA 40

```
RESULT 20
US-09-419-788-115
; Sequence 115, Application US/09419788
; Patent No. 6825325
; GENERAL INFORMATION:
; APPLICANT: FISCHER, Rainer
; APPLICANT: SCHILLBERG, Stefan
; APPLICANT: NAHRING, Jorg
; APPLICANT: SACK, Markus
; APPLICANT: MONECKE, Michael
; APPLICANT: LIAO, Yu-Cai
; APPLICANT: SPIEGEL, Holger
; APPLICANT: ZIMMERMAN, Sabine
; APPLICANT: EMANS, Neil
; TITLE OF INVENTION: Molecular Pathogenicity Mediated Plant Disease
; FILE REFERENCE: 0147-0189P
; CURRENT APPLICATION NUMBER: US/09/419,788
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 98 11 9630.6 EP
; EARLIER FILING DATE: 1998-10-16
; EARLIER APPLICATION NUMBER: 66/BOM/1998 INDIA
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 115
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic, no
US-09-419-788-115

Query Match      81.5%; Score 66; DB 2; Length 259;
Best Local Similarity 76.5%; Pred. No. 0.00095;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KSSQSVFSSSQKNYLA 17
Db      164 KSSQSVLYSSNNKNYLA 180

RESULT 21
US-09-563-222C-14
; Sequence 14, Application US/09563222C
; Patent No. 6636620
; GENERAL INFORMATION:
; APPLICANT: EPICYTE PHARMACEUTICALS, INC.
; APPLICANT: HIATT, ANDREW C.
; APPLICANT: HEIN, MICHAEL B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
; FILE REFERENCE: 068304-0501
; CURRENT APPLICATION NUMBER: US/09/563,222C
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: PCT/US01/14349
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/563,222
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 14
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-563-222C-14

Query Match      79.0%; Score 64; DB 2; Length 17;
Best Local Similarity 76.5%; Pred. No. 9.8e-05;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      1 KSSQSVFSSSQKNYLA 17
Db      1 KSSQSVLYSSNNKNYLA 17
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Db      1 KSSQSVLYSSNNKNYLA 17

RESULT 22
US-09-830-748B-7
; Sequence 7, Application US/09830748B
; Patent No. 6818749
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as represented by The
; APPLICANT: Secretary of the Department of Health and Human Services
; APPLICANT: Kashmiti, Syed V.S.
; APPLICANT: Padian, Eduardo A.
; APPLICANT: Jeffery, Schloim
; TITLE OF INVENTION: VARIANTS OF HUMANIZED ANTI-CARCINOMA MONOCLONAL ANTIBODY CC49
; FILE REFERENCE: 4239-61725
; CURRENT APPLICATION NUMBER: US/09/830,748B
; PRIOR FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: PCT/US99/25552
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/106,757
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: US 60/106,534
; PRIOR FILING DATE: 1998-10-31
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 7
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-830-748B-7

Query Match      79.0%; Score 64; DB 2; Length 17;
Best Local Similarity 76.5%; Pred. No. 9.8e-05;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      1 KSSQSVFSSSQKNYLA 17
Db      1 KSSQSVLYSSNNKNYLA 17

RESULT 23
US-10-194-975-89
; Sequence 89, Application US/10194975
; Patent No. 6881557
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; PRIOR FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 89
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-89

Query Match      79.0%; Score 64; DB 2; Length 101;
Best Local Similarity 76.5%; Pred. No. 0.00073;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      1 KSSQSVFSSSQKNYLA 17
Db      24 KSSQSVLYSSNNKNYLA 40

RESULT 24
US-10-330-613A-55
; Sequence 55, Application US/10330613A
```

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Patent No. 6924360
; GENERAL INFORMATION:
; APPLICANT: Gadae, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613A
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-330-613A-55

Query Match          79.0%; Score 64; DB 2; Length 101;
Best Local Similarity 76.5%; Pred. No. 0.00073;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KSSQSVFFSSQKNYLA 17
    |||||:|:||||
Db 24 KSSQSVLYSSNNKNYLA 40

RESULT 25
US-07-942-245-30
; Sequence 30, Application US/07942245
; Patent No. 5639641
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, Jan T.
; APPLICANT: GEARLE, Stephen M.J.
; APPLICANT: REES, Anthony R.
; APPLICANT: ROGUSKA, Michael A.
; APPLICANT: GUILD, Braydon C.
; TITLE OF INVENTION: SURFACE RESIDUE VENERING OF RODENT
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 522
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: HP 9000/700 workstation
; OPERATING SYSTEM: UNIX
; SOFTWARE: In house
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/942,245
; FILING DATE: 09-SEP-1992
; CLASSIFICATION: 530
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 293-7060
; TELEFAX: (202) 293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-942-245-30

Query Match          79.0%; Score 64; DB 1; Length 112;
Best Local Similarity 76.5%; Pred. No. 0.00083;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KSSQSVFFSSQKNYLA 17
    |||||:|:||||
```

```
Db 24 KSSQSVLYSSNNKNYLA 40

RESULT 26
US-08-525-539A-80
; Sequence 80, Application US/08525539A
; Patent No. 6309636
; GENERAL INFORMATION:
; APPLICANT: DO CUTO, FERNANDO J.R.
; APPLICANT: CERIANI, ROBERTO L.
; APPLICANT: PETERSON, JERRY A.
; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
; TITLE OF INVENTION: M63 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
; TITLE OF INVENTION: METHODS OF HUMANIZING ANTIBODY PEPTIDES
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525,539A
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DYLAN, TYLER
; REGISTRATION NUMBER: 37,612
; REFERENCE/DOCKET NUMBER: 27633-20001.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-525-539A-80

Query Match          79.0%; Score 64; DB 2; Length 113;
Best Local Similarity 76.5%; Pred. No. 0.00083;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KSSQSVFFSSQKNYLA 17
    |||||:|:||||
Db 24 KSSQSVLYSSNNKNYLA 40

RESULT 27
US-09-274-163E-16
; Sequence 16, Application US/09274163E
; Patent No. 6485943
; GENERAL INFORMATION:
; APPLICANT: STEVENS, Fred J.
; APPLICANT: WILKINS STEVENS, Priscilla
; APPLICANT: RAFFEN, Rosemarie
; APPLICANT: SCHIFFER, Marianne
; TITLE OF INVENTION: OPTIMUM RECOMBINANT ANTIBODY PRODUCTION
; FILE REFERENCE: 051583/0224
; CURRENT APPLICATION NUMBER: US/09/274,163E
; CURRENT FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: US 08/373,380
; PRIOR FILING DATE: 1995-01-17
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
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SEQ ID NO 16
LENGTH: 113
TYPE: PRT
ORGANISM: Escherichia coli
US-09-274-163E-16

Query Match 79.0%; Score 64; DB 2; Length 113;
Best Local Similarity 76.5%; Pred. No. 0.00083;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KSSQSVFSSSQKNYLA 17
|||||:|:|:|
DB 24 KSSQSVLYSSNSKNYLA 40

RESULT 28

US-09-025-769B-17
Sequence 17, Application US/09025769B
Patent No. 6300064

GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Haag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090

INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid

STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-09-025-769B-17

Query Match 79.0%; Score 64; DB 2; Length 114;
Best Local Similarity 76.5%; Pred. No. 0.00084;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KSSQSVFSSSQKNYLA 17
|||||:|:|:|
DB 24 KSSQSVLYSSNSKNYLA 40

RESULT 29

US-09-274-163E-2

Sequence 2, Application US/09274163E
Patent No. 6485943
GENERAL INFORMATION:
APPLICANT: STEVENS, Fred J.
APPLICANT: WILKINS STEVENS, Priscilla
APPLICANT: RAFFEN, Rosemarie
APPLICANT: SCHIFFER, Marianne
TITLE OF INVENTION: OPTIMUM RECOMBINANT ANTIBODY PRODUCTION
FILE REFERENCE: 051583/0224
CURRENT APPLICATION NUMBER: US/09/274,163E
CURRENT FILING DATE: 1999-03-22
PRIOR APPLICATION NUMBER: US 08/373,380
PRIOR FILING DATE: 1995-01-17
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 114
TYPE: PRT
ORGANISM: Escherichia coli
US-09-274-163E-2

Query Match 79.0%; Score 64; DB 2; Length 114;
Best Local Similarity 76.5%; Pred. No. 0.00084;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KSSQSVFSSSQKNYLA 17
|||||:|:~|:|
DB 24 KSSQSVLYSSNSKNYLA 40

RESULT 30

US-09-274-163E-4
Sequence 4, Application US/09274163E
Patent No. 6485943

GENERAL INFORMATION:
APPLICANT: STEVENS, Fred J.
APPLICANT: WILKINS STEVENS, Priscilla
APPLICANT: RAFFEN, Rosemarie
APPLICANT: SCHIFFER, Marianne
TITLE OF INVENTION: OPTIMUM RECOMBINANT ANTIBODY PRODUCTION
FILE REFERENCE: 051583/0224
CURRENT APPLICATION NUMBER: US/09/274,163E
CURRENT FILING DATE: 1999-03-22
PRIOR APPLICATION NUMBER: US 08/373,380
PRIOR FILING DATE: 1995-01-17
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.1

SEQ ID NO 4
LENGTH: 114
TYPE: PRT

ORGANISM: Escherichia coli
US-09-274-163E-4

Query Match 79.0%; Score 64; DB 2; Length 114;
Best Local Similarity 76.5%; Pred. No. 0.00084;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KSSQSVFSSSQKNYLA 17
|||||:|:~|:|
DB 24 KSSQSVLYSSNSKNYLA 40

RESULT 31

US-09-274-163E-6
Sequence 6, Application US/09274163E
Patent No. 6485943

GENERAL INFORMATION:
APPLICANT: STEVENS, Fred J.
APPLICANT: WILKINS STEVENS, Priscilla
APPLICANT: RAFFEN, Rosemarie
APPLICANT: SCHIFFER, Marianne
TITLE OF INVENTION: OPTIMUM RECOMBINANT ANTIBODY PRODUCTION
FILE REFERENCE: 051583/0224

```

; CURRENT APPLICATION NUMBER: US/09/274,163E
; CURRENT FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: US 08/373,380
; PRIOR FILING DATE: 1995-01-17
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 6
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-274-163E-6

Query Match          79.0%; Score 64; DB 2; Length 114;
Best Local Similarity 76.5%; Pred. No. 0.00084;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      1 KSSQSVFFSSSQKNYLA 17
        |||||:|:|:|
        24 KSSQSVLYSSNNKNYLA 40

Db

RESULT 32
US-09-490-070A-17
; Sequence 17, Application US/09490070A
; Patent No. 6696248
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckhuhn, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Colin G. Sandercock, Esq. c/o Heller Ehrman
; White & McAlliffe
; STREET: 1666 K Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,070A
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Colin G. Sandercock, Esq.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37629-0005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 912-2020
; TELEFAX: (202) 912-2020
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-490-070A-17

Query Match          79.0%; Score 64; DB 2; Length 114;
Best Local Similarity 76.5%; Pred. No. 0.00084;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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Qy      1 KSSQSVFFSSSQKNYLA 17
        |||||:|:|:|
        24 KSSQSVLYSSNNKNYLA 40

Db

RESULT 33
US-09-490-153-17
; Sequence 17, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckhuhn, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSER: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,153
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9090
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-490-153-17

Query Match          79.0%; Score 64; DB 2; Length 114;
Best Local Similarity 76.5%; Pred. No. 0.00084;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      1 KSSQSVFFSSSQKNYLA 17
        |||||:|:~|~|
        24 KSSQSVLYSSNNKNYLA 40

Db

RESULT 34
US-09-810-502-38
; Sequence 38, Application US/09810502
; Patent No. 6797492
; GENERAL INFORMATION:
; APPLICANT: Padlan, Eduardo A.
; Daugherty, Bruce L.
; Mark, George E.
```

TITLE OF INVENTION: A METHOD FOR REDUCING THE IMMUNOGENICITY
OF ANTIBODY VARIABLE DOMAINS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000, 126 E. Lincoln Ave.
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/810,502
FILING DATE: 16-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/905,280
FILING DATE: 01-Aug-1997
APPLICATION NUMBER: 08/609,218
FILING DATE: 01-Mar-1996
APPLICATION NUMBER: 08/109,187
FILING DATE: 19-Aug-1993
APPLICATION NUMBER: 07/702,217
FILING DATE: 17-May-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hand, J. Mark
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 18410CC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-3905
TELEFAX: 732-594-4720
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-09-810-502-38
Query Match 79.0%; Score 64; DB 2; Length 114;
Best Local Similarity 76.5%; Pred. No. 0.00084;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 KSSQSVFPSSQKNYLA 17
|||:|:|:|
Db 24 KSSQSVLYSSNSKNYLA 40
RESULT 35
US-09-490-324-17
Sequence 17, Application US/09490324
Patent No. 6828422
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Jiming
Moroney, Simon
Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York

COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-490-324-17
Query Match 79.0%; Score 64; DB 2; Length 114;
Best Local Similarity 76.5%; Pred. No. 0.00084;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 KSSQSVFPSSQKNYLA 17
|||:|:|:|
Db 24 KSSQSVLYSSNNKYLA 40
RESULT 36
US-08-026-320A-4
Sequence 4, Application US/08026320A
Patent No. 5419904
GENERAL INFORMATION:
APPLICANT: Itie, Reiko F
TITLE OF INVENTION: HUMAN B-LYMPHOBLASTOID CELL LINE
SECRETING ANTI-GANGLIOSIDE ANTIBODY
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pons, Smith, Lande & Rosé
STREET: 2029 Century Park East, Suite 3800
CITY: Los Angeles
STATE: California
COUNTRY: United States of America
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/026,320A
FILING DATE: 26-FEB-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/609803
FILING DATE: 05-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Oldenkamp, David J
REGISTRATION NUMBER: 29421
REFERENCE/DOCKET NUMBER: 94268

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 3107885046
; TELEFAX: 3102771297
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-026-320A-4

Query Match
Best Local Similarity 79.0%; Score 64; DB 1; Length 120;
Pred. No. 0.00089;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KSSQSVFFSSQKNYLA 17
    |||||:|:|:||||
Db 20 KSSQSVLYSSNNKNYLA 36

RESULT 37
US-08-463-903-4
; Sequence 4, Application US/08463903
; Patent No. 6071515
; GENERAL INFORMATION:
; APPLICANT: Mezes, Peter S.
; APPLICANT: Alfholtzer, Joseph A.
; APPLICANT: Kottke, Nicholas J.
; TITLE OF INVENTION: Dimer and Multimer Forms of Single Chain Polypeptides
; FILE REFERENCE: 40224A US
; CURRENT APPLICATION NUMBER: US/08/463,903
; EARLIER FILING DATE: 1995-06-05
; EARLIER FILING DATE: 1992-08-21
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: MS-Word for Windows, Ver. 7.0
; SEQ ID NO 4
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Human kappa subgroup IV VL (Hum4 VL) from pRL1001
; LOCATION: 1..133
US-08-463-903-4

Query Match
Best Local Similarity 79.0%; Score 64; DB 2; Length 133;
Pred. No. 0.001;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KSSQSVFFSSQKNYLA 17
    |||||:|:|:||||
Db 44 KSSQSVLYSSNNKNYLA 60

RESULT 38
US-07-935-695-4
; Sequence 4, Application US/07935695
; Patent No. 6329507
; GENERAL INFORMATION:
; APPLICANT: Mezes, Peter S.
; APPLICANT: Richard, Ruth A.
; APPLICANT: Alfholtzer, Joseph A.
; APPLICANT: Kottke, Nicholas J.
; TITLE OF INVENTION: Dimer and Multimer Forms of Single Chain Polypeptides
; FILE REFERENCE: 40224A US
; CURRENT APPLICATION NUMBER: US/07/935,695
; PRIOR FILING DATE: 1992-08-21
; PRIOR APPLICATION NUMBER: US 08/463,903
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: MS-Word for Windows, Ver. 7.0
; SEQ ID NO 4
```

```

; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Human kappa subgroup IV VL (Hum4 VL) from pRL1001
; LOCATION: 1..133
US-07-935-695-4

Query Match
Best Local Similarity 79.0%; Score 64; DB 2; Length 133;
Pred. No. 0.001;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KSSQSVFFSSQKNYLA 17
    |||||:|:|:||||
Db 44 KSSQSVLYSSNNKNYLA 60

RESULT 39
US-08-961-309-58
; Sequence 58, Application US/08961309
; Patent No. 6495137
; GENERAL INFORMATION:
; APPLICANT: Mezes, Peter S.
; APPLICANT: Richard, Ruth A.
; APPLICANT: Johnson, Kimberly S.
; APPLICANT: Schlom, Jeffrey
; APPLICANT: Kashmiri, Syed V.S.
; APPLICANT: Shu, Liming
; APPLICANT: Padlan, Eduardo A.
; TITLE OF INVENTION: Composite Antibodies of Humanized Human Subgroup IV Light Chain
; FILE REFERENCE: 37777E
; CURRENT APPLICATION NUMBER: US/08/961,309
; EARLIER FILING DATE: 1997-10-30
; EARLIER FILING DATE: 1996-10-31
; EARLIER FILING DATE: 1994-06-16
; EARLIER FILING DATE: 1992-10-20
; EARLIER FILING DATE: 1990-07-17
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 58
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Hum4 VL
; LOCATION: 1..134
US-08-961-309-58

Query Match
Best Local Similarity 79.0%; Score 64; DB 2; Length 134;
Pred. No. 0.001;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KSSQSVFFSSQKNYLA 17
    |||||:|:~|:||||
Db 44 KSSQSVLYSSNNKNYLA 60

RESULT 40
US-08-828-741B-11
; Sequence 11, Application US/08828741B
; Patent No. 6043069
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; APPLICANT: Sues, Gabriele M.
; APPLICANT: Tarlinton, David M.
; APPLICANT: Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
; PRODUCING SAME
```

```

; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States of America
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,741B
; FILING DATE: 26-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 10591
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 155 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-828-741B-11

Query Match          79.0%; Score 64; DB 2; Length 155;
Best Local Similarity 76.5%; Pred. No. 0.0012;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KSSQSVFFSSQKNYLA 17
    |||||:|:|:||||
Db 53 KSSQSVLYSSNSKNYLA 69

RESULT 41
US-09-160-567-11
; Sequence 11, Application US/09160567
; Patent No. 6326179
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; APPLICANT: Sues, Gabriele M.
; APPLICANT: Tarlinton, David M.
; APPLICANT: Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States of America
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/160,567
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/828,741
; FILING DATE:
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; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 10591
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 155 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-160-567-11

Query Match          79.0%; Score 64; DB 2; Length 155;
Best Local Similarity 76.5%; Pred. No. 0.0012;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KSSQSVFFSSQKNYLA 17
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Db 53 KSSQSVLYSSNSKNYLA 69

RESULT 42
US-09-710-299-11
; Sequence 11, Application US/09710299
; Patent No. 6521741
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; APPLICANT: Sues, Gabriele M.
; APPLICANT: Tarlinton, David M.
; APPLICANT: Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States of America
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/710,299
; FILING DATE: 09-NO. 6521741-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/828,741
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 10591
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 155 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
; US-09-710-299-11
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Query Match 79.0%; Score 64; DB 2; Length 155;
Best Local Similarity 76.5%; Pred. No. 0.0012;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 KSSQSVFFSSSQKNYLA 17
|||||:|:|:|
Db 53 KSSQSVLYSSNKNYLA 69

RESULT 43
US-09-509-031-11
; Sequence 11, Application US/09509031
; Patent No. 6590080
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; APPLICANT: Sues, Gabriele M.
; APPLICANT: Tarlinton, David M.
; APPLICANT: Treutlein, Hebert R.
; TITLE OF INVENTION: CATALYTIC ANTIBOIDS AND A METHOD OF PRODUCING SAME
; FILE REFERENCE: 13474
; CURRENT APPLICATION NUMBER: US/09/509,031
; CURRENT FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Kappa
US-09-509-031-11

Query Match 79.0%; Score 64; DB 2; Length 155;
Best Local Similarity 76.5%; Pred. No. 0.0012;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 KSSQSVFFSSSQKNYLA 17
|||||:|:|:|
Db 53 KSSQSVLYSSNKNYLA 69

RESULT 44
US-08-463-903-20
; Sequence 20, Application US/08463903
; Patent No. 6071515
; GENERAL INFORMATION:
; APPLICANT: Mezes, Peter S.
; APPLICANT: Richard, Ruth A.
; APPLICANT: Affholter, Joseph A.
; APPLICANT: Kotite, Nicolas J.
; TITLE OF INVENTION: Dimer and Multimer Forms of Single Chain Polypeptides
; FILE REFERENCE: 40224A US
; CURRENT APPLICATION NUMBER: US/08/463,903
; CURRENT FILING DATE: 1995-06-05
; EARLIER APPLICATION NUMBER: US 07/935,695
; EARLIER FILING DATE: 1992-08-21
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: MS-Word for Windows, Ver. 7.0
; SEQ ID NO 20
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Hum4 VL-UNIHOPe linker-FLAG peptide construct in pATDFLAG
; LOCATION: 1..171
US-08-463-903-20

Query Match 79.0%; Score 64; DB 2; Length 171;
Best Local Similarity 76.5%; Pred. No. 0.0013;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 KSSQSVFFSSSQKNYLA 17

Db 46 KSSQSVLYSSNKNYLA 62
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RESULT 45
US-07-935-695-20
; Sequence 20, Application US/07935695
; Patent No. 6329507
; GENERAL INFORMATION:
; APPLICANT: Mezes, Peter S.
; APPLICANT: Richard, Ruth A.
; APPLICANT: Affholter, Joseph A.
; APPLICANT: Kotite, Nicolas J.
; TITLE OF INVENTION: Dimer and Multimer Forms of Single Chain Polypeptides
; FILE REFERENCE: 40224A US
; CURRENT APPLICATION NUMBER: US/07/935,695
; CURRENT FILING DATE: 1992-08-21
; PRIOR APPLICATION NUMBER: US 08/463,903
; PRIOR FILING DATE: 1995-06-05
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: MS-Word for Windows, Ver. 7.0
; SEQ ID NO 20
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Hum4 VL-UNIHOPe linker-FLAG peptide construct in pATDFLAG
; LOCATION: 1..171
; OTHER INFORMATION: :
US-07-935-695-20

Query Match 79.0%; Score 64; DB 2; Length 171;
Best Local Similarity 76.5%; Pred. No. 0.0013;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 KSSQSVFFSSSQKNYLA 17
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Db 46 KSSQSVLYSSNKNYLA 62

RESULT 46
US-08-812-586-29
; Sequence 29, Application US/08812586
; Patent No. 6048704
; GENERAL INFORMATION:
; APPLICANT: Martin David Tilson
; TITLE OF INVENTION: PURIFIED AND RECOMBINANT ANTIGENIC
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH ABDOMINAL AORTIC ANEURISM (AAA)
; TITLE OF INVENTION: DISEASE, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/812,586
; FILING DATE: 07-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/53862-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525

INFORMATION FOR SEQ ID NO: 29;
SEQUENCE CHARACTERISTICS:
LENGTH: 239 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-812-586-29

Query Match 79.0%; Score 64; DB 2; Length 239;
Best Local Similarity 76.5%; Pred. No. 0.0019;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KSSQSVFSSSQKNYLA 17
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Db 43 KSSQSVLYSSNNKNYLA 59

RESULT 47
US-09-535-832A-30
Sequence 30, Application US/09535832A
Patent No. 6537769
GENERAL INFORMATION:
APPLICANT: Tilson, Martin David
TITLE OF INVENTION: Purified and Recombinant Antigenic Proteins Associated
TITLE OF INVENTION: with Abdominal Aortic Aneurysm (AAA) Disease, and
FILE REFERENCE: 53862-A2
CURRENT APPLICATION NUMBER: US/09/535,832A
CURRENT FILING DATE: 2000-03-28
NUMBER OF SEQ ID NOS: 57
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 30
LENGTH: 239
TYPE: PRT
ORGANISM: Homo sapiens
US-09-535-832A-30

Query Match 79.0%; Score 64; DB 2; Length 239;
Best Local Similarity 76.5%; Pred. No. 0.0019;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KSSQSVFSSSQKNYLA 17
||| :|||
Db 43 KSSQSVLYSSNNKNYLA 59

RESULT 48
US-08-463-903-2
Sequence 2, Application US/08463903
Patent No. 6071515
GENERAL INFORMATION:
APPLICANT: Mezes, Peter S.
APPLICANT: Richard, Ruth A.
APPLICANT: Affholter, Joseph A.
APPLICANT: Kotite, Nicholas J.
TITLE OF INVENTION: Dimer and Multimer Forms of Single Chain Polypeptides
FILE REFERENCE: 40224A US
CURRENT APPLICATION NUMBER: US/08/463,903
CURRENT FILING DATE: 1995-06-05
EARLIER APPLICATION NUMBER: US 07/935,695
EARLIER FILING DATE: 1992-08-21
NUMBER OF SEQ ID NOS: 102
SOFTWARE: MS-Word for Windows, Ver. 7.0
SEQ ID NO 2
LENGTH: 260
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: SCFV1 from pCCGS515
LOCATION: 1..260
US-08-463-903-2

Query Match 79.0%; Score 64; DB 2; Length 260;
Best Local Similarity 76.5%; Pred. No. 0.0021;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KSSQSVFSSSQKNYLA 17
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Db 43 KSSQSVLYSSNNKNYLA 59

RESULT 49
US-07-935-695-2
Sequence 2, Application US/07935695
Patent No. 6329507
GENERAL INFORMATION:
APPLICANT: Mezes, Peter S.
APPLICANT: Richard, Ruth A.
APPLICANT: Affholter, Joseph A.
APPLICANT: Kotite, Nicholas J.
TITLE OF INVENTION: Dimer and Multimer Forms of Single Chain Polypeptides
FILE REFERENCE: 40224A US
CURRENT APPLICATION NUMBER: US/07/935,695
CURRENT FILING DATE: 1992-08-21
PRIOR APPLICATION NUMBER: US 08/463,903
PRIOR FILING DATE: 1995-06-05
NUMBER OF SEQ ID NOS: 102
SOFTWARE: MS-Word for Windows, Ver. 7.0
SEQ ID NO 2
LENGTH: 260
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: SCFV1 from pCCGS515
LOCATION: 1..260
OTHER INFORMATION: :
US-07-935-695-2

Query Match 79.0%; Score 64; DB 2; Length 260;
Best Local Similarity 76.5%; Pred. No. 0.0021;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KSSQSVFSSSQKNYLA 17
||| :|||
Db 43 KSSQSVLYSSNNKNYLA 59

RESULT 50
US-08-961-309-64
Sequence 64, Application US/08961309
Patent No. 6495137
GENERAL INFORMATION:
APPLICANT: Mezes, Peter S.
APPLICANT: Richard, Ruth A.
APPLICANT: Johnson, Kimberly S.
APPLICANT: Schiom, Jeffrey
APPLICANT: Kashmiri, Syed V.S.
APPLICANT: Shu, Liming
APPLICANT: Padian, Eduardo A.
TITLE OF INVENTION: Composite Antibodies of Humanized Human Subgroup IV Light Chain
FILE REFERENCE: 37777E
CURRENT APPLICATION NUMBER: US/08/961,309
CURRENT FILING DATE: 1997-10-30
EARLIER APPLICATION NUMBER: US 60/030,173
EARLIER FILING DATE: 1996-10-31
EARLIER APPLICATION NUMBER: US 08/261,354
EARLIER FILING DATE: 1994-06-16
EARLIER APPLICATION NUMBER: US 07/964,536
EARLIER FILING DATE: 1992-10-20
EARLIER APPLICATION NUMBER: US 07/510,697
EARLIER FILING DATE: 1990-07-17
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Microsoft Word 97 SR-2
SEQ ID NO 64

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; LENGTH: 260
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: SCFV1
; LOCATION: 1..260
; OTHER INFORMATION: Single chain anti-TAG-72 antibody, SCFV1
; FEATURE:
; NAME/KEY: Leader sequence
; LOCATION: 1..19
; OTHER INFORMATION: Invertase leader sequence from yeast
; FEATURE:
; NAME/KEY: Hum4 VL
; LOCATION: 20..129
; OTHER INFORMATION: Human kappa subgroup 4 light chain variable region in SCFV1
; FEATURE:
; NAME/KEY: Linker
; LOCATION: 130..147
; OTHER INFORMATION: 18-amino acid VL-VH linker in SCFV1
; FEATURE:
; NAME/KEY: CC49 VH
; LOCATION: 148..260
; OTHER INFORMATION: Murine CC49 heavy chain variable region in SCFV1
US-08-961-309-64
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Query Match          79.0%; Score 64; DB 2; Length 260;
Best Local Similarity 76.5%; Pred.No. 0.0021;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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QY      1 KSSQSVFFSSSOKNYLA 17
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Db      43 KSSQSVLYSSNNKNYLA 59
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Job time : 46.3175 secs
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GenCore version 5.1.1.7
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OM protein - protein search, using sw model

Run on: May 4, 2006, 13:43:49 ; Search time 123.317 Seconds
(without alignments)
57.600 Million cell updates/sec

Title: US-10-700-632-4
Perfect score: 81
Sequence: 1 KSSQSVFFSSGQKNYLA 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published Applications_AA_Main:*
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2: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	81	100.0	17	5	US-10-700-632-4	Sequence 4, Appl
2	81	100.0	17	5	US-10-700-632-48	Sequence 48, App
3	81	100.0	113	5	US-10-700-632-8	Sequence 8, Appl
4	81	100.0	113	5	US-10-700-632-10	Sequence 10, App
5	81	100.0	114	5	US-10-700-632-62	Sequence 62, App
6	88.9	272	4	US-10-207-655-14	Sequence 14, App	
7	88.9	272	4	US-10-053-530-14	Sequence 14, App	
8	88.9	272	6	US-11-089-511-14	Sequence 14, App	
9	88.9	272	6	US-11-089-190-14	Sequence 14, App	
10	88.9	272	6	US-11-088-570-14	Sequence 14, App	
11	88.9	272	6	US-11-088-737-14	Sequence 14, App	
12	88.9	272	6	US-11-088-569-14	Sequence 14, App	
13	88.9	272	6	US-11-088-693-14	Sequence 14, App	
14	88.9	272	6	US-11-089-367-14	Sequence 14, App	
15	88.9	272	6	US-11-089-368-14	Sequence 14, App	
16	88.9	85.2	17	5	US-10-893-576-61	Sequence 61, App
17	69	85.2	99	5	US-10-700-632-60	Sequence 60, App
18	69	85.2	112	4	US-10-056-052-6	Sequence 6, Appl
19	69	85.2	112	4	US-10-056-052-10	Sequence 10, App
20	69	85.2	112	4	US-10-056-052-18	Sequence 18, App
21	69	85.2	112	4	US-10-229-335-4	Sequence 4, Appl
22	69	85.2	112	4	US-10-229-335-28	Sequence 28, Appl
23	69	85.2	112	5	US-10-816-938-31	Sequence 31, Appl
24	69	85.2	113	5	US-10-722-849-2	Sequence 2, Appl
25	69	85.2	113	5	US-10-722-849-4	Sequence 4, Appl
26	69	85.2	113	5	US-10-893-576-174	Sequence 174, Appl
27	69	85.2	113	6	US-11-004-659-2	Sequence 2, Appl

28	69	85.2	113	6	US-11-004-659-4	Sequence 4, Appli
29	69	85.2	133	5	US-10-723-003-10	Sequence 10, Appl
30	69	85.2	133	5	US-10-893-576-26	Sequence 26, Appl
31	69	85.2	133	6	US-11-004-639-10	Sequence 10, Appl
32	69	85.2	135	5	US-10-723-003-18	Sequence 18, Appl
33	69	85.2	135	6	US-11-004-639-18	Sequence 18, Appl
34	69	85.2	239	6	US-10-723-003-14	Sequence 14, Appl
35	69	85.2	239	6	US-11-004-639-14	Sequence 14, Appl
36	69	85.2	241	6	US-10-723-003-22	Sequence 22, Appl
37	69	85.2	241	6	US-11-004-639-22	Sequence 22, Appl
38	69	85.2	352	3	US-09-203-958A-2	Sequence 2, Appli
39	69	85.2	352	5	US-10-764-131-2	Sequence 2, Appli
40	69	85.2	661	5	US-10-723-003-28	Sequence 28, Appl
41	69	85.2	661	5	US-10-723-003-34	Sequence 34, Appl
42	69	85.2	661	6	US-11-004-639-28	Sequence 28, Appl
43	69	85.2	661	6	US-11-004-639-34	Sequence 34, Appl
44	67	82.7	17	3	US-09-828-708-36	Sequence 36, Appl
45	67	82.7	17	3	US-09-828-708-39	Sequence 39, Appl
46	67	82.7	17	5	US-10-630-009-36	Sequence 36, Appl
47	67	82.7	17	5	US-10-630-009-39	Sequence 39, Appl
48	67	82.7	109	3	US-09-828-708-1	Sequence 66, Appl
49	67	82.7	109	3	US-09-828-708-4	Sequence 1, Appli
50	67	82.7	109	3	US-09-828-708-1	Sequence 1, Appli
51	67	82.7	109	5	US-10-630-009-1	Sequence 1, Appli
52	67	82.7	109	5	US-10-630-009-4	Sequence 4, Appli
53	67	82.7	133	5	US-10-893-576-173	Sequence 173, App
54	67	82.7	133	5	US-10-893-576-36	Sequence 36, Appl
55	66	81.5	17	6	US-11-015-558-4	Sequence 4, Appli
56	66	81.5	112	4	US-10-056-052-14	Sequence 14, Appli
57	66	81.5	112	6	US-11-015-958-8	Sequence 8, Appli
58	66	81.5	132	6	US-11-013-537-2	Sequence 2, Appli
59	66	81.5	154	5	US-10-644-277-48	Sequence 48, Appl
60	66	81.5	220	3	US-09-995-699-1	Sequence 1, Appli
61	66	81.5	220	4	US-10-232-409-1	Sequence 1, Appli
62	66	81.5	238	6	US-11-013-537-1	Sequence 1, Appli
63	64	79.0	17	3	US-09-563-222-14	Sequence 14, Appl
64	64	79.0	17	4	US-10-467-253-1	Sequence 1, Appli
65	64	79.0	17	4	US-10-783-950-14	Sequence 14, Appl
66	64	79.0	17	5	US-10-726-332-164	Sequence 164, App
67	64	79.0	17	5	US-10-726-332-188	Sequence 188, App
68	64	79.0	17	5	US-10-927-433-7	Sequence 7, Appli
69	64	79.0	82	4	US-10-078-958-15	Sequence 15, Appl
70	64	79.0	101	4	US-10-194-975-89	Sequence 89, Appl
71	64	79.0	101	4	US-10-125-687-25	Sequence 25, Appl
72	64	79.0	101	4	US-10-308-817-36	Sequence 36, Appl
73	64	79.0	101	4	US-10-453-698-36	Sequence 36, Appl
74	64	79.0	101	4	US-10-379-392-103	Sequence 103, App
75	64	79.0	101	5	US-10-996-191-25	Sequence 25, Appl
76	64	79.0	112	4	US-10-467-253-7	Sequence 7, Appli
77	64	79.0	113	3	US-09-274-163E-16	Sequence 16, Appl
78	64	79.0	113	3	US-09-956-206A-80	Sequence 80, Appl
79	64	79.0	113	3	US-09-995-529-6	Sequence 6, Appli
80	64	79.0	113	3	US-09-995-529-6	Sequence 6, Appli
81	64	79.0	113	5	US-10-880-028-29	Sequence 29, Appl
82	64	79.0	113	5	US-10-880-320-29	Sequence 29, Appl
83	64	79.0	113	5	US-10-965-616-80	Sequence 80, Appl
84	64	79.0	113	6	US-11-003-819-14	Sequence 14, Appl
85	64	79.0	114	3	US-09-810-502-38	Sequence 38, Appl
86	64	79.0	114	3	US-09-274-163E-2	Sequence 2, Appli
87	64	79.0	114	3	US-09-274-163E-4	Sequence 4, Appli
88	64	79.0	114	3	US-09-274-163E-6	Sequence 6, Appli
89	64	79.0	114	5	US-10-884-133-38	Sequence 38, Appl
90	64	79.0	114	5	US-10-938-153-112	Sequence 112, App
91	64	79.0	114	5	US-10-700-632-70	Sequence 70, Appl
92	64	79.0	114	6	US-11-031-485-117	Sequence 17, Appl
93	64	79.0	119	4	US-10-010-729-13	Sequence 13, Appl
94	64	79.0	122	4	US-10-010-729-51	Sequence 51, Appl
95	64	79.0	126	5	US-10-473-287-51	Sequence 51, Appl
96	64	79.0	134	4	US-10-255-478-58	Sequence 58, Appl
97	64	79.0	134	5	US-10-644-277-28	Sequence 28, Appl
98	64	79.0	155	4	US-10-345-618-11	Sequence 11, Appl
99	64	79.0	159	4	US-10-644-277-112	Sequence 112, App
100	64	79.0	159	5	US-10-644-277-116	Sequence 116, App


```
977 34 42.0 528 4 US-10-282-122A-52047 Sequence 52047, A
978 34 42.0 532 4 US-10-424-589-172364 Sequence 172364, A
979 34 42.0 538 3 US-09-723-920-5 Sequence 5, Appl1
980 34 42.0 538 3 US-09-892-360-2 Sequence 2, Appl1
981 34 42.0 538 5 US-10-887-932-5 Sequence 5, Appl1
982 34 42.0 538 5 US-10-923-035-46 Sequence 46, Appl1
983 34 42.0 543 3 US-09-729-920-2 Sequence 2, Appl1
984 34 42.0 543 3 US-09-852-386-73 Sequence 73, Appl1
985 34 42.0 543 4 US-10-332-175-2 Sequence 2, Appl1
986 34 42.0 543 4 US-10-262-511-106 Sequence 106, App
987 34 42.0 543 5 US-10-887-932-2 Sequence 2, Appl1
988 34 42.0 549 4 US-09-115-150-4 Sequence 4, Appl1
989 34 42.0 550 4 US-10-437-963-121892 Sequence 121892,
990 34 42.0 557 4 US-10-424-599-236485 Sequence 236485,
991 34 42.0 604 4 US-10-282-122A-61472 Sequence 61472, A
992 34 42.0 609 4 US-10-437-963-115531 Sequence 115531,
993 34 42.0 620 4 US-10-425-115-193645 Sequence 193645,
994 34 42.0 623 4 US-10-437-963-102986 Sequence 102986,
995 34 42.0 625 5 US-10-450-763-38996 Sequence 38996, A
996 34 42.0 625 5 US-10-450-763-44874 Sequence 44874, A
997 34 42.0 626 5 US-10-450-763-37212 Sequence 37212, A
998 34 42.0 629 6 US-11-097-143-28182 Sequence 28182, A
999 34 42.0 636 4 US-10-425-114-64076 Sequence 64076, A
1000 34 42.0 652 4 US-10-282-122A-46281 Sequence 46281, A
```

ALIGNMENTS

```
RESULT 1
US-10-700-632-4
; Sequence 4, Application US/10700632
; Publication No. US20050118183A1
; GENERAL INFORMATION:
; APPLICANT: Immunogen, Inc.
; TITLE OF INVENTION: ANTI-CD33 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID
; FILE REFERENCE: A8427
; CURRENT APPLICATION NUMBER: US/10/700,632
; CURRENT FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: US 60/424,332
; PRIOR FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-700-632-4

Query Match 100.0%; Score 81; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 KSSQSVFFSSSQKNYLA 17
|||
Db 1 KSSQSVFFSSSQKNYLA 17

RESULT 2
US-10-700-632-48
; Sequence 48, Application US/10700632
; Publication No. US20050118183A1
; GENERAL INFORMATION:
; APPLICANT: Immunogen, Inc.
; TITLE OF INVENTION: ANTI-CD33 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID
; FILE REFERENCE: A8427
; CURRENT APPLICATION NUMBER: US/10/700,632
; CURRENT FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: US 60/424,332
; PRIOR FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 94
```

```
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-700-632-48

Query Match 100.0%; Score 81; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Cy 1 KSSQSVFFSSSQKNYLA 17
|||
Db 1 KSSQSVFFSSSQKNYLA 17
```

```
RESULT 3
US-10-700-632-8
; Sequence 8, Application US/10700632
; Publication No. US20050118183A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Immunogen, Inc.
; TITLE OF INVENTION: ANTI-CD33 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID
; FILE REFERENCE: A8427
; CURRENT APPLICATION NUMBER: US/10/700,632
; CURRENT FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: US 60/424,332
; PRIOR FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-700-632-8
```

```
Query Match 100.0%; Score 81; DB 5; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Cy 1 KSSQSVFFSSSQKNYLA 17
|||
Db 24 KSSQSVFFSSSQKNYLA 40
```

```
RESULT 4
US-10-700-632-10
; Sequence 10, Application US/10700632
; Publication No. US20050118183A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Immunogen, Inc.
; TITLE OF INVENTION: ANTI-CD33 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID
; FILE REFERENCE: A8427
; CURRENT APPLICATION NUMBER: US/10/700,632
; CURRENT FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: US 60/424,332
; PRIOR FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized My9-6 antibody light chain variable region
US-10-700-632-10
```

```
Query Match 100.0%; Score 81; DB 5; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```


QY 1 KSSQSVFSSSQKNYLA 17
| | | | | | | | | | | | | | | | | | | | | |
DB 24 KSSQSVFSSSQKNYLA 40

RESULT 5
US-10-700-632-62
; Sequence 62, Application US/10700632
; Publication No. US20050118183A1
; GENERAL INFORMATION:

; APPLICANT: Immunogen, Inc.
; TITLE OF INVENTION: ANTI-CD33 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID
; FILE REFERENCE: A8427
; CURRENT APPLICATION NUMBER: US/10/700,632
; CURRENT FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: US 60/424,332
; PRIOR FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 62
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-700-632-62

Query Match 100.0%; Score 81; DB 5; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSSQSVFSSSQKNYLA 17
| | | | | | | | | | | | | | | | | | | | | |
DB 24 KSSQSVFSSSQKNYLA 40

RESULT 6
US-10-207-655-14
; Sequence 14, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(272)
; OTHER INFORMATION: MOUSE ANTI-HUMAN CD22 SCFV
US-10-207-655-14

Query Match 88.9%; Score 72; DB 4; Length 272;
Best Local Similarity 82.4%; Pred. No. 0.001;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSSQSVFSSSQKNYLA 17
| | | | | | | | | | | | | | | | | | | | | |
DB 44 KSSQSVFSSSQKNYLA 60

RESULT 7
US-10-053-530-14
; Sequence 14, Application US/10053530
; Publication No. US20030133939A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey

; APPLICANT: Hayden-Ledbetter, Martha
; TITLE OF INVENTION: Binding Domain-Immunoglobulin Fusion Proteins
; FILE REFERENCE: 390069.401
; CURRENT APPLICATION NUMBER: US/10/053,530
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: US 09/765,208
; PRIOR FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(272)
; OTHER INFORMATION: MOUSE ANTI-HUMAN CD22 SCFV
US-10-053-530-14

Query Match 88.9%; Score 72; DB 4; Length 272;
Best Local Similarity 82.4%; Pred. No. 0.001;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSSQSVFSSSQKNYLA 17
| | | | | | | | | | | | | | | | | | | | | |
DB 44 KSSQSVFSSSQKNYLA 60

RESULT 8
US-11-089-511-14
; Sequence 14, Application US/11089511
; Publication No. US20050175614A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey
; APPLICANT: Hayden-Ledbetter, Martha
; TITLE OF INVENTION: Binding Domain-Immunoglobulin Fusion Proteins
; FILE REFERENCE: 390069.401
; CURRENT APPLICATION NUMBER: US/11/089,511
; CURRENT FILING DATE: 2005-03-23
; PRIOR APPLICATION NUMBER: US/10/053,530
; PRIOR FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: US 09/765,208
; PRIOR FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(272)
; OTHER INFORMATION: MOUSE ANTI-HUMAN CD22 SCFV
US-11-089-511-14

Query Match 88.9%; Score 72; DB 6; Length 272;
Best Local Similarity 82.4%; Pred. No. 0.001;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSSQSVFSSSQKNYLA 17
| | | | | | | | | | | | | | | | | | | | | |
DB 44 KSSQSVFSSSQKNYLA 60

RESULT 9
US-11-089-190-14
; Sequence 14, Application US/11089190
; Publication No. US20050180970A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey
; APPLICANT: Hayden-Ledbetter, Martha
; TITLE OF INVENTION: Binding Domain-Immunoglobulin Fusion Proteins
; FILE REFERENCE: 390069.401

```
; CURRENT APPLICATION NUMBER: US/11/089,190
; CURRENT FILING DATE: 2005-03-23
; PRIOR APPLICATION NUMBER: US/10/053,530
; PRIOR FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: US 09/765,208
; PRIOR FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(272)
; OTHER INFORMATION: MOUSE ANTI-HUMAN CD22 SCFV
US-11-089-190-14
```

```
Query Match      88.9%; Score 72; DB 6; Length 272;
Best Local Similarity 82.4%; Pred. No. 0.001;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KSSQSVFSSSQKNYLA 17
      |||||:|:|:|:|
DB      44 KSSQSVFYSSNQKNYLA 60
```

```
RESULT 10
US-11-088-570-14
; Sequence 14, Application US/11088570
; Publication No. US20050186216A1
; GENERAL INFORMATION:
; APPLICANT: Hayden-Ledbetter, Jeffrey
; TITLE OF INVENTION: Binding Domain-Immunoglobulin Fusion Proteins
; FILE REFERENCE: 390069,401
; CURRENT APPLICATION NUMBER: US/11/088,570
; CURRENT FILING DATE: 2005-03-23
; PRIOR APPLICATION NUMBER: US/10/053,530
; PRIOR FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: US 09/765,208
; PRIOR FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(272)
; OTHER INFORMATION: MOUSE ANTI-HUMAN CD22 SCFV
US-11-088-570-14
```

```
Query Match      88.9%; Score 72; DB 6; Length 272;
Best Local Similarity 82.4%; Pred. No. 0.001;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KSSQSVFSSSQKNYLA 17
      |||||:|:|:|:|
DB      44 KSSQSVFYSSNQKNYLA 60
```

```
RESULT 11
US-11-088-737-14
; Sequence 14, Application US/11088737
; Publication No. US20050202012A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey
; APPLICANT: Hayden-Ledbetter, Martha
; TITLE OF INVENTION: Binding Domain-Immunoglobulin Fusion Proteins
; FILE REFERENCE: 390069,401
; CURRENT APPLICATION NUMBER: US/11/088,737
```

```
; CURRENT FILING DATE: 2005-03-23
; PRIOR APPLICATION NUMBER: US/10/053,530
; PRIOR FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: US 09/765,208
; PRIOR FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(272)
; OTHER INFORMATION: MOUSE ANTI-HUMAN CD22 SCFV
US-11-088-737-14
```

```
Query Match      88.9%; Score 72; DB 6; Length 272;
Best Local Similarity 82.4%; Pred. No. 0.001;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KSSQSVFSSSQKNYLA 17
      |||||:|:~|:|
DB      44 KSSQSVFYSSNQKNYLA 60
```

```
RESULT 12
US-11-088-569-14
; Sequence 14, Application US/11088569
; Publication No. US20050202023A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey
; TITLE OF INVENTION: Binding Domain-Immunoglobulin Fusion Proteins
; FILE REFERENCE: 390069,401
; CURRENT APPLICATION NUMBER: US/11/088,569
; CURRENT FILING DATE: 2005-03-23
; PRIOR APPLICATION NUMBER: US/10/053,530
; PRIOR FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: US 09/765,208
; PRIOR FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(272)
; OTHER INFORMATION: MOUSE ANTI-HUMAN CD22 SCFV
US-11-088-569-14
```

```
Query Match      88.9%; Score 72; DB 6; Length 272;
Best Local Similarity 82.4%; Pred. No. 0.001;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KSSQSVFSSSQKNYLA 17
      |||||:|:~|:|
DB      44 KSSQSVFYSSNQKNYLA 60
```

```
RESULT 13
US-11-088-693-14
; Sequence 14, Application US/11088693
; Publication No. US20050202028A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey
; APPLICANT: Hayden-Ledbetter, Martha
; TITLE OF INVENTION: Binding Domain-Immunoglobulin Fusion Proteins
; FILE REFERENCE: 390069,401
; CURRENT APPLICATION NUMBER: US/11/088,693
; CURRENT FILING DATE: 2005-03-23
```

```
; PRIOR APPLICATION NUMBER: US 09/765,208
; PRIOR FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(272)
; OTHER INFORMATION: MOUSE ANTI-HUMAN CD22 SCFV
US-11-088-693-14
```

```
Query Match      88.9%; Score 72; DB 6; Length 272;
Best Local Similarity 82.4%; Pred. No. 0.001;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 KSSQSVFFSSSQKNYLA 17
|||||:|:|:|:|
Db      44 KSSQSVFYSSNQKNYLA 60
```

```
RESULT 14
; Sequence 14, Application US/11089367
; Publication No. US20050202534A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey
; TITLE OF INVENTION: Binding Domain-Immunoglobulin Fusion Proteins
; FILE REFERENCE: 390069, 401
; CURRENT APPLICATION NUMBER: US/11/089,367
; PRIOR FILING DATE: 2005-03-23
; PRIOR APPLICATION NUMBER: US/10/053,530
; PRIOR FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: US 09/765,208
; PRIOR FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(272)
; OTHER INFORMATION: MOUSE ANTI-HUMAN CD22 SCFV
US-11-089-367-14
```

```
Query Match      88.9%; Score 72; DB 6; Length 272;
Best Local Similarity 82.4%; Pred. No. 0.001;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 KSSQSVFFSSSQKNYLA 17
|||||:|:|:|:|
Db      44 KSSQSVFYSSNQKNYLA 60
```

```
RESULT 15
; Sequence 14, Application US/11089368
; Publication No. US20050238646A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey
; TITLE OF INVENTION: Binding Domain-Immunoglobulin Fusion Proteins
; FILE REFERENCE: 390069, 401
; CURRENT APPLICATION NUMBER: US/11/089,368
; PRIOR FILING DATE: 2005-03-23
; PRIOR APPLICATION NUMBER: US 09/765,208
; PRIOR FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 38
```

```
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(272)
; OTHER INFORMATION: MOUSE ANTI-HUMAN CD22 SCFV
US-11-089-368-14
```

```
Query Match      88.9%; Score 72; DB 6; Length 272;
Best Local Similarity 82.4%; Pred. No. 0.001;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 KSSQSVFFSSSQKNYLA 17
|||||:|:~|:|:|
Db      44 KSSQSVFYSSNQKNYLA 60
```

```
RESULT 16
; Sequence 61, Application US/10893576
; Publication No. US20050118643A1
; GENERAL INFORMATION:
; APPLICANT: BURGESS, TERESA L.
; APPLICANT: COXON, ANGELA
; APPLICANT: GREEN, LARRY L.
; APPLICANT: ZHANG, KE
; TITLE OF INVENTION: SPECIFIC BINDING AGENTS TO HEPATOCTYTE GROWTH FACTOR
; FILE REFERENCE: 06843, 0051-00000
; CURRENT APPLICATION NUMBER: US/10/893,576
; PRIOR FILING DATE: 2004-07-16
; PRIOR APPLICATION NUMBER: US 60/488,681
; PRIOR FILING DATE: 2003-07-18
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 61
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic light chain
US-10-893-576-61
```

```
Query Match      85.2%; Score 69; DB 5; Length 17;
Best Local Similarity 76.5%; Pred. No. 0.00017;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 KSSQSVFFSSSQKNYLA 17
|||||:|:~|:|:|
Db      1 KSSQSVFYSSNQKNYLA 17
```

```
RESULT 17
; Sequence 60, Application US/10700632
; Publication No. US20050118183A1
; GENERAL INFORMATION:
; APPLICANT: Immunogen, Inc.
; TITLE OF INVENTION: ANTI-CD3 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID
; LEUKEMIA USING THE SAME
; FILE REFERENCE: A8427
; CURRENT APPLICATION NUMBER: US/10/700,632
; PRIOR FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: US 60/424,332
; PRIOR FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 60
; LENGTH: 99
; TYPE: PRT
```

```
; ORGANISM: Mus musculus
US-10-700-632-60

Query Match      85.2%; Score 69; DB 5; Length 99;
Best Local Similarity 82.4%; Pred. No. 0.0011;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 KSSQSVFFSSQKNYLA 17
      |||||:|:|:|:|
Db      24 KSSQSVLYSSNQKNYLA 40

RESULT 18
US-10-056-052-6
; Sequence 6, Application US/10056052
; Publication No. US20030099656A1
; GENERAL INFORMATION:
; APPLICANT: PATTI, Joseph M
; APPLICANT: HUTCHINS, Jeff T
; APPLICANT: DOMANSKI, Paul
; APPLICANT: PATEL, Pratiksha
; APPLICANT: HALT, Andrea
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN . . .
; FILE REFERENCE: P07069US04/BAS
; CURRENT APPLICATION NUMBER: US/10/056,052
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/308,116
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/298,413
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/274,611
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/264,072
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-056-052-6

Query Match      85.2%; Score 69; DB 4; Length 112;
Best Local Similarity 82.4%; Pred. No. 0.0012;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 KSSQSVFFSSQKNYLA 17
      |||||:|:|:|:|
Db      24 KSSQSVLYSSNQKNYLA 40

RESULT 19
US-10-056-052-10
; Sequence 10, Application US/10056052
; Publication No. US20030099656A1
; GENERAL INFORMATION:
; APPLICANT: PATTI, Joseph M
; APPLICANT: HUTCHINS, Jeff T
; APPLICANT: DOMANSKI, Paul
; APPLICANT: PATEL, Pratiksha
; APPLICANT: HALT, Andrea
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN . . .
; FILE REFERENCE: P07069US04/BAS
; CURRENT APPLICATION NUMBER: US/10/056,052
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/308,116
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/298,413
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/274,611
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/264,072
; PRIOR FILING DATE: 2001-01-26
```

```
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-056-052-10

Query Match      85.2%; Score 69; DB 4; Length 112;
Best Local Similarity 82.4%; Pred. No. 0.0012;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 KSSQSVFFSSQKNYLA 17
      |||||:|:~|:|:|
Db      24 KSSQSVLYSSNQKNYLA 40

RESULT 20
US-10-056-052-18
; Sequence 18, Application US/10056052
; Publication No. US20030099656A1
; GENERAL INFORMATION:
; APPLICANT: PATTI, Joseph M
; APPLICANT: HUTCHINS, Jeff T
; APPLICANT: DOMANSKI, Paul
; APPLICANT: PATEL, Pratiksha
; APPLICANT: HALT, Andrea
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN . . .
; FILE REFERENCE: P07069US04/BAS
; CURRENT APPLICATION NUMBER: US/10/056,052
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/308,116
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/298,413
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/274,611
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/264,072
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-056-052-18

Query Match      85.2%; Score 69; DB 4; Length 112;
Best Local Similarity 82.4%; Pred. No. 0.0012;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 KSSQSVFFSSQKNYLA 17
      |||||:|:~|:|:|
Db      24 KSSQSVLYSSNQKNYLA 40

RESULT 21
US-10-229-335-4
; Sequence 4, Application US/10229335
; Publication No. US2003014483A1
; GENERAL INFORMATION:
; APPLICANT: MEDAREX, INC.
; TITLE OF INVENTION: HUMANIZED ANTIBODIES TO FC RECEPTORS FOR
IMMUNOBLOBLIN & ON HUMAN MONONUCLEAR PHAGOCYTES
; NUMBER OF SEQUENCES: 28
; STREET: P.O. Box 953, 1545 Route 22 East
; CITY: Annandale
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08801
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
```

```
/
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: ASCII text
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/229,335
/ FILING DATE: 26-Aug-2002
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/435,516
/ FILING DATE: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Arnold, Beth E.
/ REGISTRATION NUMBER: 35,430
/ REFERENCE/DOCKET NUMBER: MXI-013
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 227-7400
/ TELEFAX: (617) 227-5941
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 112 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ FRAGMENT TYPE: internal
/ SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-229-335-4

Query Match      85.2%; Score 69; DB 4; Length 112;
Best Local Similarity 82.4%; Pred. No. 0.0012;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 KSSQSVFFSSQKNYLA 17
        |||||:|||||
Db      24 KSSQSVLYSSNQKNYLA 40

RESULT 22
US-10-229-335-28
/ Sequence 28, Application US/10229335
/ Publication No. US20030144483A1
/ GENERAL INFORMATION:
/ APPLICANT: MEDAREX, INC.
/ TITLE OF INVENTION: HUMANIZED ANTIBODIES TO FC RECEPTORS FOR
/ IMMUNOBLOBLIN G ON HUMAN MONONUCLEAR PHAGOCYTES
/ NUMBER OF SEQUENCES: 28
/ STREET: P.O. Box 953, 1545 Route 22 East
/ CITY: Annandale
/ STATE: New Jersey
/ COUNTRY: USA
/ ZIP: 08801
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: ASCII text
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/229,335
/ FILING DATE: 26-Aug-2002
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/435,516
/ FILING DATE: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Arnold, Beth E.
/ REGISTRATION NUMBER: 35,430
/ REFERENCE/DOCKET NUMBER: MXI-013
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 227-7400
/ TELEFAX: (617) 227-5941
/ INFORMATION FOR SEQ ID NO: 28:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 112 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
```

```
/
/ MOLECULE TYPE: peptide
/ FRAGMENT TYPE: internal
/ SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-10-229-335-28

Query Match      85.2%; Score 69; DB 4; Length 112;
Best Local Similarity 82.4%; Pred. No. 0.0012;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 KSSQSVFFSSQKNYLA 17
        |||||:|||||
Db      24 KSSQSVLYSSNQKNYLA 40

RESULT 23
US-10-816-938-31
/ Sequence 31, Application US/10816938
/ Publication No. US20040229301A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Baiyang
/ TITLE OF INVENTION: Tissue Factor Antibodies and Uses Thereof
/ FILE REFERENCE: 1861.1670002
/ CURRENT APPLICATION NUMBER: US/10/816,938
/ CURRENT FILING DATE: 2004-04-05
/ NUMBER OF SEQ ID NOS: 35
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 31
/ LENGTH: 112
/ TYPE: PRT
/ ORGANISM: Mus sp.
US-10-816-938-31

Query Match      85.2%; Score 69; DB 5; Length 112;
Best Local Similarity 82.4%; Pred. No. 0.0012;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 KSSQSVFFSSQKNYLA 17
        |||||:|||||
Db      24 KSSQSVLYSSNQKNYLA 40
```

```
RESULT 24
US-10-722-849-2
/ Sequence 2, Application US/10722849
/ Publication No. US20050031617A1
/ GENERAL INFORMATION:
/ APPLICANT: MA, Jing
/ APPLICANT: GUO, Yajun
/ TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR CANCER
/ FILE REFERENCE: 549062000100
/ CURRENT APPLICATION NUMBER: US/10/722,849
/ CURRENT FILING DATE: 2003-11-26
/ PRIOR APPLICATION NUMBER: CN 03129123.6
/ PRIOR FILING DATE: 2003-06-06
/ NUMBER OF SEQ ID NOS: 14
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 2
/ LENGTH: 113
/ TYPE: PRT
/ ORGANISM: Homo Sapiens
US-10-722-849-2

Query Match      85.2%; Score 69; DB 5; Length 113;
Best Local Similarity 82.4%; Pred. No. 0.0013;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 KSSQSVFFSSQKNYLA 17
        |||||:|||||
Db      24 KSSQSVLYSSNQKNYLA 40

RESULT 25
```

```
US-10-722-849-4
; Sequence 4, Application US/10722849
; Publication No. US20050031617A1
; GENERAL INFORMATION:
; APPLICANT: MA, Jing
; APPLICANT: GUO, Yajun
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR CANCER
; FILE REFERENCE: 549062000100
; CURRENT APPLICATION NUMBER: US/10/722,849
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: CN 03129123.6
; PRIOR FILING DATE: 2003-06-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 113
; TYPE: PRP
; ORGANISM: Mus Musculus
US-10-722-849-4
```

```
Query Match      85.2%; Score 69; DB 5; Length 113;
Best Local Similarity 82.4%; Pred. No. 0.0013;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 KSSQSVFSSSQKNYLA 17
|||||:|||||
Db      24 KSSQSVLYSSNQKNYLA 40
```

```
RESULT 26
US-10-893-576-174
; Sequence 174, Application US/10893576
; Publication No. US20050118643A1
; GENERAL INFORMATION:
; APPLICANT: BURGESS, TERESA L.
; APPLICANT: COXON, ANGELA
; APPLICANT: GREEN, LARRY L.
; APPLICANT: ZHANG, KE
; TITLE OF INVENTION: SPECIFIC BINDING AGENTS TO HEPATOCTYTE GROWTH FACTOR
; FILE REFERENCE: 06843.0051-00000
; CURRENT APPLICATION NUMBER: US/10/893,576
; CURRENT FILING DATE: 2004-07-16
; PRIOR APPLICATION NUMBER: US 60/488,681
; PRIOR FILING DATE: 2003-07-18
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 174
; LENGTH: 113
; TYPE: PRP
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic kappa light
US-10-893-576-174
```

```
Query Match      85.2%; Score 69; DB 5; Length 113;
Best Local Similarity 76.5%; Pred. No. 0.0013;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 KSSQSVFSSSQKNYLA 17
|||||:|||||
Db      24 KSSQSVLYSSNQKNYLA 40
```

```
RESULT 27
US-11-004-659-2
; Sequence 2, Application US/11004659
; Publication No. US20050232926A1
; GENERAL INFORMATION:
; APPLICANT: MA, Jing
; APPLICANT: GUO, Yajun
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR CANCER
```

```
; TITLE OF INVENTION: ASSOCIATED ANTIGEN SMs-1 AND USES THEREOF
; FILE REFERENCE: 549062000100
; CURRENT APPLICATION NUMBER: US/11/004,659
; CURRENT FILING DATE: 2004-12-02
; PRIOR APPLICATION NUMBER: US/10/722,849
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: CN 03129123.6
; PRIOR FILING DATE: 2003-06-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 113
; TYPE: PRP
; ORGANISM: Homo Sapiens
US-11-004-659-2
```

```
Query Match      85.2%; Score 69; DB 6; Length 113;
Best Local Similarity 82.4%; Pred. No. 0.0013;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 KSSQSVFSSSQKNYLA 17
|||||:|||||
Db      24 KSSQSVLYSSNQKNYLA 40
```

```
RESULT 28
US-11-004-659-4
; Sequence 4, Application US/11004659
; Publication No. US20050232926A1
; GENERAL INFORMATION:
; APPLICANT: MA, Jing
; APPLICANT: GUO, Yajun
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR CANCER
; FILE REFERENCE: 549062000100
; CURRENT APPLICATION NUMBER: US/11/004,659
; CURRENT FILING DATE: 2004-12-02
; PRIOR APPLICATION NUMBER: US/10/722,849
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: CN 03129123.6
; PRIOR FILING DATE: 2003-06-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 113
; TYPE: PRP
; ORGANISM: Mus Musculus
US-11-004-659-4
```

```
Query Match      85.2%; Score 69; DB 6; Length 113;
Best Local Similarity 82.4%; Pred. No. 0.0013;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 KSSQSVFSSSQKNYLA 17
|||||:|||||
Db      24 KSSQSVLYSSNQKNYLA 40
```

```
RESULT 29
US-10-723-003-10
; Sequence 10, Application US/10723003
; Publication No. US20040254108A1
; GENERAL INFORMATION:
; APPLICANT: MA, Jing
; APPLICANT: GUO, Yajun
; TITLE OF INVENTION: PREPARATION AND APPLICATION OF
; FILE REFERENCE: 549062000200
; CURRENT APPLICATION NUMBER: US/10/723,003
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: CN 2003101199300
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: CN 031292909
```

;; PRIOR FILING DATE: 2003-06-13
;; NUMBER OF SEQ ID NOS: 68
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 10
;; LENGTH: 133
;; TYPE: PRT
;; ORGANISM: Mus musculus
US-10-723-003-10

Query Match 85.2%; Score 69; DB 5; Length 133;
Best Local Similarity 82.4%; Pred. No. 0.0015;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSSQSVFSSSQKNYLA 17
|||||:|||||
Db 44 KSSQSVLYSSNQKNYLA 60

RESULT 30
US-10-893-576-26
; Sequence 26, Application US/10893576
; Publication No. US20050118643A1
; GENERAL INFORMATION:
; APPLICANT: BURGESS, TERESA L.
; APPLICANT: COXON, ANGELA
; APPLICANT: GREEN, LARRY L.
; APPLICANT: ZHANG, KE
; TITLE OF INVENTION: SPECIFIC BINDING AGENTS TO HEPATOCYTE GROWTH FACTOR
; FILE REFERENCE: 06843.0051-00000
; CURRENT APPLICATION NUMBER: US/10/893,576
; CURRENT FILING DATE: 2004-07-16
; PRIOR APPLICATION NUMBER: US 60/488,681
; PRIOR FILING DATE: 2003-07-18
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 26
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HGF 1.29.1
US-10-893-576-26

Query Match 85.2%; Score 69; DB 5; Length 133;
Best Local Similarity 76.5%; Pred. No. 0.0015;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSSQSVFSSSQKNYLA 17
|||||:|||||
Db 44 KSSQSVLYSSNQKNYLA 60

RESULT 31
US-11-004-639-10
; Sequence 10, Application US/11004639
; Publication No. US20050232931A1
; GENERAL INFORMATION:
; APPLICANT: MA, Jing
; APPLICANT: GUO, Yajun
; TITLE OF INVENTION: PREPARATION AND APPLICATION OF
; TITLE OF INVENTION: ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS
; FILE REFERENCE: 549062000200
; CURRENT APPLICATION NUMBER: US/11/004,639
; CURRENT FILING DATE: 2004-12-02
; PRIOR APPLICATION NUMBER: US/10/723,003
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: CN 2003101199300
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: CN 031292909
; PRIOR FILING DATE: 2003-06-13
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0

;; SEQ ID NO 10
;; LENGTH: 133
;; TYPE: PRT
;; ORGANISM: Mus musculus
US-11-004-639-10

Query Match 85.2%; Score 69; DB 6; Length 133;
Best Local Similarity 82.4%; Pred. No. 0.0015;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSSQSVFSSSQKNYLA 17
|||||:|||||
Db 44 KSSQSVLYSSNQKNYLA 60

RESULT 32
US-10-723-003-18
; Sequence 18, Application US/10723003
; Publication No. US20040254108A1
; GENERAL INFORMATION:
; APPLICANT: MA, Jing
; APPLICANT: GUO, Yajun
; TITLE OF INVENTION: PREPARATION AND APPLICATION OF
; TITLE OF INVENTION: ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS
; FILE REFERENCE: 549062000200
; CURRENT APPLICATION NUMBER: US/10/723,003
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: CN 2003101199300
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: CN 031292909
; PRIOR FILING DATE: 2003-06-13
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-723-003-18

Query Match 85.2%; Score 69; DB 5; Length 135;
Best Local Similarity 82.4%; Pred. No. 0.0015;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSSQSVFSSSQKNYLA 17
|||||:|||||
Db 46 KSSQSVLYSSNQKNYLA 62

RESULT 33
US-11-004-639-18
; Sequence 18, Application US/11004639
; Publication No. US20050232931A1
; GENERAL INFORMATION:
; APPLICANT: MA, Jing
; APPLICANT: GUO, Yajun
; TITLE OF INVENTION: PREPARATION AND APPLICATION OF
; TITLE OF INVENTION: ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS
; FILE REFERENCE: 549062000200
; CURRENT APPLICATION NUMBER: US/11/004,639
; CURRENT FILING DATE: 2004-12-02
; PRIOR APPLICATION NUMBER: US/10/723,003
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: CN 2003101199300
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: CN 031292909
; PRIOR FILING DATE: 2003-06-13
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 135
; TYPE: PRT

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-11-004-639-18

Query Match      85.2%; Score 69; DB 6; Length 135;
Best Local Similarity 82.4%; Pred. No. 0.0015;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 KSSQSVFSSSQKNYLA 17
        |||||:|||||
        46 KSSQSVLYSSNQKNYLA 62

Db

RESULT 34
US-10-723-003-14
; Sequence 14, Application US/10723003
; Publication No. US20040254108A1
; GENERAL INFORMATION:
; APPLICANT: MA, Jing
; APPLICANT: GUO, Yajun
; TITLE OF INVENTION: PREPARATION AND APPLICATION OF
; TITLE OF INVENTION: ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS
; FILE REFERENCE: 549062000200
; CURRENT APPLICATION NUMBER: US/10/723,003
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: CN 2003101199300
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: CN 031292909
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-723-003-14

Query Match      85.2%; Score 69; DB 5; Length 239;
Best Local Similarity 82.4%; Pred. No. 0.0028;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 KSSQSVFSSSQKNYLA 17
        |||||:|||||
        44 KSSQSVLYSSNQKNYLA 60

Db

RESULT 35
US-11-004-639-14
; Sequence 14, Application US/11004639
; Publication No. US20050232931A1
; GENERAL INFORMATION:
; APPLICANT: MA, Jing
; APPLICANT: GUO, Yajun
; TITLE OF INVENTION: PREPARATION AND APPLICATION OF
; TITLE OF INVENTION: ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS
; FILE REFERENCE: 549062000200
; CURRENT APPLICATION NUMBER: US/11/004,639
; PRIOR FILING DATE: 2004-12-02
; PRIOR APPLICATION NUMBER: US/10/723,003
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: CN 2003101199300
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: CN 031292909
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-11-004-639-14

Query Match      85.2%; Score 69; DB 6; Length 239;
Best Local Similarity 82.4%; Pred. No. 0.0028;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 KSSQSVFSSSQKNYLA 17
        |||||:|||||
        44 KSSQSVLYSSNQKNYLA 60

Db

RESULT 36
US-10-723-003-22
; Sequence 22, Application US/10723003
; Publication No. US20040254108A1
; GENERAL INFORMATION:
; APPLICANT: MA, Jing
; APPLICANT: GUO, Yajun
; TITLE OF INVENTION: PREPARATION AND APPLICATION OF
; TITLE OF INVENTION: ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS
; FILE REFERENCE: 549062000200
; CURRENT APPLICATION NUMBER: US/10/723,003
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: CN 2003101199300
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: CN 031292909
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-723-003-22

Query Match      85.2%; Score 69; DB 5; Length 241;
Best Local Similarity 82.4%; Pred. No. 0.0028;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 KSSQSVFSSSQKNYLA 17
        |||||:|||||
        46 KSSQSVLYSSNQKNYLA 62

Db

RESULT 37
US-11-004-639-22
; Sequence 22, Application US/11004639
; Publication No. US20050232931A1
; GENERAL INFORMATION:
; APPLICANT: MA, Jing
; APPLICANT: GUO, Yajun
; TITLE OF INVENTION: PREPARATION AND APPLICATION OF
; TITLE OF INVENTION: ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS
; FILE REFERENCE: 549062000200
; CURRENT APPLICATION NUMBER: US/11/004,639
; PRIOR FILING DATE: 2004-12-02
; PRIOR APPLICATION NUMBER: US/10/723,003
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: CN 2003101199300
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: CN 031292909
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Artificial Sequence
```



```
/ OTHER INFORMATION: Synthetic Construct
US-11-004-639-22

Query Match      85.2%; Score 69; DB 6; Length 241;
Best Local Similarity 82.4%; Pred. No. 0.0028;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KSSQSVFPSSSQKNYLA 17
      |||||:|:|:|:|:|
Db      46 KSSQSVLYSSNQKNYLA 62

RESULT 38
US-09-203-958A-2
; Sequence 2, Application US/09203958A
; Publication No. US20030039641A1
; GENERAL INFORMATION:
; APPLICANT: KELLER, Tibor
; APPLICANT: GOLDSTEIN, Joel
; APPLICANT: GRAZIANO, Robert
; APPLICANT: DEO, Yashwant M.
; TITLE OF INVENTION: CELLS EXPRESSING ANTI-PC RECEPTOR
; FILE REFERENCE: MX1-099CPA
; CURRENT APPLICATION NUMBER: US/09/203,958A
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 60/067232
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-203-958A-2

Query Match      85.2%; Score 69; DB 3; Length 352;
Best Local Similarity 82.4%; Pred. No. 0.0042;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KSSQSVFPSSSQKNYLA 17
      |||||:|:|:|:|:|
Db      61 KSSQSVLYSSNQKNYLA 77

RESULT 39
US-10-764-131-2
; Sequence 2, Application US/10764131
; Publication No. US20050142120A1
; GENERAL INFORMATION:
; APPLICANT: KELLER, Tibor
; APPLICANT: GOLDSTEIN, Joel
; APPLICANT: GRAZIANO, Robert
; APPLICANT: DEO, Yashwant M.
; TITLE OF INVENTION: CELLS EXPRESSING ANTI-PC RECEPTOR
; FILE REFERENCE: MX1-099CPA
; CURRENT APPLICATION NUMBER: US/10/764,131
; PRIOR FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: US/09/203,958
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 60/067232
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
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```
US-10-764-131-2

Query Match      85.2%; Score 69; DB 5; Length 352;
Best Local Similarity 82.4%; Pred. No. 0.0042;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KSSQSVFPSSSQKNYLA 17
      |||||:|:|:|:|:|
Db      61 KSSQSVLYSSNQKNYLA 77

RESULT 40
US-10-723-003-28
; Sequence 28, Application US/10723003
; Publication No. US20040254108A1
; GENERAL INFORMATION:
; APPLICANT: GUO, Yajun
; APPLICANT: GUO, Yajun
; TITLE OF INVENTION: PREPARATION AND APPLICATION OF
; FILE REFERENCE: 549062000200
; CURRENT APPLICATION NUMBER: US/10/723,003
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: CN 2003101199300
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: CN 031292909
; PRIOR FILING DATE: 2003-06-13
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 661
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-723-003-28

Query Match      85.2%; Score 69; DB 5; Length 661;
Best Local Similarity 82.4%; Pred. No. 0.0082;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KSSQSVFPSSSQKNYLA 17
      |||||:|:~|:|:|:|
Db      572 KSSQSVLYSSNQKNYLA 588

RESULT 41
US-10-723-003-34
; Sequence 34, Application US/10723003
; Publication No. US20040254108A1
; GENERAL INFORMATION:
; APPLICANT: MA, Jing
; APPLICANT: GUO, Yajun
; TITLE OF INVENTION: PREPARATION AND APPLICATION OF
; FILE REFERENCE: 549062000200
; CURRENT APPLICATION NUMBER: US/10/723,003
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: CN 2003101199300
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: CN 031292909
; PRIOR FILING DATE: 2003-06-13
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 661
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-723-003-34

Query Match      85.2%; Score 69; DB 5; Length 661;
```

Best Local Similarity 82.4%; Pred. No. 0.0082;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KSSQSVFSSSQKNYLA 17
|||||:|||||
Db 572 KSSQSVLYSSNQKNYLA 588

RESULT 42

US-11-004-639-28
; Sequence 28, Application US/11004639
; Publication No. US20050232931A1
; GENERAL INFORMATION:
; APPLICANT: MA, JING
; APPLICANT: GUO, YAJUN
; TITLE OF INVENTION: PREPARATION AND APPLICATION OF
; FILE REFERENCE: 549062000200
; CURRENT FILING DATE: 2004-12-02
; PRIOR APPLICATION NUMBER: US/11/004,639
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: CN 2003101199300
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: CN 031292909
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 661
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-11-004-639-28

Query Match 85.2%; Score 69; DB 6; Length 661;
Best Local Similarity 82.4%; Pred. No. 0.0082;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KSSQSVFSSSQKNYLA 17
|||||:|||||
Db 572 KSSQSVLYSSNQKNYLA 588

RESULT 43

US-11-004-639-34
; Sequence 34, Application US/11004639
; Publication No. US20050232931A1
; GENERAL INFORMATION:
; APPLICANT: MA, JING
; APPLICANT: GUO, YAJUN
; TITLE OF INVENTION: PREPARATION AND APPLICATION OF
; FILE REFERENCE: 549062000200
; CURRENT FILING DATE: 2004-12-02
; PRIOR APPLICATION NUMBER: US/11/004,639
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: CN 2003101199300
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: CN 031292909
; PRIOR FILING DATE: 2003-06-13
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 661
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-11-004-639-34

Query Match 85.2%; Score 69; DB 6; Length 661;
Best Local Similarity 82.4%; Pred. No. 0.0082;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KSSQSVFSSSQKNYLA 17
|||||:|||||
Db 572 KSSQSVLYSSNQKNYLA 588

RESULT 44

US-09-828-708-36
; Sequence 36, Application US/09828708
; Patent No. US20020146753A1
; GENERAL INFORMATION:
; APPLICANT: DITZEL, H.
; APPLICANT: BURTON, D.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partici
; FILE REFERENCE: 1361.005081
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: US/09/828,708
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-708-36

Query Match 82.7%; Score 67; DB 3; Length 17;
Best Local Similarity 76.5%; Pred. No. 0.0036;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KSSQSVFSSSQKNYLA 17
|||||:|||||
Db 1 KSSQSVFYTSNNKNYLA 17

RESULT 45

US-09-828-708-39
; Sequence 39, Application US/09828708
; Patent No. US20020146753A1
; GENERAL INFORMATION:
; APPLICANT: DITZEL, H.
; APPLICANT: BURTON, D.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partici
; FILE REFERENCE: 1361.005081
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: US/09/828,708
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-708-39

Query Match 82.7%; Score 67; DB 3; Length 17;
Best Local Similarity 76.5%; Pred. No. 0.0036;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KSSQSVFSSSQKNYLA 17
|||||:|||||
Db 1 KSSQSVFYTSNNKNYLA 17

RESULT 46

US-10-630-009-36
; Sequence 36, Application US/10630009
; Publication No. US20050080239A1

```
; GENERAL INFORMATION:
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their particl
; FILE REFERENCE: 1361.005US2
; CURRENT APPLICATION NUMBER: US/10/630,009
; PRIOR FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: US 09/828,708
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-630-009-36
```

```
Query Match      82.7%; Score 67; DB 5; Length 17;
Best Local Similarity 76.5%; Pred. No. 0.00036;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 KSSQSVFSSSQKNYLA 17
      |||||:|:|:|:|:|
Db      1 KSSQSVFYTSNNKNYLA 17
```

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RESULT 47
US-10-630-009-39
; Sequence 39, Application US/10630009
; Publication No. US20050080239A1
; GENERAL INFORMATION:
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their particl
; FILE REFERENCE: 1361.005US2
; CURRENT APPLICATION NUMBER: US/10/630,009
; PRIOR FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: US 09/828,708
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-630-009-39
```

```
Query Match      82.7%; Score 67; DB 5; Length 17;
Best Local Similarity 76.5%; Pred. No. 0.00036;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 KSSQSVFSSSQKNYLA 17
      |||||:|:|:|:|:|
Db      1 KSSQSVFYTSNNKNYLA 17
```

```
RESULT 48
US-10-893-576-66
; Sequence 66, Application US/10893576
; Publication No. US20050118643A1
; GENERAL INFORMATION:
; APPLICANT: BURGESS, TERESA L.
; APPLICANT: COXON, ANGELA
; APPLICANT: GREEN, LARRY L.
; APPLICANT: ZHANG, KE
; TITLE OF INVENTION: SPECIFIC BINDING AGENTS TO HEPATOCYTE GROWTH FACTOR
; FILE REFERENCE: 06843.0051-00000
; CURRENT APPLICATION NUMBER: US/10/893,576
; CURRENT FILING DATE: 2004-07-16
```

```
; PRIOR APPLICATION NUMBER: US 60/488,681
; PRIOR FILING DATE: 2003-07-18
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 66
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic light chain
US-10-893-576-66
```

```
Query Match      82.7%; Score 67; DB 5; Length 17;
Best Local Similarity 82.4%; Pred. No. 0.00036;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      1 KSSQSVFSSSQKNYLA 17
      |||||:|:|:|:|:|
Db      1 KSSQSVLFSSNNKNYLA 17
```

```
RESULT 49
US-09-828-708-1
; Sequence 1, Application US/09828708
; Patent No. US20020146753A1
; GENERAL INFORMATION:
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their particl
; FILE REFERENCE: 1361.005US1
; CURRENT APPLICATION NUMBER: US/09/828,708
; PRIOR FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-708-1
```

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Query Match      82.7%; Score 67; DB 3; Length 109;
Best Local Similarity 76.5%; Pred. No. 0.0026;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
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```
Qy      1 KSSQSVFSSSQKNYLA 17
      |||||:|:~|:~|:~|
Db      17 KSSQSVFYTSNNKNYLA 33
```

```
RESULT 50
US-09-828-708-4
; Sequence 4, Application US/09828708
; Patent No. US20020146753A1
; GENERAL INFORMATION:
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their particl
; FILE REFERENCE: 1361.005US1
; CURRENT APPLICATION NUMBER: US/09/828,708
; PRIOR FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-708-4
```

Query Match 82.7%; Score 67; DB 3; Length 109;
 Best Local Similarity 76.5%; Pred No. 0.0026;
 Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KSSQSVFPSSSQKNTLA 17
 |||||:::|
 Db 17 KSSQSVFYTSNNKNTLA 33

Search completed: May 4, 2006, 13:53:20
 Job time : 132.484 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 4, 2006, 13:46:13 ; Search time 19.6984 Seconds
(without alignments)
39.944 Million cell updates/sec

Title: US-10-700-632-4
Perfect score: 81
Sequence: 1 KSSQSVFRSSQKNVLA 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 235405 seqs, 46284737 residues

Total number of hits satisfying chosen parameters: 235405

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :

Published Applications AA_New:*
1: /SIDS5/ptodata/2/pubppaa/US08_NEW_PUB.pep1:*
2: /SIDS5/ptodata/2/pubppaa/US06_NEW_PUB.pep1:*
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12: /SIDS5/ptodata/2/pubppaa/US60_NEW_PUB.pep1:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	69	85.2	17	9	US-10-981-356A-24
2	69	85.2	17	11	US-11-096-046-24
3	69	85.2	17	11	US-11-136-559-27
4	69	85.2	112	11	US-11-136-559-6
5	69	85.2	112	11	US-11-136-559-10
6	69	85.2	112	11	US-11-136-559-18
7	69	85.2	112	11	US-11-136-559-22
8	69	85.2	116	11	US-11-096-046-1
9	69	85.2	116	11	US-11-096-046-1
10	69	85.2	666	9	US-10-981-356A-29
11	69	85.2	667	11	US-11-096-046-29
12	69	85.2	112	11	US-11-136-559-14
13	66	81.5	259	9	US-10-512-184-31
14	66	81.5	329	9	US-10-512-184-68
15	64	79.0	101	10	US-11-221-902-63
16	64	79.0	101	10	US-11-221-902-63
17	64	79.0	101	11	US-11-054-669-89
18	64	79.0	101	11	US-11-084-554-120
19	64	79.0	101	11	US-11-004-590-94
20	64	79.0	101	11	US-11-136-250-120
21	64	79.0	114	9	US-10-771-257-72

22	64	79.0	114	9	US-10-834-397-17	Sequence 17, Appl
23	64	79.0	114	11	US-11-127-677-27	Sequence 27, Appl
24	64	79.0	114	11	US-11-127-677-27	Sequence 70, Appl
25	64	79.0	115	9	US-10-771-257-72	Sequence 27, Appl
26	64	79.0	133	8	US-10-511-937-2965	Sequence 2965, Ap
27	63	77.8	17	9	US-10-981-356A-18	Sequence 18, Appl
28	63	77.8	116	11	US-11-096-046-18	Sequence 3, Appl
29	63	77.8	116	11	US-11-096-046-18	Sequence 18, Appl
30	63	77.8	116	11	US-11-096-046-3	Sequence 3, Appl
31	63	77.8	666	9	US-10-981-356A-25	Sequence 25, Appl
32	63	77.8	666	9	US-10-981-356A-27	Sequence 27, Appl
33	63	77.8	666	9	US-10-981-356A-28	Sequence 28, Appl
34	63	77.8	666	9	US-10-981-356A-30	Sequence 30, Appl
35	63	77.8	666	11	US-11-096-046-27	Sequence 27, Appl
36	63	77.8	667	11	US-11-096-046-25	Sequence 25, Appl
37	63	77.8	667	11	US-11-096-046-28	Sequence 28, Appl
38	63	77.8	667	11	US-11-096-046-30	Sequence 30, Appl
39	63	77.8	692	11	US-10-981-356A-26	Sequence 26, Appl
40	63	77.8	695	11	US-11-096-046-26	Sequence 26, Appl
41	62	76.5	242	11	US-11-239-510-23	Sequence 23, Appl
42	62	76.5	244	11	US-11-239-510-13	Sequence 13, Appl
43	62	76.5	483	11	US-11-239-510-19	Sequence 19, Appl
44	61	75.3	115	9	US-10-834-397-31	Sequence 31, Appl
45	61	75.3	115	9	US-10-834-397-49	Sequence 49, Appl
46	61	75.3	135	11	US-11-158-505-35	Sequence 35, Appl
47	60	74.1	259	9	US-10-512-184-33	Sequence 33, Appl
48	60	74.1	259	9	US-10-512-184-34	Sequence 34, Appl
49	60	74.1	329	9	US-10-512-184-70	Sequence 70, Appl
50	60	74.1	329	9	US-10-512-184-71	Sequence 71, Appl
51	60	74.1	626	9	US-10-512-184-49	Sequence 49, Appl
52	58	71.6	174	11	US-11-072-512-3202	Sequence 3202, Ap
53	56	69.1	109	9	US-10-771-257-101	Sequence 101, Appl
54	56	69.1	109	9	US-10-771-257-105	Sequence 105, Appl
55	56	69.1	109	9	US-10-771-257-107	Sequence 107, Appl
56	56	69.1	113	10	US-11-219-563-71	Sequence 71, Appl
57	56	69.1	113	10	US-11-219-563-91	Sequence 91, Appl
58	56	69.1	113	11	US-11-076-395-16	Sequence 16, Appl
59	56	69.1	113	11	US-11-076-395-21	Sequence 21, Appl
60	56	69.1	113	11	US-11-076-395-45	Sequence 45, Appl
61	56	69.1	113	11	US-11-076-395-46	Sequence 46, Appl
62	56	69.1	113	11	US-11-076-395-70	Sequence 70, Appl
63	56	69.1	113	11	US-11-076-395-71	Sequence 71, Appl
64	56	69.1	113	11	US-11-218-813-91	Sequence 91, Appl
65	56	69.1	113	11	US-11-218-813-91	Sequence 91, Appl
66	55	67.9	17	9	US-10-530-171-4	Sequence 4, Appl
67	55	67.9	109	9	US-10-771-257-112	Sequence 112, Appl
68	55	67.9	114	9	US-10-771-257-74	Sequence 74, Appl
69	55	67.9	114	9	US-10-530-171-8	Sequence 8, Appl
70	55	67.9	114	11	US-11-127-677-72	Sequence 72, Appl
71	52	64.2	118	10	US-11-075-891-26	Sequence 26, Appl
72	52	64.2	263	9	US-10-512-184-29	Sequence 29, Appl
73	51	63.0	678	11	US-11-202-507A-11	Sequence 11, Appl
74	51	63.0	679	11	US-11-202-507A-5	Sequence 5, Appl
75	47	58.0	17	11	US-11-105-708-23	Sequence 23, Appl
76	45	55.6	293	11	US-11-116-939-10	Sequence 10, Appl
77	45	55.6	412	11	US-11-116-939-12	Sequence 12, Appl
78	45	55.6	824	11	US-11-116-939-11	Sequence 11, Appl
79	44	54.3	114	9	US-10-771-257-68	Sequence 68, Appl
80	44	54.3	114	11	US-11-127-677-66	Sequence 66, Appl
81	42	51.9	115	10	US-11-219-563-92	Sequence 92, Appl
82	42	51.9	115	11	US-11-218-813-92	Sequence 92, Appl
83	42	51.9	347	11	US-11-096-568A-22627	Sequence 22627, A
84	42	51.9	394	11	US-11-096-568A-22626	Sequence 22626, A
85	42	51.9	411	11	US-11-096-568A-22625	Sequence 22625, A
86	41	50.6	505	11	US-11-079-463-1291	Sequence 7291, Ap
87	40	49.4	185	11	US-11-087-099-11470	Sequence 11470, A
88	39	48.1	468	9	US-10-957-589-28	Sequence 28, Appl
89	39	48.1	468	11	US-11-097-589-26	Sequence 26, Appl
90	39	48.1	510	11	US-11-188-298-16887	Sequence 16887, A
91	39	48.1	897	11	US-11-188-298-15917	Sequence 15917, Ap
92	38.5	47.5	74	11	US-11-079-463-8435	Sequence 8435, Ap
93	38.5	47.5	304	11	US-11-045-004-1618	Sequence 1618, Ap
94	37	45.7	160	11	US-11-096-568A-1206	Sequence 1206, Ap


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971 29 35.8 340 11 US-11-096-568A-7704 Sequence 7704, Ap
972 29 35.8 341 11 US-11-188-298-18416 Sequence 18416, A
973 29 35.8 343 11 US-11-188-298-5930 Sequence 5930, Ap
974 29 35.8 345 9 US-10-467-657-252 Sequence 252, App
975 29 35.8 346 9 US-10-467-657-3086 Sequence 3086, Ap
976 29 35.8 346 11 US-11-096-568A-5743 Sequence 5743, Ap
977 29 35.8 352 11 US-11-096-568A-7153 Sequence 7153, Ap
978 29 35.8 354 11 US-11-188-298-19724 Sequence 19724, A
979 29 35.8 355 9 US-10-873-528-149 Sequence 149, App
980 29 35.8 355 11 US-11-096-568A-7152 Sequence 7152, Ap
981 29 35.8 355 11 US-11-096-568A-25553 Sequence 25553, A
982 29 35.8 356 11 US-11-282-495-6 Sequence 6, App11
983 29 35.8 360 11 US-11-188-298-2669 Sequence 2669, Ap
984 29 35.8 363 9 US-10-838-616-10 Sequence 10, App1
985 29 35.8 366 11 US-11-124-368A-282 Sequence 282, App
986 29 35.8 367 11 US-11-124-368A-283 Sequence 283, App
987 29 35.8 367 11 US-11-124-368A-284 Sequence 284, App
988 29 35.8 367 11 US-11-072-512-3502 Sequence 3502, Ap
989 29 35.8 367 11 US-11-096-568A-29694 Sequence 29694, A
990 29 35.8 373 11 US-11-072-463-5763 Sequence 5763, Ap
991 29 35.8 373 11 US-11-096-568A-31989 Sequence 31989, A
992 29 35.8 376 11 US-11-096-568A-7703 Sequence 7703, A
993 29 35.8 376 11 US-11-188-298-21104 Sequence 21104, A
994 29 35.8 379 11 US-11-144-833-11 Sequence 11, App1
995 29 35.8 379 11 US-11-096-568A-14738 Sequence 14738, A
996 29 35.8 379 11 US-11-188-298-1320 Sequence 1320, Ap
997 29 35.8 380 11 US-11-096-568A-39693 Sequence 39693, A
998 29 35.8 382 11 US-11-087-099-3998 Sequence 3998, A
999 29 35.8 382 11 US-11-087-099-9715 Sequence 9715, Ap
1000 29 35.8 385 11 US-11-096-568A-4426 Sequence 4426, Ap
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ALIGNMENTS

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RESULT 1
US-10-981-356A-24
; Sequence 24, Application US/10981356A
; Publication No. US20060015952A1
; GENERAL INFORMATION:
; APPLICANT: FILVAROFF, ELLEN H.
; TITLE OF INVENTION: SCREENING ASSAYS AND METHODS OF TUMOR TREATMENT
; FILE REFERENCE: P2068R1
; CURRENT APPLICATION NUMBER: US/10/981, 356A
; PRIOR FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: US 60/520,398
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/557,951
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 45
; SEQ ID NO 24
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-981-356A-24
```

```
Query Match 85.2%; Score 69; DB 9; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.9e-05;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 KSSQSVFSSSQKNYLA 17
Db 1 KSSQSVLYSSNQKNYLA 17
```

```
RESULT 2
US-11-096-046-24
; Sequence 24, Application US/11096046
; Publication No. US20050276802A1
; GENERAL INFORMATION:
; APPLICANT: ADAMS, CAMELLIA W.
; APPLICANT: FERRARA, NAPOLEONE
; APPLICANT: FILVAROFF, ELLEN H.
```

```
; APPLICANT: MAO, WEIGUANG
; APPLICANT: PRESTA, LEONARD G.
; APPLICANT: TEJADA, MAX L.
; TITLE OF INVENTION: Humanized Anti-TGF-Beta Antibodies
; FILE REFERENCE: P1954R1US
; CURRENT APPLICATION NUMBER: US/11/096,046
; PRIOR FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: US 60/558,290
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 24
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-096-046-24
```

```
Query Match 85.2%; Score 69; DB 11; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.9e-05;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 KSSQSVFSSSQKNYLA 17
Db 1 KSSQSVLYSSNQKNYLA 17
```

```
RESULT 3
US-11-136-559-27
; Sequence 27, Application US/11136559
; Publication No. US20050287164A1
; GENERAL INFORMATION:
; APPLICANT: HUTCHINS, Jeff T
; APPLICANT: HUTCHINS, Paul
; APPLICANT: DOMANSKI, Paul
; APPLICANT: PATEL, Pratiksha
; APPLICANT: HALL, Andrea
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN . . .
; FILE REFERENCE: P0706US04/BAS
; CURRENT APPLICATION NUMBER: US/11/136,559
; PRIOR FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US/10/056,052
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: 60/308,116
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/298,413
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/274,611
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/264,072
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-11-136-559-27
```

```
Query Match 85.2%; Score 69; DB 11; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.9e-05;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 KSSQSVFSSSQKNYLA 17
Db 1 KSSQSVLYSSNQKNYLA 17
```

```
RESULT 4
US-11-136-559-6
; Sequence 6, Application US/11136559
; Publication No. US20050287164A1
; GENERAL INFORMATION:
; APPLICANT: PATTI, Joseph M
; APPLICANT: HUTCHINS, Jeff T
```

```

; APPLICANT: DOMANSKI, Paul
; APPLICANT: PATEL, Pratiksha
; APPLICANT: HALU, Andrea
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN . . .
; FILE REFERENCE: P07069US04/BAS
; CURRENT APPLICATION NUMBER: US/11/136,559
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: 60/308,116
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: 60/298,413
; PRIOR FILING DATE: 2001-07-30
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/274,611
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/264,072
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-11-136-559-6

```

```

Query Match      85.2%; Score 69; DB 11; Length 112;
Best Local Similarity 82.4%; Pred. No. 0.0002;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1 KSSQSVFSSSQKNYLA 17
        |||||:|||||
        24 KSSQSVLYSSNQKNYLA 40

```

```

RESULT 5
US-11-136-559-10
; Sequence 10, Application US/11/136559
; Publication No. US20050287164A1
; GENERAL INFORMATION:
; APPLICANT: PATTI, Joseph M
; APPLICANT: HUTCHINS, Jeff T
; APPLICANT: DOMANSKI, Paul
; APPLICANT: PATEL, Pratiksha
; APPLICANT: HALU, Andrea
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN . . .
; FILE REFERENCE: P07069US04/BAS
; CURRENT APPLICATION NUMBER: US/11/136,559
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: 60/308,116
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: 60/298,413
; PRIOR FILING DATE: 2001-07-30
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/274,611
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/264,072
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-11-136-559-10

```

```

Query Match      85.2%; Score 69; DB 11; Length 112;
Best Local Similarity 82.4%; Pred. No. 0.0002;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1 KSSQSVFSSSQKNYLA 17
        |||||:|||||
        24 KSSQSVLYSSNQKNYLA 40

```

```

RESULT 6
US-11-136-559-18
; Sequence 18, Application US/11/136559
; Publication No. US20050287164A1
; GENERAL INFORMATION:
; APPLICANT: PATTI, Joseph M
; APPLICANT: HUTCHINS, Jeff T
; APPLICANT: DOMANSKI, Paul
; APPLICANT: PATEL, Pratiksha
; APPLICANT: HALU, Andrea
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN . . .
; FILE REFERENCE: P07069US04/BAS
; CURRENT APPLICATION NUMBER: US/11/136,559
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: 60/308,116
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: 60/298,413
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/274,611
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/264,072
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/264,072
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-11-136-559-18

```

```

Query Match      85.2%; Score 69; DB 11; Length 112;
Best Local Similarity 82.4%; Pred. No. 0.0002;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1 KSSQSVFSSSQKNYLA 17
        |||||:|||||
        24 KSSQSVLYSSNQKNYLA 40

```

```

RESULT 7
US-11-136-559-22
; Sequence 22, Application US/11/136559
; Publication No. US20050287164A1
; GENERAL INFORMATION:
; APPLICANT: PATTI, Joseph M
; APPLICANT: HUTCHINS, Jeff T
; APPLICANT: DOMANSKI, Paul
; APPLICANT: PATEL, Pratiksha
; APPLICANT: HALU, Andrea
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN . . .
; FILE REFERENCE: P07069US04/BAS
; CURRENT APPLICATION NUMBER: US/11/136,559
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: 60/308,116
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: 60/298,413
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/274,611
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/264,072
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/264,072
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Staphylococcus aureus

```

US-11-136-559-22

Query Match 85.2%; Score 69; DB 11; Length 112;
Best Local Similarity 82.4%; Pred. No. 0.0002;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSSQSVFFSSQKNYLA 17
|||||:|||||
DB 24 KSSQSVLYSSNQKNYLA 40

RESULT 8

US-10-981-356A-1
; Sequence 1, Application US/10981356A
; Publication No. US20060015952A1
; GENERAL INFORMATION:
; APPLICANT: FILVAROFF, ELLEN H.
; TITLE OF INVENTION: SCREENING ASSAYS AND METHODS OF TUMOR TREATMENT
; FILE REFERENCE: P2068R1
; CURRENT APPLICATION NUMBER: US/10/981,356A
; PRIOR FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: US 60/520,398
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/557,951
; NUMBER OF SEQ ID NOS: 45
; SEQ ID NO 1
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-981-356A-1

Query Match 85.2%; Score 69; DB 9; Length 116;
Best Local Similarity 82.4%; Pred. No. 0.00021;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSSQSVFFSSQKNYLA 17
|||||:|||||
DB 24 KSSQSVLYSSNQKNYLA 40

RESULT 9
US-11-096-046-1
; Sequence 1, Application US/11096046
; Publication No. US20050276802A1
; GENERAL INFORMATION:
; APPLICANT: ADAMS, CAMELLIA W.
; APPLICANT: FERRARA, NAPOLEONE
; APPLICANT: FILVAROFF, ELLEN H.
; APPLICANT: MAO, WEIGUANG
; APPLICANT: PRESTA, LEONARD G.
; APPLICANT: TEJADA, MAX L.
; TITLE OF INVENTION: Humanized Anti-TGF-Beta Antibodies
; FILE REFERENCE: P1954R1US
; CURRENT APPLICATION NUMBER: US/11/096,046
; PRIOR FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: US 60/558,290
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 1
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-096-046-1

Query Match 85.2%; Score 69; DB 11; Length 116;
Best Local Similarity 82.4%; Pred. No. 0.00021;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSSQSVFFSSQKNYLA 17
|||||:|||||
DB 24 KSSQSVLYSSNQKNYLA 40

RESULT 10

US-10-981-356A-29
; Sequence 29, Application US/10981356A
; Publication No. US20060015952A1
; GENERAL INFORMATION:
; APPLICANT: FILVAROFF, ELLEN H.
; TITLE OF INVENTION: SCREENING ASSAYS AND METHODS OF TUMOR TREATMENT
; FILE REFERENCE: P2068R1
; CURRENT APPLICATION NUMBER: US/10/981,356A
; PRIOR FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: US 60/520,398
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/557,951
; NUMBER OF SEQ ID NOS: 45
; SEQ ID NO 29
; LENGTH: 666
; TYPE: PRT
; ORGANISM: Artificial sequence
; OTHER INFORMATION: Sequence is synthesized
US-10-981-356A-29

Query Match 85.2%; Score 69; DB 9; Length 666;
Best Local Similarity 82.4%; Pred. No. 0.0013;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSSQSVFFSSQKNYLA 17
|||||:|||||
DB 24 KSSQSVLYSSNQKNYLA 40

RESULT 11
US-11-096-046-29
; Sequence 29, Application US/11096046
; Publication No. US20050276802A1
; GENERAL INFORMATION:
; APPLICANT: ADAMS, CAMELLIA W.
; APPLICANT: FERRARA, NAPOLEONE
; APPLICANT: FILVAROFF, ELLEN H.
; APPLICANT: MAO, WEIGUANG
; APPLICANT: PRESTA, LEONARD G.
; APPLICANT: TEJADA, MAX L.
; TITLE OF INVENTION: Humanized Anti-TGF-Beta Antibodies
; FILE REFERENCE: P1954R1US
; CURRENT APPLICATION NUMBER: US/11/096,046
; PRIOR FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: US 60/558,290
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 29
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
; NAME/KEY: Unsure
; LOCATION: 220
; OTHER INFORMATION: Unknown amino acid
US-11-096-046-29

Query Match 85.2%; Score 69; DB 11; Length 667;
Best Local Similarity 82.4%; Pred. No. 0.0013;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSSQSVFFSSQKNYLA 17
|||||:|||||
DB 24 KSSQSVLYSSNQKNYLA 40

RESULT 12

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US-11-136-559-14
; Sequence 14, Application US/11136559
; Publication No. US20050287164A1
; GENERAL INFORMATION:
; APPLICANT: PATTI, Joseph M
; APPLICANT: HUTCHINS, Jeff T
; APPLICANT: DOMANSKI, Paul
; APPLICANT: PATEL, Pratiksha
; APPLICANT: HALL, Andrea
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN . . .
; FILE REFERENCE: P07069US04/BAS
; CURRENT APPLICATION NUMBER: US/11/136,559
; PRIOR FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US/10/056,052
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: 60/308,116
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/298,413
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/274,611
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/264,072
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-11-136-559-14

Query Match      81.5%; Score 66; DB 11; Length 112;
Best Local Similarity 76.5%; Pred. No. 0.00063;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 KSSQSVFSSSQKNYLA 17
      :||||:|:|:|:|:|
      24 KSSQSVLYSSNNKNYLA 40

Db

RESULT 13
US-10-512-184-31
; Sequence 31, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: scFv VDCw with
; OTHER INFORMATION: specificity against Verticillium dahliae;
; OTHER INFORMATION: originates from Mus musculus.
US-10-512-184-31

Query Match      81.5%; Score 66; DB 9; Length 259;
Best Local Similarity 76.5%; Pred. No. 0.0015;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 KSSQSVFSSSQKNYLA 17
      :||||:|:|:|:|:|
      161 KSSQSVLYSSNNKNYLA 177

Db
```

```
RESULT 14
US-10-512-184-68
; Sequence 68, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 68
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: precursor
; OTHER INFORMATION: fusion protein comprising RS - linker scFv VDC.
US-10-512-184-68

Query Match      81.5%; Score 66; DB 9; Length 329;
Best Local Similarity 76.5%; Pred. No. 0.0019;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 KSSQSVFSSSQKNYLA 17
      :||||:|:|:|:|:|
      231 KSSQSVLYSSNNKNYLA 247

Db

RESULT 15
US-11-221-902-63
; Sequence 63, Application US/11221902
; Publication No. US20060088522A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: HUMANIZED ANTI-5T4 ANTIBODIES AND ANTI-5T4/CALICHEAMICIN CONJUGAT
; FILE REFERENCE: 040000-0317285
; CURRENT APPLICATION NUMBER: US/11/221,902
; CURRENT FILING DATE: 2005-09-09
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 63
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-221-902-63

Query Match      79.0%; Score 64; DB 10; Length 101;
Best Local Similarity 76.5%; Pred. No. 0.0012;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 KSSQSVFSSSQKNYLA 17
      :||||:|:|:|:|:|
      24 KSSQSVLYSSNNKNYLA 40

Db

RESULT 16
US-11-239-308-57
; Sequence 57, Application US/11239308
; Publication No. US20060088883A1
; GENERAL INFORMATION:
; APPLICANT: Smider, Vaughn
; APPLICANT: Lattick, James W.
; APPLICANT: Integritgen, Inc.
; TITLE OF INVENTION: Recombinant Catalytic Polypeptides and Their Uses
; FILE REFERENCE: 021216-000310US
; CURRENT APPLICATION NUMBER: US/11/239,308
; CURRENT FILING DATE: 2005-09-28
; PRIOR APPLICATION NUMBER: US/10/683,733
; PRIOR FILING DATE: 2003-10-09
```

PRIOR APPLICATION NUMBER: US 60/417,979
PRIOR FILING DATE: 2002-10-09
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 57
LENGTH: 101
TYPE: PRT
ORGANISM: Homo sapiens
US-11-239-308-57

Query Match 79.0%; Score 64; DB 10; Length 101;
Best Local Similarity 76.5%; Pred. No. 0.0012;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KSSQSVFSSSQKNYLA 17
||| | | | | : ||| | | | |
Db 24 KSSQSVLYSSNNKNYLA 40

RESULT 17
US-11-054-669-89
Sequence 89, Application US/11054669
Publication No. US20050261480A1
GENERAL INFORMATION:
APPLICANT: Foote, Jefferson
TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
FILE REFERENCE: 30219/US/3
CURRENT APPLICATION NUMBER: US/11/054,669
CURRENT FILING DATE: 2005-02-08
PRIOR APPLICATION NUMBER: US 10/194,975
PRIOR FILING DATE: 2002-07-12
PRIOR APPLICATION NUMBER: US 60/305,111
PRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 124
SOFTWARE: Patent In version 3.3
SEQ ID NO 89
LENGTH: 101
TYPE: PRT
ORGANISM: Homo sapiens
US-11-054-669-89

Query Match 79.0%; Score 64; DB 11; Length 101;
Best Local Similarity 76.5%; Pred. No. 0.0012;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KSSQSVFSSSQKNYLA 17
||| | | | | : ||| | | | |
Db 24 KSSQSVLYSSNNKNYLA 40

RESULT 18
US-11-084-554-120
Sequence 120, Application US/11084554
Publication No. US20050260679A1
GENERAL INFORMATION:
APPLICANT: Kellermann, Strid-Ai
APPLICANT: Green, Larry L.
APPLICANT: Korver, Wouter
TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
TITLE OF INVENTION: ANTIBODIES THROUGH V GENE MANIPULATION
FILE REFERENCE: ABGENIX.100A
CURRENT APPLICATION NUMBER: US/11/084,554
CURRENT FILING DATE: 2005-03-17
PRIOR APPLICATION NUMBER: 60/554,372
PRIOR FILING DATE: 2004-03-19
PRIOR APPLICATION NUMBER: 60/574,661
PRIOR FILING DATE: 2004-05-24
NUMBER OF SEQ ID NOS: 266
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 120
LENGTH: 101
TYPE: PRT
ORGANISM: Homo sapiens

US-11-084-554-120

Query Match 79.0%; Score 64; DB 11; Length 101;
Best Local Similarity 76.5%; Pred. No. 0.0012;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KSSQSVFSSSQKNYLA 17
||| | | | | : ||| | | | |
Db 24 KSSQSVLYSSNNKNYLA 40

RESULT 19
US-11-004-590-94
Sequence 94, Application US/11004590
Publication No. US2006008883A1
GENERAL INFORMATION:
APPLICANT: Lazar, Gregory Alan
APPLICANT: Desjardais, John R.
APPLICANT: Hammond, Phillip W.
TITLE OF INVENTION: METHODS OF GENERATING VARIANT PROTEINS WITH INCREASED HOST STRING
TITLE OF INVENTION: CONTENT AND COMPOSITIONS THEREOF
FILE REFERENCE: 185832/US/5
CURRENT APPLICATION NUMBER: US/11/004,590
CURRENT FILING DATE: 2004-12-03
PRIOR APPLICATION NUMBER: US 60/527,167
PRIOR FILING DATE: 2003-12-04
PRIOR APPLICATION NUMBER: US 60/581,613
PRIOR FILING DATE: 2004-06-21
PRIOR APPLICATION NUMBER: US 60/601,665
PRIOR FILING DATE: 2004-08-13
PRIOR APPLICATION NUMBER: US 60/619,483
PRIOR FILING DATE: 2004-10-14
NUMBER OF SEQ ID NOS: 458
SOFTWARE: Patent In version 3.3
SEQ ID NO 94
LENGTH: 101
TYPE: PRT
ORGANISM: Homo sapiens
US-11-004-590-94

US-11-004-590-94

Query Match 79.0%; Score 64; DB 11; Length 101;
Best Local Similarity 76.5%; Pred. No. 0.0012;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KSSQSVFSSSQKNYLA 17
||| | | | | : ||| | | | |
Db 24 KSSQSVLYSSNNKNYLA 40

RESULT 20
US-11-136-250-120
Sequence 120, Application US/11136250
Publication No. US20060021074A1
GENERAL INFORMATION:
APPLICANT: Kellermann, Strid-Ai
APPLICANT: Green, Larry L.
APPLICANT: Korver, Wouter
TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
TITLE OF INVENTION: ANTIBODIES THROUGH V GENE MANIPULATION
FILE REFERENCE: ABGENIX.100A2
CURRENT APPLICATION NUMBER: US/11/136,250
CURRENT FILING DATE: 2005-05-23
PRIOR APPLICATION NUMBER: 60/554,554
PRIOR FILING DATE: 2005-03-17
PRIOR APPLICATION NUMBER: PCT/US2005/009306
PRIOR FILING DATE: 2005-03-17
PRIOR APPLICATION NUMBER: 60/574,661
PRIOR FILING DATE: 2004-05-24
PRIOR APPLICATION NUMBER: 60/554,372
PRIOR FILING DATE: 2004-03-19
NUMBER OF SEQ ID NOS: 266
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 120

LENGTH: 101
TYPE: PRT
ORGANISM: Homo sapiens
US-11-136-250-120

Query Match 79.0%; Score 64; DB 11; Length 101;
Best Local Similarity 76.5%; Pred. No. 0.0012;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KSSQSVFFSSQKNYLA 17
|||||:|:|:|
DB 24 KSSQSVLYSSNNKNYLA 40

RESULT 21
US-10-771-257-72
Sequence 72, Application US/10771257
Publication No.: US2005028864A1
GENERAL INFORMATION:
APPLICANT: Medical Research Council
APPLICANT: SISSA - Scuola Superiore Internazionale di Studi Avanzati
APPLICANT: Cattaneo, Antonino
APPLICANT: Martean, Amos
APPLICANT: Visintin, Michela
APPLICANT: Rabbits, Terence H
APPLICANT: Settemi, Giovanni
TITLE OF INVENTION: Intracellular antibodies
FILE REFERENCE: 18396/2272
CURRENT APPLICATION NUMBER: US/10/771,257
CURRENT FILING DATE: 2004-02-03
PRIOR APPLICATION NUMBER: PCT/GB02/03512
PRIOR FILING DATE: 2002-08-01
PRIOR APPLICATION NUMBER: GB 0119004.0
PRIOR FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: GB 0121577.1
PRIOR FILING DATE: 2001-09-06
PRIOR APPLICATION NUMBER: GB 0200928.0
PRIOR FILING DATE: 2002-01-16
PRIOR APPLICATION NUMBER: GB 0203569.9
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: IT RM2001A000633
PRIOR FILING DATE: 2001-10-25
NUMBER OF SEQ ID NOS: 124
SOFTWARE: PatentIn version 3.1
SEQ ID NO 72
LENGTH: 114
TYPE: PRT
ORGANISM: Homo sapiens
US-10-771-257-72

Query Match 79.0%; Score 64; DB 9; Length 114;
Best Local Similarity 76.5%; Pred. No. 0.0014;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KSSQSVFFSSQKNYLA 17
|||||:|:|:|
DB 24 KSSQSVLYSSNNKNYLA 40

RESULT 22
US-10-834-397-17
Sequence 17, Application US/10834397
Publication No. US2006000334A1
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Laming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly) peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/834,397
FILING DATE: 29-Apr-2004
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-Jan-2000
APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 17:

US-10-834-397-17
Query Match 79.0%; Score 64; DB 9; Length 114;
Best Local Similarity 76.5%; Pred. No. 0.0014;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KSSQSVFFSSQKNYLA 17
|||||:|:~|:|:|
DB 24 KSSQSVLYSSNNKNYLA 40

RESULT 23
US-11-127-677-27
Sequence 27, Application US/11127677
Publication No. US20050272107A1
GENERAL INFORMATION:
APPLICANT: Medical Research Council
APPLICANT: Rabbits, Terence H
APPLICANT: Tanaka, Tomoyuki
TITLE OF INVENTION: Intracellular antibodies
FILE REFERENCE: 18396/2462
CURRENT APPLICATION NUMBER: US/11/127,677
CURRENT FILING DATE: 2005-05-12
PRIOR APPLICATION NUMBER: PCT/GB03/04942
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: GB 0226729.2
PRIOR FILING DATE: 2002-11-15
NUMBER OF SEQ ID NOS: 150
SOFTWARE: PatentIn version 3.1
SEQ ID NO 27
LENGTH: 114
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Derived protein sequence of scFv
US-11-127-677-27

Query Match 79.0%; Score 64; DB 11; Length 114;
Best Local Similarity 76.5%; Pred. No. 0.0014;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KSSQSVFPSSSQKNYLA 17
|||||:|:|:|
DB 24 KSSQSVLYSSNNKNYLA 40

RESULT 24
US-11-127-677-70
; Sequence 70, Application US/11127677
; Publication No. US20050272107A1
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; APPLICANT: Rabbitts, Terence H
; APPLICANT: Tanaka, Tomoyuki
; TITLE OF INVENTION: Intracellular antibodies
; FILE REFERENCE: 18396/2462
; CURRENT APPLICATION NUMBER: US/11/127,677
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: PCT/GB03/04942
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: GB 0226729.2
; PRIOR FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 70
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Derived protein sequence of scFv
US-11-127-677-70

Query Match 79.0%; Score 64; DB 11; Length 114;
Best Local Similarity 76.5%; Pred. No. 0.0014;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KSSQSVFPSSSQKNYLA 17
|||||:|:|:|
DB 24 KSSQSVLYSSNNKNYLA 40

RESULT 25
US-10-771-257-27
; Sequence 27, Application US/10771257
; Publication No. US2005028864A1
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; APPLICANT: SISGA - Scuola Superiore Internazionale di Studi Avanzati
; APPLICANT: Cattaneo, Antonino
; APPLICANT: Maritan, Amos
; APPLICANT: Visintin, Michela
; APPLICANT: Rabbitts, Terence H
; APPLICANT: Settanni, Giovanni
; TITLE OF INVENTION: Intracellular antibodies
; FILE REFERENCE: 18396/2272
; CURRENT APPLICATION NUMBER: US/10/771,257
; CURRENT FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: PCT/GB02/03512
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: GB 0119004.0
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: GB 0121577.1
; PRIOR FILING DATE: 2001-09-06
; PRIOR APPLICATION NUMBER: GB 0200928.0
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: GB 0203569.9
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: IT RM2001A000633
; PRIOR FILING DATE: 2001-10-25
; NUMBER OF SEQ ID NOS: 124

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-771-257-27

Query Match 79.0%; Score 64; DB 9; Length 115;
Best Local Similarity 76.5%; Pred. No. 0.0014;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KSSQSVFPSSSQKNYLA 17
|||||:|:|:|
DB 24 KSSQSVLYSSNNKNYLA 40

RESULT 26
US-10-511-937-2965
; Sequence 2965, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 317
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2965
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2965

Query Match 79.0%; Score 64; DB 8; Length 133;
Best Local Similarity 76.5%; Pred. No. 0.0016;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KSSQSVFPSSSQKNYLA 17
|||||:|:|:|
DB 44 KSSQSVLYSSNNKNYLA 60

RESULT 27
US-10-981-356A-18
; Sequence 18, Application US/10981356A
; Publication No. US20060015952A1
; GENERAL INFORMATION:
; APPLICANT: FLIVAROFF, ELLEN H.
; TITLE OF INVENTION: SCREENING ASSAYS AND METHODS OF TUMOR TREATMENT
; FILE REFERENCE: P206681
; CURRENT APPLICATION NUMBER: US/10/981,356A
; CURRENT FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: US 60/520,398
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/557,951
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 45
; SEQ ID NO 18

```
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-10-981-356A-18
```

```
Query Match          77.8%; Score 63; DB 9; Length 17;
Best Local Similarity 70.6%; Pred. No. 0.00029;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 KSSQSVFFSSSQKNYLA 17
       ::|||:|||||
DB      1 RASQSVLYSSNQKNYLA 17
```

```
RESULT 28
US-11-096-046-18
; Sequence 18, Application US/11096046
; Publication No. US20050276802A1
; GENERAL INFORMATION:
; APPLICANT: ADAMS, CAMELIA W.
; APPLICANT: FERRARA, NAPOLEONE
; APPLICANT: FILVAROFF, ELLEN H.
; APPLICANT: MAO, WEIGUANG
; APPLICANT: PRESTA, LEONARD G.
; APPLICANT: TEJADA, MAX L.
; TITLE OF INVENTION: Humanized Anti-TGF-Beta Antibodies
; FILE REFERENCE: P1954RIUS
; CURRENT APPLICATION NUMBER: US/11/096,046
; CURRENT FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: US 60/558,290
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 18
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-096-046-18
```

```
Query Match          77.8%; Score 63; DB 11; Length 17;
Best Local Similarity 70.6%; Pred. No. 0.00029;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 KSSQSVFFSSSQKNYLA 17
       ::|||:|||||
DB      1 RASQSVLYSSNQKNYLA 17
```

```
RESULT 29
US-10-981-356A-3
; Sequence 3, Application US/10981356A
; Publication No. US20060015952A1
; GENERAL INFORMATION:
; APPLICANT: FILVAROFF, ELLEN H.
; TITLE OF INVENTION: SCREENING ASSAYS AND METHODS OF TUMOR TREATMENT
; FILE REFERENCE: P2068R1
; CURRENT APPLICATION NUMBER: US/10/981,356A
; CURRENT FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: US 60/520,398
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/557,951
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 45
; SEQ ID NO 3
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-10-981-356A-3
```

```
; Query Match          77.8%; Score 63; DB 9; Length 116;
Best Local Similarity 70.6%; Pred. No. 0.002;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 KSSQSVFFSSSQKNYLA 17
       ::|||:|||||
DB      24 RASQSVLYSSNQKNYLA 40
```

```
RESULT 30
US-11-096-046-3
; Sequence 3, Application US/11096046
; Publication No. US20050276802A1
; GENERAL INFORMATION:
; APPLICANT: ADAMS, CAMELIA W.
; APPLICANT: FERRARA, NAPOLEONE
; APPLICANT: FILVAROFF, ELLEN H.
; APPLICANT: MAO, WEIGUANG
; APPLICANT: PRESTA, LEONARD G.
; APPLICANT: TEJADA, MAX L.
; TITLE OF INVENTION: Humanized Anti-TGF-Beta Antibodies
; FILE REFERENCE: P1954RIUS
; CURRENT APPLICATION NUMBER: US/11/096,046
; CURRENT FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: US 60/558,290
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 3
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-096-046-3
```

```
Query Match          77.8%; Score 63; DB 11; Length 116;
Best Local Similarity 70.6%; Pred. No. 0.002;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 KSSQSVFFSSSQKNYLA 17
       ::|||:|||||
DB      24 RASQSVLYSSNQKNYLA 40
```

```
RESULT 31
US-10-981-356A-25
; Sequence 25, Application US/10981356A
; Publication No. US20060015952A1
; GENERAL INFORMATION:
; APPLICANT: FILVAROFF, ELLEN H.
; TITLE OF INVENTION: SCREENING ASSAYS AND METHODS OF TUMOR TREATMENT
; FILE REFERENCE: P2068R1
; CURRENT APPLICATION NUMBER: US/10/981,356A
; CURRENT FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: US 60/520,398
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/557,951
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 45
; SEQ ID NO 25
; LENGTH: 666
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-10-981-356A-25
```

```
Query Match          77.8%; Score 63; DB 9; Length 666;
Best Local Similarity 70.6%; Pred. No. 0.012;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 KSSQSVFFSSSQKNYLA 17
```

```
Db      24 RASQSVLYSSNQKNYLA 40
      ::|||:|||||
RESULT 32
US-10-981-356A-27
; Sequence 27, Application US/10981356A
; Publication No. US20060015952A1
; GENERAL INFORMATION:
; APPLICANT: FILVAROFF, ELLEN H.
; TITLE OF INVENTION: SCREENING ASSAYS AND METHODS OF TUMOR TREATMENT
; FILE REFERENCE: P2068R1
; CURRENT APPLICATION NUMBER: US/10/981,356A
; PRIOR FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: US 60/520,398
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/557,951
; NUMBER OF SEQ ID NOS: 45
; SEQ ID NO 27
; LENGTH: 666
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-10-981-356A-27

Query Match      77.8%; Score 63; DB 9; Length 666;
Best Local Similarity 70.6%; Pred. No. 0.012;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      1 KSSQSVFFSSSQKNYLA 17
      ::|||:|||||
Db      24 RASQSVLYSSNQKNYLA 40

RESULT 33
US-10-981-356A-28
; Sequence 28, Application US/10981356A
; Publication No. US20060015952A1
; GENERAL INFORMATION:
; APPLICANT: FILVAROFF, ELLEN H.
; TITLE OF INVENTION: SCREENING ASSAYS AND METHODS OF TUMOR TREATMENT
; FILE REFERENCE: P2068R1
; CURRENT APPLICATION NUMBER: US/10/981,356A
; PRIOR FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: US 60/520,398
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/557,951
; NUMBER OF SEQ ID NOS: 45
; SEQ ID NO 28
; LENGTH: 666
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-10-981-356A-28

Query Match      77.8%; Score 63; DB 9; Length 666;
Best Local Similarity 70.6%; Pred. No. 0.012;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      1 KSSQSVFFSSSQKNYLA 17
      ::|||:|||||
Db      24 RASQSVLYSSNQKNYLA 40

RESULT 34
US-10-981-356A-30
; Sequence 30, Application US/10981356A
; Publication No. US20060015952A1
; GENERAL INFORMATION:
```

```
; APPLICANT: FILVAROFF, ELLEN H.
; TITLE OF INVENTION: SCREENING ASSAYS AND METHODS OF TUMOR TREATMENT
; FILE REFERENCE: P2068R1
; CURRENT APPLICATION NUMBER: US/10/981,356A
; PRIOR FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: US 60/520,398
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/557,951
; NUMBER OF SEQ ID NOS: 45
; SEQ ID NO 30
; LENGTH: 666
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-10-981-356A-30

Query Match      77.8%; Score 63; DB 9; Length 666;
Best Local Similarity 70.6%; Pred. No. 0.012;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      1 KSSQSVFFSSSQKNYLA 17
      ::|||:|||||
Db      24 RASQSVLYSSNQKNYLA 40

RESULT 35
US-11-096-046-27
; Sequence 27, Application US/11096046
; Publication No. US20050276802A1
; GENERAL INFORMATION:
; APPLICANT: ADAMS, CAMELLIA W.
; APPLICANT: FERRARA, NAPOLEONE
; APPLICANT: FILVAROFF, ELLEN H.
; APPLICANT: MAO, WEIGUANG
; APPLICANT: PRESTA, LEONARD G.
; TITLE OF INVENTION: Humanized Anti-TGF-Beta Antibodies
; FILE REFERENCE: P1954R1US
; CURRENT APPLICATION NUMBER: US/11/096,046
; PRIOR FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: US 60/558,290
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 27
; LENGTH: 666
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-096-046-27

Query Match      77.8%; Score 63; DB 11; Length 666;
Best Local Similarity 70.6%; Pred. No. 0.012;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      1 KSSQSVFFSSSQKNYLA 17
      ::|||:|||||
Db      24 RASQSVLYSSNQKNYLA 40

RESULT 36
US-11-096-046-25
; Sequence 25, Application US/11096046
; Publication No. US20050276802A1
; GENERAL INFORMATION:
; APPLICANT: ADAMS, CAMELLIA W.
; APPLICANT: FERRARA, NAPOLEONE
; APPLICANT: FILVAROFF, ELLEN H.
; APPLICANT: MAO, WEIGUANG
; APPLICANT: PRESTA, LEONARD G.
; APPLICANT: TEJADA, MAX L.
```

```
; TITLE OF INVENTION: Humanized Anti-TGF-Beta Antibodies
; FILE REFERENCE: P1954RIUS
; CURRENT APPLICATION NUMBER: US/11/096,046
; CURRENT FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: US 60/558,290
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 25
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
; NAME/KEY: Unsure
; LOCATION: 220
; OTHER INFORMATION: Unknown amino acid
US-11-096-046-25
```

```
Query Match          77.8%; Score 63; DB 11; Length 667;
Best Local Similarity 70.6%; Pred. No. 0.012;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 KSSQSVFFSSSQKNYLA 17
       ::|||:|||||
Db      24 RASQSVLYSSNQKNYLA 40
```

```
RESULT 37
US-11-096-046-28
; Sequence 28, Application US/11096046
; Publication No. US20050276802A1
; GENERAL INFORMATION:
; APPLICANT: ADAMS, CAMELLIA W.
; APPLICANT: FERRARA, NAPOLEONE
; APPLICANT: FILVAROFF, ELLEN H.
; APPLICANT: MAO, WEIGUANG
; APPLICANT: PRESTA, LEONARD G.
; APPLICANT: TEJADA, MAX L.
; TITLE OF INVENTION: Humanized Anti-TGF-Beta Antibodies
; FILE REFERENCE: P1954RIUS
; CURRENT APPLICATION NUMBER: US/11/096,046
; CURRENT FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: US 60/558,290
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 28
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
; NAME/KEY: Unsure
; LOCATION: 220
; OTHER INFORMATION: Unknown amino acid
US-11-096-046-28
```

```
Query Match          77.8%; Score 63; DB 11; Length 667;
Best Local Similarity 70.6%; Pred. No. 0.012;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
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```
QY      1 KSSQSVFFSSSQKNYLA 17
       ::|||:|||||
Db      24 RASQSVLYSSNQKNYLA 40
```

```
RESULT 38
US-11-096-046-30
; Sequence 30, Application US/11096046
; Publication No. US20050276802A1
; GENERAL INFORMATION:
; APPLICANT: ADAMS, CAMELLIA W.
```

```
; APPLICANT: FERRARA, NAPOLEONE
; APPLICANT: FILVAROFF, ELLEN H.
; APPLICANT: MAO, WEIGUANG
; APPLICANT: PRESTA, LEONARD G.
; APPLICANT: TEJADA, MAX L.
; TITLE OF INVENTION: Humanized Anti-TGF-Beta Antibodies
; FILE REFERENCE: P1954RIUS
; CURRENT APPLICATION NUMBER: US/11/096,046
; CURRENT FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: US 60/558,290
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 30
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
; NAME/KEY: Unsure
; LOCATION: 220
; OTHER INFORMATION: Unknown amino acid
US-11-096-046-30
```

```
Query Match          77.8%; Score 63; DB 11; Length 667;
Best Local Similarity 70.6%; Pred. No. 0.012;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 KSSQSVFFSSSQKNYLA 17
       ::|||:|||||
Db      24 RASQSVLYSSNQKNYLA 40
```

```
RESULT 39
US-10-981-356A-26
; Sequence 26, Application US/10981356A
; Publication No. US20060015952A1
; GENERAL INFORMATION:
; APPLICANT: FILVAROFF, ELLEN H.
; TITLE OF INVENTION: SCREENING ASSAYS AND METHODS OF TUMOR TREATMENT
; FILE REFERENCE: P2068RI
; CURRENT APPLICATION NUMBER: US/10/981,356A
; CURRENT FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: US 60/520,398
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/557,951
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 45
; SEQ ID NO 26
; LENGTH: 692
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-10-981-356A-26
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```
Query Match          77.8%; Score 63; DB 9; Length 692;
Best Local Similarity 70.6%; Pred. No. 0.013;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
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```
QY      1 KSSQSVFFSSSQKNYLA 17
       ::|||:|||||
Db      24 RASQSVLYSSNQKNYLA 40
```

```
RESULT 40
US-11-096-046-26
; Sequence 26, Application US/11096046
; Publication No. US20050276802A1
; GENERAL INFORMATION:
; APPLICANT: ADAMS, CAMELLIA W.
; APPLICANT: FERRARA, NAPOLEONE
; APPLICANT: FILVAROFF, ELLEN H.
```

```

; APPLICANT: MAO, WEIGUANG
; APPLICANT: PRESTA, LEONARD G.
; APPLICANT: TEJADA, MAX L.
; TITLE OF INVENTION: Humanized Anti-TGF-Beta Antibodies
; FILE REFERENCE: P1954R1US
; CURRENT APPLICATION NUMBER: US/11/096,046
; CURRENT FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: US 60/558,290
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 26
; LENGTH: 695
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
; NAME/KEY: Unsure
; LOCATION: 220, 668, 673
; OTHER INFORMATION: Unknown amino acid
; US-11-096-046-26

Query Match      77.8%; Score 63; DB 11; Length 695;
Best Local Similarity 70.6%; Pred. No. 0.013;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      1 KSSQSVFFSSQKNYLA 17
Db      24 RASQSVLYSSNQKNYLA 40

RESULT 41
; US-11-239-510-23
; Sequence 23, Application US/11239510
; Publication No. US20060063715A1
; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; Wood, James F.
; Hardman, Karl
; Bird, Robert
; Filpula, David
; Rolence, Michelle
; TITLE OF INVENTION: Multivalent Antigen-Binding Proteins
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, NW
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/239,510
; FILING DATE: 29-Sep-2005
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/10/137,297
; FILING DATE: 03-May-2002
; APPLICATION NUMBER: US/09/443,213
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 09/166,094
; FILING DATE: 05-OCT-1998
; APPLICATION NUMBER: US 08/392,338
; FILING DATE: 22-FEB-1995
; APPLICATION NUMBER: US 07/989,846
; FILING DATE: 20-NOV-1992
; APPLICATION NUMBER: US 07/796,936
; FILING DATE: 25-NOV-1991

```

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0977.003000E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 242 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
; US-11-239-510-23

Query Match      76.5%; Score 62; DB 11; Length 242;
Best Local Similarity 70.6%; Pred. No. 0.0063;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      1 KSSQSVFFSSQKNYLA 17
Db      24 RASQSVLYSSNQKNYLA 40

RESULT 42
; US-11-239-510-13
; Sequence 13, Application US/11239510
; Publication No. US20060063715A1
; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; Wood, James F.
; Hardman, Karl
; Bird, Robert
; Filpula, David
; Rolence, Michelle
; TITLE OF INVENTION: Multivalent Antigen-Binding Proteins
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, NW
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/239,510
; FILING DATE: 29-Sep-2005
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/10/137,297
; FILING DATE: 03-May-2002
; APPLICATION NUMBER: US/09/443,213
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 09/166,094
; FILING DATE: 05-OCT-1998
; APPLICATION NUMBER: US 08/392,338
; FILING DATE: 22-FEB-1995
; APPLICATION NUMBER: US 07/989,846
; FILING DATE: 20-NOV-1992
; APPLICATION NUMBER: US 07/796,936
; FILING DATE: 25-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0977.003000E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600

```

TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 244 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-11-239-510-13

Query Match 76.5%; Score 62; DB 11; Length 244;
Best Local Similarity 70.6%; Pred. No. 0.0064;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 KSSQSVFFSSQKNTLA 17
| | | | | : | : | | | | |
Db 24 KSSQSLVYSGNQKNTLA 40

RESULT 43
US-11-239-510-19
Sequence 19, Application US/11239510
Publication No. US20060063715A1
GENERAL INFORMATION:
APPLICANT: Whitlow, Marc
Wood, James F.
Hardman, Karl
Bird, Robert
Filipula, David
Rollence, Michelle
TITLE OF INVENTION: Multivalent Antigen-Binding Proteins
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSER: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, NW
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/239,510
FILING DATE: 29-Sep-2005
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/137,297
FILING DATE: 03-May-2002
APPLICATION NUMBER: US/09/443,213
FILING DATE: <Unknown>
APPLICATION NUMBER: US 09/166,094
FILING DATE: 05-OCT-1998
APPLICATION NUMBER: US 08/392,338
FILING DATE: 22-FEB-1995
APPLICATION NUMBER: US 07/989,846
FILING DATE: 20-NOV-1992
APPLICATION NUMBER: US 07/796,936
FILING DATE: 25-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0977.003000E
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 483 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-11-239-510-19

Query Match 76.5%; Score 62; DB 11; Length 483;
Best Local Similarity 70.6%; Pred. No. 0.013;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 KSSQSVFFSSQKNTLA 17
| | | | | : | : | | | | |
Db 24 KSSQSLVYSGNQKNTLA 40

RESULT 44
US-10-834-397-31
Sequence 31, Application US/10834397
Publication No. US2006000334A1
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSER: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/834,397
FILING DATE: 29-Apr-2004
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-Jan-2000
APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-10-834-397-31

Query Match 75.3%; Score 61; DB 9; Length 115;
Best Local Similarity 70.6%; Pred. No. 0.0043;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 KSSQSVFFSSQKNTLA 17
| | | | | : | : | | | | |
Db 24 KSSQSLVYSGNQKNTLA 40

RESULT 45
US-10-834-397-49
; Sequence 49, Application US/10834397
; Publication No. US20060003334A1
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckhuhn, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/834,397
; FILING DATE: 29-Apr-2004
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,324
; FILING DATE: 24-Jan-2000
; APPLICATION NUMBER: US/09/025,769
; FILING DATE: 18-Feb-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-Aug-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 115 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 49:
US-10-834-397-49
Query Match 75.3%; Score 61; DB 9; Length 115;
Best Local Similarity 70.6%; Pred. No. 0.0043;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 KSSQSVFSSSQKNYLA 17
;|||||:|||||
DB 24 RSSQSVLYSSNNKNYLA 40
RESULT 46
US-11-158-505-35
; Sequence 35, Application US/11158505
; Publication No. US20060002921A1
; GENERAL INFORMATION:
; APPLICANT: WINSOR-HINES, DAMN
; APPLICANT: RAO, PATRICIA
; APPLICANT: RINGIER, DOUGLAS J
; APPLICANT: PONATH, PAUL
; TITLE OF INVENTION: OPTIMIZED DOSING OF ANTI-CD4 ANTIBODIES FOR TOLERANCE
; TITLE OF INVENTION: INDUCTION IN PRIMATES
; FILE REFERENCE: T1N-031

; CURRENT APPLICATION NUMBER: US/11/158,505
; CURRENT FILING DATE: 2005-06-21
; PRIOR APPLICATION NUMBER: 60/582,181
; PRIOR FILING DATE: 2004-06-22
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 35
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-158-505-35
Query Match 75.3%; Score 61; DB 11; Length 135;
Best Local Similarity 70.6%; Pred. No. 0.0051;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 KSSQSVFSSSQKNYLA 17
;|||||:|||||
DB 44 KSSQSVLYSSNNKNYLA 60
RESULT 47
US-10-512-184-33
; Sequence 33, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antitoxins, recombinant plant disease
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: gctv p12 with
; OTHER INFORMATION: specifically against Phoma lingam; originates from
US-10-512-184-33
Query Match 74.1%; Score 60; DB 9; Length 259;
Best Local Similarity 70.6%; Pred. No. 0.014;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 KSSQSVFSSSQKNYLA 17
;|||||:|||||
DB 161 KFSQSVLYSSNNKNYLA 177
RESULT 48
US-10-512-184-34
; Sequence 34, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antitoxins, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: scFv PL2 with
 OTHER INFORMATION: specificity against Phoma lingam; originates from
 OTHER INFORMATION: Mus musculus.
 US-10-512-184-34

Query Match 74.1%; Score 60; DB 9; Length 259;
 Best Local Similarity 76.5%; Pred. No. 0.014;
 Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 KSSQSVFSSSQKNYLA 17
 |||||:|||||
 DB 168 KSSQSLNSSNQKNYLA 184

RESULT 49
 US-10-512-184-70
 ; Sequence 70, Application US/10512184
 ; Publication No. US20050244901A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Fraunhofer Gesellschaft zur Forderung der angewandten Forschung e.V.
 ; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
 ; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
 ; TITLE OF INVENTION: resistance against fungi
 ; FILE REFERENCE: 3581.01US01
 ; CURRENT APPLICATION NUMBER: US/10/512,184
 ; CURRENT FILING DATE: 2004-10-22
 ; NUMBER OF SEQ ID NOS: 72
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 70
 ; LENGTH: 329
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: precursor
 ; OTHER INFORMATION: fusion protein comprising RS - linker - scFv VDM2.
 US-10-512-184-70

Query Match 74.1%; Score 60; DB 9; Length 329;
 Best Local Similarity 70.6%; Pred. No. 0.018;
 Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 KSSQSVFSSSQKNYLA 17
 |||||:|||||
 DB 231 KFSQSLYSSNQKNYLA 247

RESULT 50
 US-10-512-184-71
 ; Sequence 71, Application US/10512184
 ; Publication No. US20050244901A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Fraunhofer Gesellschaft zur Forderung der angewandten Forschung e.V.
 ; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
 ; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
 ; TITLE OF INVENTION: resistance against fungi
 ; FILE REFERENCE: 3581.01US01
 ; CURRENT APPLICATION NUMBER: US/10/512,184
 ; CURRENT FILING DATE: 2004-10-22
 ; NUMBER OF SEQ ID NOS: 72
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 71
 ; LENGTH: 371
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: precursor
 ; OTHER INFORMATION: fusion protein comprising ACE - linker -
 ; OTHER INFORMATION: scFv PL2.
 US-10-512-184-71

Query Match 74.1%; Score 60; DB 9; Length 371;
 Best Local Similarity 76.5%; Pred. No. 0.021;
 Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KSSQSVFSSSQKNYLA 17
 |||||:|||||
 DB 280 KSSQSLNSSNQKNYLA 296

Search completed: May 4, 2006, 13:54:22
 Job time : 24.6984 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 4, 2006, 12:46:10 ; Search time 62.2222 Seconds
(without alignments)
49.430 Million cell updates/sec

Title: US-10-700-632-5
Perfect score: 38
Sequence: 1 WASTRES 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A: Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	100.0	7	2	AAR30157 MAB GAH v
2	38	100.0	7	2	AAR57966 MAB NPS2
3	38	100.0	7	2	AAR50317 MAB NPS2
4	38	100.0	7	2	AAR57964 MAB NPS2
5	38	100.0	7	2	AAV08713 Human m1
6	38	100.0	7	3	AAV95234 Human m1
7	38	100.0	7	3	AAV32227 G-CSF ago
8	38	100.0	7	3	AAV07952 CDR2 sequ
9	38	100.0	7	5	AAU81257 Human trk
10	38	100.0	7	5	ABP62361 Human imm
11	38	100.0	7	5	AAE29275 Anti-ClfA
12	38	100.0	7	5	ABG68854 CDR2 VL P
13	38	100.0	7	5	AAU70347 Mouse Kap
14	38	100.0	7	5	AAU70335 Human Kap
15	38	100.0	7	6	AAE34369 Escherich
16	38	100.0	7	6	ABP98689 Human GAH
17	38	100.0	7	6	ABP98681 Human GAH
18	38	100.0	7	6	ABG71653 CDR2 of H
19	38	100.0	7	6	AA38110 Human COU
20	38	100.0	7	7	ABO33872 Anti-GPI-
21	38	100.0	7	7	ABO33869 Anti-GPI-
22	38	100.0	7	7	ADC97709 Mouse mon
23	38	100.0	7	7	ADG43867 Human pep
24	38	100.0	7	8	ADL23027 Myelin as

25	38	100.0	7	8	ADO32089 Mouse ant
26	38	100.0	7	8	ADO58066 S2 cell d
27	38	100.0	7	8	ADP47268 Human pho
28	38	100.0	7	8	ADP47250 Human pho
29	38	100.0	7	8	ADP47241 Human pho
30	38	100.0	7	8	ADP47271 Human pho
31	38	100.0	7	8	ADP47286 Human pho
32	38	100.0	7	8	ADQ28264 Method of
33	38	100.0	7	8	ADS88787 Light cha
34	38	100.0	7	8	ADT50351 Human mon
35	38	100.0	7	9	ADV21417 Human ant
36	38	100.0	7	9	ADW47139 Anti-CD20
37	38	100.0	7	9	ADW77439 Human pla
38	38	100.0	7	9	ADW77433 Human pla
39	38	100.0	7	9	ADX98304 Human ant
40	38	100.0	7	9	ADX98299 Human ant
41	38	100.0	7	9	ADY59130 Anti-TAg-
42	38	100.0	7	9	ADY59136 Human mon
43	38	100.0	7	9	ADY58494 Peptide u
44	38	100.0	7	9	ADZ45515 Murine fa
45	38	100.0	7	9	ADZ45538 Murine fa
46	38	100.0	7	9	ADZ35818 Anti-glyc
47	38	100.0	7	9	ADZ35815 Anti-glyc
48	38	100.0	7	9	AEA38789 Humanized
49	38	100.0	7	9	AEA38759 Humanized
50	38	100.0	7	9	AE823167 Antibody
51	38	100.0	12	8	ADO32134 Mouse ant
52	38	100.0	15	5	ABG68859 CDR2 sequ
53	38	100.0	17	8	ADR38445 Human N-t
54	38	100.0	82	2	AAW62807 Amino aci
55	38	100.0	84	2	AAW14491 Monoclonal
56	38	100.0	84	2	AAV99878 Monoclonal
57	38	100.0	94	3	AAV56669 Partial p
58	38	100.0	94	8	ADU04213 Human imm
59	38	100.0	94	8	ADU04221 Human imm
60	38	100.0	98	7	ADC99827 Anti-huma
61	38	100.0	98	7	ADD05431 Anti-MUC1
62	38	100.0	98	7	ADP09869 Anti-MUC1
63	38	100.0	99	8	ADO32144 Mouse ant
64	38	100.0	101	6	ABJ18696 Antibody
65	38	100.0	101	6	ABO27156 Human ger
66	38	100.0	101	7	ADC99826 Germ line
67	38	100.0	101	7	ADD05430 Anti-MUC1
68	38	100.0	101	7	ADP10202 Anti-body
69	38	100.0	101	7	ADF09998 Anti-body
70	38	100.0	101	7	ADP10100 VEGF anti
71	38	100.0	101	7	ADF09868 Anti-MUC1
72	38	100.0	101	9	ADJ80276 Human ant
73	38	100.0	101	8	ADJ80275 Human ant
74	38	100.0	101	9	ADY75450 Human ger
75	38	100.0	101	9	ABE13654 Human var
76	38	100.0	101	5	ABE20819 Human var
77	38	100.0	105	5	ABB07184 MS119E5 I
78	38	100.0	105	8	AD126684 Human ant
79	38	100.0	107	2	AAW80814 Amino aci
80	38	100.0	107	2	AAW80817 Amino aci
81	38	100.0	107	2	AAV17955 Human Kap
82	38	100.0	108	6	AAE38116 Human can
83	38	100.0	109	7	ABO33830 Human ant
84	38	100.0	109	9	ABO33827 Human ant
85	38	100.0	109	9	ADZ35773 Anti-glyc
86	38	100.0	109	9	ADZ35776 Anti-glyc
87	38	100.0	110	2	AAR30012 Light cha
88	38	100.0	110	2	AAW56520 Anti-DNA
89	38	100.0	110	2	AAW56517 H221 anti
90	38	100.0	110	8	ADN08040 Human ant
91	38	100.0	111	2	AAW52059 Light cha
92	38	100.0	111	6	ABR42303 Mouse mon
93	38	100.0	111	6	ABR42302 Mouse mon
94	38	100.0	112	2	AAW28807 S48 VL 3
95	38	100.0	112	2	AAW54932 FC recept
96	38	100.0	112	2	AAW54933 MAB 022 V
97	38	100.0	112	5	ABG76524 HCV E1 an

98	38	100.0	112	5	ABG76548	Abg76548 HCV E1 an
99	38	100.0	112	5	ABG76514	Abg76514 HCV E1 an
100	38	100.0	112	5	AAE29270	AAE29270 S. aureus
101	38	100.0	112	5	AAE29268	AAE29268 S. aureus
102	38	100.0	112	5	AAE29264	AAE29264 S. aureus
103	38	100.0	112	5	AAE29266	AAE29266 S. aureus
104	38	100.0	112	8	ADP03685	Adp03685 Human ant
105	38	100.0	112	8	ADT02527	Adt02527 Anti-CD22
106	38	100.0	112	8	ADU39970	Adu39970 Anti-body
107	38	100.0	113	2	AAE25407	AAE25407 Light cha
108	38	100.0	113	2	AAE50322	AAE50322 MAb NFS2
109	38	100.0	113	2	AAE50314	AAE50314 Humanised
110	38	100.0	113	2	AAE50313	AAE50313 Humanised
111	38	100.0	113	2	AAE59513	AAE59513 Sequence
112	38	100.0	113	2	AAE92215	AAE92215 Lf2 MAb V
113	38	100.0	113	2	AAE92217	AAE92217 Humanised
114	38	100.0	113	2	AAW27695	AAW27695 Variable
115	38	100.0	113	2	AAW50145	AAW50145 Antibody
116	38	100.0	113	2	AAW50143	AAW50143 Antibody
117	38	100.0	113	2	AAW50144	AAW50144 Antibody
118	38	100.0	113	2	AAW21818	AAW21818 11E10 ant
119	38	100.0	113	3	AAW90819	AAW90819 260F9 Hyb
120	38	100.0	113	3	AAW18873	AAW18873 Amino aci
121	38	100.0	113	3	AAW18877	AAW18877 Amino aci
122	38	100.0	113	3	AAW18855	AAW18855 Amino aci
123	38	100.0	113	3	AAW18871	AAW18871 Amino aci
124	38	100.0	113	3	AAW18857	AAW18857 Amino aci
125	38	100.0	113	3	AAW18859	AAW18859 Amino aci
126	38	100.0	113	3	AAW18861	AAW18861 Amino aci
127	38	100.0	113	3	AAW18879	AAW18879 Amino aci
128	38	100.0	113	3	AAW18869	AAW18869 Amino aci
129	38	100.0	113	3	AAW18881	AAW18881 Amino aci
130	38	100.0	113	3	AAW18863	AAW18863 Amino aci
131	38	100.0	113	3	AAW18875	AAW18875 Amino aci
132	38	100.0	113	4	AAW62769	AAW62769 Human HIV
133	38	100.0	113	6	ABW89748	ABW89748 Human res
134	38	100.0	113	6	ABW89749	ABW89749 Human res
135	38	100.0	113	6	ABW89747	ABW89747 Human res
136	38	100.0	113	6	ABW89877	ABW89877 Human res
137	38	100.0	113	6	ABW89874	ABW89874 Human res
138	38	100.0	113	6	ABW89875	ABW89875 Human res
139	38	100.0	113	6	ABW89876	ABW89876 Human res
140	38	100.0	113	6	ABW89877	ABW89877 Human res
141	38	100.0	113	6	ABW89878	ABW89878 Human res
142	38	100.0	113	6	ABW89879	ABW89879 Human res
143	38	100.0	113	6	ABW89880	ABW89880 Human res
144	38	100.0	113	6	ABW89881	ABW89881 Human res
145	38	100.0	113	6	ABW89882	ABW89882 Human res
146	38	100.0	113	6	ABW89883	ABW89883 Human res
147	38	100.0	113	6	ABW89884	ABW89884 Human res
148	38	100.0	113	6	ABW89885	ABW89885 Human res
149	38	100.0	113	6	ABW89886	ABW89886 Human res
150	38	100.0	113	6	ABW89887	ABW89887 Human res
151	38	100.0	113	6	ABW89888	ABW89888 Human res
152	38	100.0	113	6	ABW89889	ABW89889 Human res
153	38	100.0	113	6	ABW89890	ABW89890 Human res
154	38	100.0	113	6	ABW89891	ABW89891 Human res
155	38	100.0	113	6	ABW89892	ABW89892 Human res
156	38	100.0	113	6	ABW89893	ABW89893 Human res
157	38	100.0	113	6	ABW89894	ABW89894 Human res
158	38	100.0	113	6	ABW89895	ABW89895 Human res
159	38	100.0	113	6	ABW89896	ABW89896 Human res
160	38	100.0	113	6	ABW89897	ABW89897 Human res
161	38	100.0	113	6	ABW89898	ABW89898 Human res
162	38	100.0	113	6	ABW89899	ABW89899 Human res
163	38	100.0	113	6	ABW89900	ABW89900 Human res
164	38	100.0	113	6	ABW89901	ABW89901 Human res
165	38	100.0	113	6	ABW89902	ABW89902 Human res
166	38	100.0	113	6	ABW89903	ABW89903 Human res
167	38	100.0	113	6	ABW89904	ABW89904 Human res
168	38	100.0	113	6	ABW89905	ABW89905 Human res
169	38	100.0	113	6	ABW89906	ABW89906 Human res
170	38	100.0	113	6	ABW89907	ABW89907 Human res

244	38	100.0	116	9	ADx02149	SARS	coro	317	38	100.0	141	2	AAy24374	Human mon
245	38	100.0	116	9	ADx02201	SARS	coro	318	38	100.0	144	9	ADw47080	Light cha
246	38	100.0	116	9	ADx02077	SARS	coro	319	38	100.0	147	2	AAw09817	Pelb-VL4
247	38	100.0	116	9	ADx02177	SARS	coro	320	38	100.0	147	2	AAy34314	Igm antiB
248	38	100.0	116	9	ADx02185	SARS	coro	321	38	100.0	148	1	AAp93078	Light cha
249	38	100.0	116	9	ADx02089	SARS	coro	322	38	100.0	149	8	ADK52402	Igm antiB
250	38	100.0	116	9	ADx02141	SARS	coro	323	38	100.0	149	8	ADK52402	Human ant
251	38	100.0	116	9	ADx02133	SARS	coro	324	38	100.0	149	8	ADy21959	Antibody
252	38	100.0	116	9	ADx02129	SARS	coro	325	38	100.0	153	3	AEa17763	Hybridoma
253	38	100.0	116	9	ADx02061	SARS	coro	326	38	100.0	154	3	AAb53686	Human col
254	38	100.0	116	9	ADx02085	SARS	coro	327	38	100.0	154	6	AB004851	Human epi
255	38	100.0	116	9	ADx02169	SARS	coro	328	38	100.0	154	8	ADK52342	Human ant
256	38	100.0	116	9	ADx02105	SARS	coro	329	38	100.0	154	8	AEa17778	Hybridoma
257	38	100.0	116	9	ADx02137	SARS	coro	330	38	100.0	155	2	AAW32483	Kappa 1:9
258	38	100.0	116	9	ADx02157	SARS	coro	331	38	100.0	155	2	AAy06912	Human var
259	38	100.0	116	9	ADx02161	SARS	coro	332	38	100.0	157	6	AB004855	Human epi
260	38	100.0	116	9	ADx02173	SARS	coro	333	38	100.0	157	9	AEa17779	Hybridoma
261	38	100.0	116	9	ADx02053	SARS	coro	334	38	100.0	159	8	ADK52382	Human ant
262	38	100.0	116	9	ADx02153	SARS	coro	335	38	100.0	159	8	ADK52410	Human ant
263	38	100.0	116	9	ADx02193	SARS	coro	336	38	100.0	159	8	ADK52302	Human ant
264	38	100.0	116	9	ADx02145	SARS	coro	337	38	100.0	159	8	AEa17767	Hybridoma
265	38	100.0	116	9	ADx02165	SARS	coro	338	38	100.0	161	7	ADG46871	Protein e
266	38	100.0	116	9	AEa38741	Murine an		339	38	100.0	163	8	ADK52310	Human ant
267	38	100.0	116	9	AEa38743	Humanized		340	38	100.0	163	8	ADK52346	Human ant
268	38	100.0	117	9	ADx02109	SARS	coro	341	38	100.0	163	8	ADK52394	Human ant
269	38	100.0	119	9	ABB07172	ebvH1gM M		342	38	100.0	163	8	ADK52398	Human ant
270	38	100.0	119	8	AD126660	Human ant		343	38	100.0	166	7	ADD28248	Human het
271	38	100.0	120	4	AAg65565	Amino aci		344	38	100.0	166	9	AAr38635	Bacillus
272	38	100.0	120	4	AAg65565	Amino aci		345	38	100.0	171	2	AAr38320	Sequence
273	38	100.0	122	8	AD126708	Human ant		346	38	100.0	171	2	AAy50693	Plasmid p
274	38	100.0	124	2	AAy57181	Amino aci		347	38	100.0	171	2	AAy57184	Amino aci
275	38	100.0	126	6	ABR55903	Human mab		348	38	100.0	173	8	ADK52438	Human ant
276	38	100.0	128	3	AAy56734	Amino aci		349	38	100.0	173	8	ADK52430	Human ant
277	38	100.0	130	6	AAE34366	Escherich		350	38	100.0	179	8	ADK52434	Human ant
278	38	100.0	132	2	AAW21651	Humanized		351	38	100.0	208	7	ADD05282	Female mo
279	38	100.0	132	3	AAE07964	Amino aci		352	38	100.0	211	5	ABP43134	Human ova
280	38	100.0	132	3	AAE07966	A light c		353	38	100.0	214	9	ABP43144	Human ant
281	38	100.0	132	9	ABE08042	H1A-DR sp		354	38	100.0	218	7	ADD05274	Female mo
282	38	100.0	133	1	AAE08094	V region		355	38	100.0	218	8	ADMO80365	Murine ho
283	38	100.0	133	2	AAE59509	Sequence		356	38	100.0	219	2	AAr44495	Sequence
284	38	100.0	133	2	AAE59511	Sequence		357	38	100.0	220	2	AAW07528	Anti-HGF
285	38	100.0	133	2	AAE48633	Sequence		358	38	100.0	220	2	AAy50172	Anti-body
286	38	100.0	133	3	AAy50154	Murine mo		359	38	100.0	220	2	AAy08601	JP1112785
287	38	100.0	133	3	AAy83647	Consensus		360	38	100.0	220	8	ADK52386	Human res
288	38	100.0	133	8	ABG71660	Abp71660		361	38	100.0	220	8	ADK52334	Human ant
289	38	100.0	133	8	ADP12956	Protein e		362	38	100.0	228	7	ADBE4203	IL2LC pro
290	38	100.0	133	9	ADy92466	Mouse SMS		363	38	100.0	238	8	ADL23052	Mouse/hum
291	38	100.0	133	9	ADy98529	Novel chl		364	38	100.0	238	8	ADL23055	Humanised
292	38	100.0	133	9	ADx98264	Human ant		365	38	100.0	238	8	ADK588793	A mouse/h
293	38	100.0	134	2	AAE30485	Human ant		366	38	100.0	238	8	ADK588804	Humanised
294	38	100.0	134	2	AAE30485	V kappa r		367	38	100.0	238	9	ABE08041	Murine/hu
295	38	100.0	134	2	AAE38317	Sequence		368	38	100.0	239	9	ADy92470	SMS-1 chi
296	38	100.0	134	2	AAE81841	E-selecti		369	38	100.0	239	9	ADy98533	Novel chl
297	38	100.0	134	2	AAE81838	E-selecti		370	38	100.0	240	2	AAy50156	Chimeric
298	38	100.0	134	2	AAW06206	Xenograft		371	38	100.0	240	4	AAy50161	Human res
299	38	100.0	134	2	AAy50690	Human Hum		372	38	100.0	240	4	AAU00815	Human imm
300	38	100.0	134	6	ABW74792	Anti-CA12		373	38	100.0	240	9	ADW23408	Human L61
301	38	100.0	134	6	ADB17730	Human Hum		374	38	100.0	240	9	ADZ51047	Amino aci
302	38	100.0	134	7	ADG46850	Human Hum		375	38	100.0	240	9	ADZ56181	Protein s
303	38	100.0	135	6	AAE03714	Immunoglo		376	38	100.0	241	9	AEA41033	Human ant
304	38	100.0	135	6	ADA47343	Human ant		377	38	100.0	241	2	AAE28809	Vecfor pM
305	38	100.0	135	7	ADB72875	Human AAA		378	38	100.0	241	9	ADy92478	SMS-1 hum
306	38	100.0	135	8	ADP88458	Human ant		379	38	100.0	241	9	ADy98541	Novel chl
307	38	100.0	135	8	AD087927	Human HSI		380	38	100.0	241	9	ADW23426	Human L55
308	38	100.0	135	9	ADy92474	SMS-1 hum		381	38	100.0	242	4	AAU80338	Human m1l
309	38	100.0	135	9	ADy98537	Novel chl		382	38	100.0	242	4	AAU97949	HMGFI Fab
310	38	100.0	137	2	AAW21653	Mouse Mab		383	38	100.0	242	4	AAU80039	HMGFI Fab
311	38	100.0	137	2	AAW21655	Chimeric		384	38	100.0	242	6	ADA91406	Anti-Abet
312	38	100.0	137	2	AAW10544	Humanised		385	38	100.0	244	3	AAy96305	Human IGF
313	38	100.0	137	2	AAW10545	Humanised		386	38	100.0	244	8	ADG17481	Anti-CD22
314	38	100.0	137	5	ABP62187	Wild type		387	38	100.0	244	8	ADG17477	Anti-CD22
315	38	100.0	137	5	ABP62187	Human Imm		388	38	100.0	244	8	ADG17487	Anti-CD22
316	38	100.0	139	2	AAE99469	Monoclonal		389	38	100.0	244	8	ADG17479	Anti-CD22

390	38	100.0	244	8	ADG17482	Adg17482	Anti-CD22
391	38	100.0	244	8	ADG17483	Adg17483	Anti-CD22
392	38	100.0	244	8	ADG17485	Adg17485	Anti-CD22
393	38	100.0	244	8	ADG17476	Adg17476	Anti-CD22
394	38	100.0	244	8	ADG17480	Adg17480	Anti-CD22
395	38	100.0	244	8	ADG17486	Adg17486	Anti-CD22
396	38	100.0	244	8	ADG17478	Adg17478	Anti-CD22
397	38	100.0	244	8	ADG17484	Adg17484	Anti-CD22
398	38	100.0	244	8	ADG59117	Adg59117	Anti-K88/
399	38	100.0	246	8	ADG27057	Adg27057	Human ant
400	38	100.0	247	7	ADC03132	Adc03132	Colon spe
401	38	100.0	247	7	ADG76001	Adg76001	huHMG1 (
402	38	100.0	248	2	AAI17964	Aai17964	Mouse scf
403	38	100.0	249	2	AAW60770	Aaw60770	Single ch
404	38	100.0	250	8	ADi61980	Adi61980	Human scf
405	38	100.0	251	2	AAAR48632	Aar48632	Sequence
406	38	100.0	251	4	AAH74793	Aah74793	Single ch
407	38	100.0	251	8	ADY21486	Ady21486	Mature fo
408	38	100.0	252	8	ADG58062	Adg58062	S2 cell d
409	38	100.0	252	9	ADX01996	Adx01996	SARS coro
410	38	100.0	252	9	ADX01974	Adx01974	SARS coro
411	38	100.0	252	9	ADX02024	Adx02024	SARS coro
412	38	100.0	252	9	ADX01970	Adx01970	SARS coro
413	38	100.0	252	9	ADX02010	Adx02010	SARS coro
414	38	100.0	252	9	ADX01998	Adx01998	SARS coro
415	38	100.0	252	9	ADX02000	Adx02000	SARS coro
416	38	100.0	252	9	ADX02004	Adx02004	SARS coro
417	38	100.0	252	9	ADX02006	Adx02006	SARS coro
418	38	100.0	252	9	ADX02002	Adx02002	SARS coro
419	38	100.0	252	9	ADX02014	Adx02014	SARS coro
420	38	100.0	252	9	ADX01976	Adx01976	SARS coro
421	38	100.0	252	9	ADX01972	Adx01972	SARS coro
422	38	100.0	252	9	ADX02008	Adx02008	SARS coro
423	38	100.0	252	9	ADX02032	Adx02032	SARS coro
424	38	100.0	252	9	ADX02012	Adx02012	SARS coro
425	38	100.0	252	9	ADX02016	Adx02016	SARS coro
426	38	100.0	253	9	ADX01988	Adx01988	SARS coro
427	38	100.0	254	9	ADX02018	Adx02018	SARS coro
428	38	100.0	254	9	ADX01958	Adx01958	SARS coro
429	38	100.0	254	9	ADX02020	Adx02020	SARS coro
430	38	100.0	254	9	ADX01962	Adx01962	SARS coro
431	38	100.0	254	9	ADX02028	Adx02028	SARS coro
432	38	100.0	254	9	ADX01984	Adx01984	SARS coro
433	38	100.0	255	5	ADU72870	Adu72870	PS-23 sin
434	38	100.0	255	5	ADU72870	Adu72870	SARS coro
435	38	100.0	255	5	ADU72870	Adu72870	SARS coro
436	38	100.0	258	2	AAW09820	Aaw09820	VI3418-11
437	38	100.0	258	4	AAH74794	Aah74794	Single ch
438	38	100.0	258	5	AAU72865	Aau72865	PS-2 sing
439	38	100.0	258	5	AAU72865	Aau72865	3B10XP4-3
440	38	100.0	259	3	AAU72862	Aau72862	Anti-viral
441	38	100.0	259	7	AAU72862	Aau72862	PA-3 sin
442	38	100.0	259	7	ADG32324	Adg32324	Mouse scf
443	38	100.0	259	8	ADG32322	Adg32322	Mouse scf
444	38	100.0	259	8	ADV02698	Adv02698	scFv-3 ml
445	38	100.0	260	2	AAH38318	Aah38318	Sequence
446	38	100.0	260	2	AAH38318	Aah38318	Human scf
447	38	100.0	260	2	AAH38318	Aah38318	Human scf
448	38	100.0	260	2	AAH38318	Aah38318	Human scf
449	38	100.0	260	2	AAH38318	Aah38318	Human scf
450	38	100.0	260	2	AAH38318	Aah38318	Human scf
451	38	100.0	260	2	AAH38318	Aah38318	Human scf
452	38	100.0	260	2	AAH38318	Aah38318	Human scf
453	38	100.0	260	2	AAH38318	Aah38318	Human scf
454	38	100.0	260	2	AAH38318	Aah38318	Human scf
455	38	100.0	260	2	AAH38318	Aah38318	Human scf
456	38	100.0	260	2	AAH38318	Aah38318	Human scf
457	38	100.0	260	2	AAH38318	Aah38318	Human scf
458	38	100.0	260	2	AAH38318	Aah38318	Human scf
459	38	100.0	260	2	AAH38318	Aah38318	Human scf
460	38	100.0	260	2	AAH38318	Aah38318	Human scf
461	38	100.0	260	2	AAH38318	Aah38318	Human scf
462	38	100.0	260	2	AAH38318	Aah38318	Human scf

536	38	100.0	497	9	AD283643	Ad283643 CD3 specti	609	34	89.5	171	8	ADK52422	AdK52422 Human ant
537	38	100.0	497	9	AD283623	Ad283623 CD3 specti	610	34	89.5	220	8	ADK52362	AdK52362 Human ant
538	38	100.0	497	9	AD283631	Ad283631 CD3 specti	611	33	86.8	7	3	AAy59233	AAy59233 Humanised
539	38	100.0	497	9	AD283617	Ad283617 CD3 specti	612	33	86.8	7	9	ADY59152	ADY59152 Anti-Tag-
540	38	100.0	500	9	ADV66095	Adv66095 Anti-CD3-	613	33	86.8	7	9	ADZ48268	AdZ48268 Pharmaceu
541	38	100.0	500	9	ADV66097	Adv66097 Anti-CD3-	614	33	86.8	12	8	ADJ25673	AdJ25673 Mouse apC
542	38	100.0	501	9	ADV21519	Adv21519 Mature fo	615	33	86.8	113	2	AAy56964	AAy56964 CC49 V-11
543	38	100.0	501	9	ADV21529	Adv21529 Mature fo	616	33	86.8	113	2	AAy42269	AAy42269 Humanised
544	38	100.0	502	9	ADY21971	Ady21971 Antibody	617	33	86.8	113	2	AAy42267	AAy42267 Murine ant
545	38	100.0	502	9	ADY21969	Ady21969 Antibody	618	33	86.8	113	2	AAW97177	AAW97177 Monoclonal
546	38	100.0	503	9	ADV66087	Adv66087 Anti-CD3-	619	33	86.8	113	2	AAy05759	AAy05759 Anti-Tag-
547	38	100.0	503	9	ADV66081	Adv66081 Anti-CD3-	620	33	86.8	113	5	AAU78327	AAU78327 Human CC4
548	38	100.0	504	9	ADV21525	Adv21525 Mature fo	621	33	86.8	113	5	AAU78320	AAU78320 Murine CC
549	38	100.0	504	9	ADV21535	Adv21535 Mature fo	622	33	86.8	113	5	AAU78322	AAU78322 Humanised
550	38	100.0	505	5	AAU72875	Aau72875 Human NKG	623	33	86.8	113	6	ABR54914	ABR54914 Light cha
551	38	100.0	506	9	ADV21505	Adv21505 Mature fo	624	33	86.8	113	6	ABU09367	ABU09367 Murine ant
552	38	100.0	506	9	ADV21515	Adv21515 Mature fo	625	33	86.8	113	6	ABU09371	ABU09371 Light cha
553	38	100.0	515	9	AD283441	Ad283441 Deimmuniz	626	33	86.8	113	6	ABU09372	ABU09372 Light cha
554	38	100.0	521	9	ADV66121	Adv66121 Anti-CD3-	627	33	86.8	113	6	ABU09365	ABU09365 Murine mo
555	38	100.0	523	3	AAy44994	AAy44994 HD708CFV-	628	33	86.8	113	6	ABU10146	ABU10146 Murine TA
556	38	100.0	524	3	AAy44995	AAy44995 HD708CFV-	629	33	86.8	113	6	ABU10142	ABU10142 Humanised
557	38	100.0	532	2	AAW35565	Aaw35565 HindIII-E	630	33	86.8	113	6	ABU10140	ABU10140 Murine TA
558	38	100.0	553	2	AAW11508	Aaw11508 Single ch	631	33	86.8	113	6	ABU10147	ABU10147 Humanised
559	38	100.0	553	2	AAW73223	Aaw73223 H22-anti-	632	33	86.8	113	6	ADBI17745	ADBI17745 Humanised
560	38	100.0	553	4	AAW61960	Aab61960 Bispecific	633	33	86.8	113	6	ADBI17743	ADBI17743 Native CC
561	38	100.0	553	4	AAW85455	Aab85455 Bispecific	634	33	86.8	113	6	ABU62757	ABU62757 Murine mo
562	38	100.0	556	2	AAW90218	Aaw90218 Bispecific	635	33	86.8	113	6	ABU62759	ABU62759 Humanised
563	38	100.0	580	5	AAW90217	Aaw90217 Bispecific	636	33	86.8	113	6	ABU62763	ABU62763 Murine mo
564	38	100.0	601	5	AAW49760	Aam49760 TNF-select	637	33	86.8	113	6	ABU62764	ABU62764 Light cha
565	38	100.0	614	5	AAO17454	Aao17454 Antibody-	638	33	86.8	113	6	ABU97820	ABU97820 HEV relat
566	38	100.0	638	8	ADL27332	AdL27332 Amino aci	639	33	86.8	113	7	AAE39070	AAE39070 Humanised
567	38	100.0	638	8	ADL27333	AdL27333 Amino aci	640	33	86.8	113	7	AAE39069	AAE39069 Murine CC
568	38	100.0	658	5	AAW49759	Aam49759 TNF-select	641	33	86.8	113	7	AAE39063	AAE39063 Murine CC
569	38	100.0	661	9	ADV92484	Adv92484 FL/Rc/hus	642	33	86.8	113	7	AAE39065	AAE39065 Humanised
570	38	100.0	661	9	ADV92480	Adv92480 FL/Rc/hus	643	33	86.8	113	7	ADG46863	ADG46863 Murine CC
571	38	100.0	661	9	ADV98553	Adv98553 Novel chl	644	33	86.8	113	7	ADG46865	ADG46865 Humanised
572	38	100.0	661	9	ADV98547	Adv98547 Novel chl	645	33	86.8	113	8	ADP71407	ADP71407 Humanised
573	38	100.0	666	9	AEA38766	Aea38766 Humanized	646	33	86.8	113	8	ADP71406	ADP71406 Mouse CC4
574	38	100.0	667	9	AEA38767	Aea38767 Humanized	647	33	86.8	113	8	ADJ25652	ADJ25652 Mouse act
575	38	100.0	667	9	AEA38768	Aea38768 Humanized	648	33	86.8	113	9	ADM77055	ADM77055 Murine CC
576	38	100.0	667	9	AEA38764	Aea38764 Humanized	649	33	86.8	113	9	ADM77058	ADM77058 Human CC4
577	38	100.0	695	9	AEA38765	Aea38765 Humanized	650	33	86.8	113	9	ADM77057	ADM77057 Human CC4
578	38	100.0	702	9	AEA54975	Aea54975 Monoclonal	651	33	86.8	113	9	ADY59145	ADY59145 Anti-Tag-
579	38	100.0	956	9	AEA36460	Aea36460 SCFV-GalV	652	33	86.8	113	9	ADY59201	ADY59201 Anti-Tag-
580	38	100.0	984	9	AEA54976	Aea54976 Bivalent	653	33	86.8	113	9	ADZ48271	ADZ48271 Pharmaceu
581	35	92.1	7	2	AAW70909	Aaw70909 CDR2 of t	654	33	86.8	113	9	ABE19290	ABE19290 Igg kappa
582	35	92.1	7	8	ADP47274	Adp47274 Human pho	655	33	86.8	114	8	ADP03701	ADP03701 Human ant
583	35	92.1	19	2	AAW70915	Aaw70915 Peptide p	656	33	86.8	116	2	AAK04386	AAK04386 Coloon Can
584	35	92.1	100	2	AAW70948	Aab18865 Amino aci	657	33	86.8	133	3	AAy57051	AAy57051 Amino aci
585	35	92.1	113	3	AAI18865	Aab18867 Amino aci	658	33	86.8	133	3	AAV90719	AAV90719 CC49 VL r
586	35	92.1	113	3	AAI18867	Aab18867 Amino aci	659	33	86.8	133	4	AAU02138	AAU02138 Mouse par
587	35	92.1	113	7	ADO51595	Ado51595 Human TNF	660	33	86.8	133	6	ADB17751	ADB17751 Humanised
588	35	92.1	116	9	ADX02057	Adx02057 SHRS coro	661	33	86.8	133	7	ADG46872	ADG46872 Humanised
589	35	92.1	124	4	AAW24229	Aam24229 Human EST	662	33	86.8	133	7	ADK66824	ADK66824 Mouse CC4
590	35	92.1	133	3	AAW85909	AaW85909 Monoclonal	663	33	86.8	137	7	AAV95243	AAV95243 Humanised
591	35	92.1	174	7	ADB65048	AdB65048 Human pro	664	33	86.8	199	6	ADB09034	ADB09034 Alloloccoc
592	35	92.1	242	2	AAW94962	Adw94962 Single ch	665	33	86.8	220	9	ADM77054	ADM77054 Light cha
593	35	92.1	254	9	ADX01960	Adx01960 SARS coro	666	33	86.8	220	9	ADM77046	ADM77046 Light cha
594	35	92.1	264	5	ABP43142	Abp43142 Human ova	667	33	86.8	220	9	ADM44589	ADM44589 Antibody
595	35	92.1	293	2	AAW59928	Aaw59928 Human AAA	668	33	86.8	240	5	AAE27927	AAE27927 Human CC4
596	35	92.1	293	3	AAW803671	AAW803671 Recombina	669	33	86.8	240	6	ABB82836	ABB82836 Antibody
597	35	92.1	328	7	ADB72835	AdB72835 Human AAA	670	33	86.8	242	2	AAW55865	AAW55865 CC49 VL/
598	35	92.1	328	3	AAW803696	AAW803696 Human aor	671	33	86.8	242	2	AAW95439	AAW95439 Linked fu
599	35	92.1	328	7	ADB72861	AdB72861 Human AAA	672	33	86.8	242	2	AAW88101	AAW88101 Single ch
600	34	89.5	11	8	ADO32135	Ado32135 Mouse ant	673	33	86.8	242	3	AAW07937	AAW07937 A single-
601	34	89.5	94	2	AAW62808	Aaw62808 Amino aci	674	33	86.8	242	3	AAV57256	AAV57256 4-4-20 Vh
602	34	89.5	114	8	ADP03707	Adp03707 Human ant	675	33	86.8	242	3	AAW27681	AAW27681 Bivalent
603	34	89.5	114	8	ADP03711	Adp03711 Human ant	676	33	86.8	242	3	AAW80926	AAW80926 Single ch
604	34	89.5	114	8	ADP03697	Adp03697 Human ant	677	33	86.8	242	3	AAW54835	AAW54835 Antibody
605	34	89.5	114	8	ADP03703	Adp03703 Human ant	678	33	86.8	242	4	AAW31422	AAW31422 Protein u
606	34	89.5	151	6	ABO04847	AbO04847 Human epi	679	33	86.8	242	6	ABU61811	ABU61811 Antigen b
607	34	89.5	151	9	ABE17759	AbE17759 Hybridoma	680	33	86.8	244	2	AAW88096	AAW88096 Single-ch
608	34	89.5	159	8	ADK52406	AdK52406 Human ant	681	33	86.8	244	3	AAW07932	AAW07932 A heterob

652	33	86.8	244	3	AAV51251	AAV51251 4-4-20 Vh	755	32	84.2	255	9	ADX01982	ADX01982 SARS coro
653	33	86.8	244	3	AAV27676	AAV27676 Bivalent	756	32	84.2	258	9	AAW82773	AAW82773 Fusion pr
664	33	86.8	244	3	AAV80921	AAV80921 Single ch	757	32	84.2	332	7	ABO80714	ABO80714 Pseudom
685	33	86.8	244	6	ABU61806	ABU61806 Antigen b	758	32	84.2	450	9	ADV21539	ADV21539 Mature fo
686	33	86.8	246	2	AAW81523	AAW81523 Single ch	759	32	84.2	491	9	ADV21543	ADV21543 Mature fo
687	33	86.8	248	2	AAV37382	AAV37382 Sequence	760	32	84.2	497	9	ADV21497	ADV21497 Mature fo
688	33	86.8	248	2	AAV97386	AAV97386 CC49 VL-P	761	32	84.2	547	8	ADV21507	ADV21507 Mature fo
689	33	86.8	249	2	AAW97888	AAW97888 CC49/218	762	32	84.2	573	8	AAW82216	AAW82216 Bacterial
690	33	86.8	257	2	AAW81524	AAW81524 Single ch	763	32	84.2	673	2	AAW82742	AAW82742 Plasmid p
691	33	86.8	257	5	AAV75157	AAV75157 CC49/218	764	32	84.2	674	2	ABU37747	ABU37747 Protein e
692	33	86.8	257	6	ABG73145	ABG73145 CC49/218	765	31	81.6	685	6	AAV37761	AAV37761 L chain C
693	33	86.8	257	6	ABG73865	ABG73865 CC49/218	766	31	81.6	111	2	AAW71242	AAW71242 Light cna
694	33	86.8	262	2	AAV97380	AAV97380 CC49/212	767	31	81.6	113	2	AAV63770	AAV63770 Mature l
695	33	86.8	262	2	AAV31421	AAV31421 Protein u	768	31	81.6	113	2	AAV63769	AAV63769 Mature l
696	33	86.8	264	2	AAV97381	AAV97381 PIAP CC49	769	31	81.6	228	4	AAW86682	AAW86682 Human pro
697	33	86.8	265	5	AAV75158	AAV75158 CC49/218	770	31	81.6	228	4	AAW67740	AAW67740 Amino aci
698	33	86.8	269	5	ABG73146	ABG73146 CC49/218	771	31	81.6	230	4	AAV76811	AAV76811 Corynebac
699	33	86.8	269	6	ABG73866	ABG73866 CC49/218	772	31	81.6	230	4	AAV69817	AAV69817 C glutami
700	33	86.8	271	4	AAV31423	AAV31423 Protein u	773	31	81.6	377	7	ABO75929	ABO75929 Pseudom
701	33	86.8	272	4	AAV31424	AAV31424 Protein u	774	31	81.6	504	6	ABU20953	ABU20953 Protein e
702	33	86.8	273	4	AAV49139	AAV49139 Sequence	775	31	81.6	661	7	ABO82299	ABO82299 Pseudom
703	33	86.8	275	2	AAV48636	AAV48636 Sequence	776	31	81.6	754	8	ADN17611	ADN17611 Bacterial
704	33	86.8	282	2	AAV19400	AAV19400 Amino aci	777	31	81.6	815	5	AAU72807	AAU72807 TRA-8 lig
705	33	86.8	285	2	AAV19400	AAV19400 Amino aci	778	31	81.6	815	5	AAU72807	AAU72807 TRA-8 lig
706	33	86.8	444	6	ABJ39018	ABJ39018 CC49 sing	779	30	78.9	7	5	ABO10668	ABO10668 Murine J5
707	33	86.8	444	6	AAW88099	AAW88099 A Protein	780	30	78.9	7	6	ABO29875	ABO29875 Murine J5
708	33	86.8	483	3	AAV07935	AAV07935 A divalent	781	30	78.9	7	6	ABR44632	ABR44632 Murine J5
709	33	86.8	483	3	AAV57254	AAV57254 Divalent	782	30	78.9	7	6	ABR44632	ABR44632 Murine J5
710	33	86.8	483	3	AAV27679	AAV27679 Bivalent	783	30	78.9	7	7	ADJ79793	ADJ79793 TRA-8 lig
711	33	86.8	483	3	AAV80924	AAV80924 Bivalent	784	30	78.9	7	8	ADQ90756	ADQ90756 Mouse com
712	33	86.8	483	3	AAV81809	AAV81809 Divalent	785	30	78.9	7	8	ADU67884	ADU67884 Mouse ant
713	33	86.8	486	6	AAV61809	AAV61809 Divalent	786	30	78.9	7	8	ADU67884	ADU67884 Mouse ant
714	33	86.8	515	9	ADZ48330	ADZ48330 Pharmaceu	787	30	78.9	7	8	ADU67706	ADU67706 Mouse Luc
715	33	86.8	515	9	ADZ48331	ADZ48331 Pharmaceu	788	30	78.9	7	9	ADY52291	ADY52291 SP-3b1 Ii
716	33	86.8	553	2	AAV56966	AAV56966 CC49 VL-L	789	30	78.9	7	9	ADY52291	ADY52291 SP-3b1 Ii
717	33	86.8	553	2	AAV56967	AAV56967 CC49 VL-L	790	30	78.9	7	9	ADY52291	ADY52291 SP-3b1 Ii
718	33	86.8	553	2	AAW97180	AAW97180 A multipla	791	30	78.9	7	8	ADZ45503	ADZ45503 Murine fa
719	33	86.8	553	2	AAW97180	AAW97180 A multipla	792	30	78.9	7	8	ADZ45503	ADZ45503 Murine fa
720	33	86.8	553	2	AAV05762	AAV05762 CC49 sing	793	30	78.9	15	8	ADT75086	ADT75086 Murine li
721	33	86.8	553	2	AAV05763	AAV05763 CC49 sing	794	30	78.9	15	8	ADT75086	ADT75086 Murine li
722	33	86.8	603	9	ADW44587	ADW44587 Antibody	795	30	78.9	8	ADT75086	ADT75086 Murine li	
723	33	86.8	621	9	ADW44588	ADW44588 Antibody	796	30	78.9	8	ADT75086	ADT75086 Murine li	
724	33	86.8	621	9	ADW44592	ADW44592 Antibody	797	30	78.9	8	ADT75086	ADT75086 Murine li	
725	33	86.8	661	9	ADW44593	ADW44593 Antibody	798	30	78.9	8	ADT75086	ADT75086 Murine li	
726	33	86.8	661	9	ADW44593	ADW44593 Antibody	799	30	78.9	8	ADT75086	ADT75086 Murine li	
727	32	84.2	1328	8	ADR86136	ADR86136 Aspergill	799	30	78.9	8	ADT75086	ADT75086 Murine li	
728	32	84.2	7	2	AAV76083	AAV76083 MAb 55.1	800	30	78.9	95	6	AAU44987	AAU44987 Propionib
729	32	84.2	7	9	AAV21337	AAV21337 Human ant	801	30	78.9	95	6	AAU44987	AAU44987 Propionib
730	32	84.2	97	4	ABR16002	ABR16002 Human ner	802	30	78.9	103	4	ABM41506	ABM41506 Propionib
731	32	84.2	107	4	ABR16002	ABR16002 Human ner	803	30	78.9	103	4	ABM41506	ABM41506 Propionib
732	32	84.2	114	7	AAV62781	AAV62781 Human HIV	804	30	78.9	105	6	ABM41506	ABM41506 Propionib
733	32	84.2	114	7	AAV62781	AAV62781 Human HIV	805	30	78.9	105	6	ABM41506	ABM41506 Propionib
734	32	84.2	116	9	ADW070539	ADW070539 Pseudomom	806	30	78.9	107	2	AAV55121	AAV55121 Mouse ant
735	32	84.2	117	9	ADW070539	ADW070539 Pseudomom	807	30	78.9	107	2	AAV55121	AAV55121 Mouse ant
736	32	84.2	134	2	ADW02101	ADW02101 SARS coro	808	30	78.9	107	2	AAV55121	AAV55121 Mouse ant
737	32	84.2	134	2	ADW02101	ADW02101 SARS coro	809	30	78.9	107	2	AAV55121	AAV55121 Mouse ant
738	32	84.2	145	6	ABR10316	ABR10316 Human pro	810	30	78.9	107	2	AAV55121	AAV55121 Mouse ant
739	32	84.2	151	6	ABR004853	ABR004853 Human epi	811	30	78.9	107	2	AAV55121	AAV55121 Mouse ant
740	32	84.2	151	6	ABR004853	ABR004853 Human epi	812	30	78.9	107	2	AAV55121	AAV55121 Mouse ant
741	32	84.2	152	6	ABR004849	ABR004849 Human epi	813	30	78.9	107	2	AAV55121	AAV55121 Mouse ant
742	32	84.2	152	6	ABR004849	ABR004849 Human epi	814	30	78.9	107	2	AAV55121	AAV55121 Mouse ant
743	32	84.2	158	8	AAE17761	AAE17761 HyDridoma	815	30	78.9	107	4	AAV69665	AAV69665 Humanisee
744	32	84.2	158	8	AAE17761	AAE17761 HyDridoma	816	30	78.9	107	4	AAV69665	AAV69665 Humanisee
745	32	84.2	163	8	ADK52366	ADK52366 Human ant	817	30	78.9	107	6	ABO10703	ABO10703 Variable
746	32	84.2	163	8	ADK52366	ADK52366 Human ant	818	30	78.9	107	6	ABO10703	ABO10703 Variable
747	32	84.2	178	8	ADK52418	ADK52418 Human ant	819	30	78.9	107	6	ABO10703	ABO10703 Variable
748	32	84.2	219	2	AAV76086	AAV76086 MAb 55.1	820	30	78.9	107	6	ABO10703	ABO10703 Variable
749	32	84.2	220	8	ADK52298	ADK52298 Human ant	821	30	78.9	107	6	ABO10703	ABO10703 Variable
750	32	84.2	220	8	ADK52298	ADK52298 Human ant	822	30	78.9	107	6	ABO10703	ABO10703 Variable
751	32	84.2	220	8	ADK52298	ADK52298 Human ant	823	30	78.9	107	6	ABO10703	ABO10703 Variable
752	32	84.2	239	2	AAV76087	AAV76087 MAb 55.1	824	30	78.9	107	8	ADQ47712	ADQ47712 Mouse Fd1
753	32	84.2	242	9	ADV21476	ADV21476 Mature fo	825	30	78.9	107	8	ADQ47712	ADQ47712 Mouse Fd1
754	32	84.2	252	9	ADX01968	ADX01968 SARS coro	826	30	78.9	107	8	ADQ47712	ADQ47712 Mouse Fd1
755	32	84.2	252	9	ADX01968	ADX01968 SARS coro	827	30	78.9	107	8	ADQ47712	ADQ47712 Mouse Fd1

828	30	78.9	107	8	ADU67899	AdU67899	Mouse ant	901	30	78.9	789	8	ADS23771	AdS23771	Bacterial
829	30	78.9	107	8	ADU87730	AdU87730	Humanized	902	30	78.9	804	6	ABP70828	AbP70828	Murine C1
830	30	78.9	107	8	ADU87728	AdU87728	Light cha	903	30	78.9	861	6	AAE34956	Aae34956	Aspergill
831	30	78.9	107	8	ADU87734	AdU87734	VL region	904	30	78.9	861	8	ADU82946	AdU82946	A. oryzae
832	30	78.9	107	8	ADU87693	AdU87693	Mouse Luc	905	30	78.9	861	9	ADU41873	AdU41873	Aspergill
833	30	78.9	107	8	ADU87736	AdU87736	Light cha	906	30	78.9	863	8	ADU83014	AdU83014	Aspergill
834	30	78.9	107	8	ADU52287	AdU52287	IH7 light	907	30	78.9	863	9	ADU41879	AdU41879	Aspergill
835	30	78.9	107	9	ADZ45501	AdZ45501	Murine fa	908	30	78.9	863	9	ADU41877	AdU41877	Aspergill
836	30	78.9	108	2	AAZ21817	AaZ21817	Anti-STX1	909	30	78.9	863	9	ADY53751	AdY53751	Aspergill
837	30	78.9	108	8	ADG25826	AdG25826	Anti-CD30	910	30	78.9	863	9	AEA33202	Aea33202	Aspergill
838	30	78.9	108	8	ADT75004	AdT75004	Light cha	911	30	78.9	863	9	ABE90870	AbE90870	Aspergill
839	30	78.9	108	8	ADT74999	AdT74999	Light cha	912	30	78.9	863	9	ABE90591	AbE90591	Family GH
840	30	78.9	108	9	ABE21883	AbE21883	Human DC-	913	30	78.9	1067	5	ABE92588	AbE92588	Herbicide
841	30	78.9	108	9	ABE21886	AbE21886	Human DC-	914	30	78.9	1067	5	ADT55825	AdT55825	Plant pol
842	30	78.9	109	8	ADG25817	AdG25817	Anti-CD30	915	30	78.9	1139	6	ABU35640	AbU35640	Protein e
843	30	78.9	109	8	ADJ26471	AdJ26471	Murine 14	916	30	78.9	1139	7	ABO23514	AbO23514	Mycoplasma
844	30	78.9	109	8	ADQ27995	AdQ27995	Anti-DPS	917	29	76.3	9	4	ABB56108	AbB56108	Vascular
845	30	78.9	109	8	ADT75067	AdT75067	Light cha	918	29	76.3	9	4	AAU28785	Aau28785	DPI tlypt
846	30	78.9	115	5	ABE07359	AbE07359	22A5 IGM	919	29	76.3	9	4	AAU26433	Aau26433	Depressio
847	30	78.9	116	9	AEA88778	Aea88778	Murine SA	920	29	76.3	9	4	ABE52396	AbE52396	Human API
848	30	78.9	116	9	AEA88779	Aea88779	Murine SA	921	29	76.3	9	4	ABR59159	AbR59159	Alzheimer
849	30	78.9	127	8	ADU87781	AdU87781	Anti-CS1	922	29	76.3	9	8	ADN31921	AdN31921	Human Alz
850	30	78.9	141	7	ABO79692	AbO79692	Pseudomon	923	29	76.3	22	6	ABP99543	AbP99543	Human sec
851	30	78.9	153	6	ABU11788	AbU11788	Human MDD	924	29	76.3	22	6	ABR01024	AbR01024	Human gen
852	30	78.9	183	7	ABO81415	AbO81415	Pseudomon	925	29	76.3	23	3	ABA44856	AbA44856	Human sec
853	30	78.9	212	5	AAU72815	Aau72815	DNA encod	926	29	76.3	30	8	ADU17103	AdU17103	Human sec
854	30	78.9	212	5	AAO29883	Aao29883	LM1 fusio	927	29	76.3	34	4	AAU21290	AAU21290	Peptide #
855	30	78.9	212	7	ADU79836	AdU79836	LM1-type	928	29	76.3	34	4	ABE43623	AbE43623	Peptide #
856	30	78.9	213	5	AAU72819	Aau72819	TRA-8 lig	929	29	76.3	34	4	AAU37517	AAU37517	Peptide #
857	30	78.9	213	5	AAU72819	Aau72819	DNA encod	930	29	76.3	34	4	AAU77367	AAU77367	Human bon
858	30	78.9	213	5	AAU72818	Aau72818	DNA encod	931	29	76.3	34	4	AAU64564	AAU64564	Human bra
859	30	78.9	213	5	AAU72817	Aau72817	DNA encod	932	29	76.3	34	4	ABG59000	AbG59000	Human liv
860	30	78.9	213	5	AAU72816	Aau72816	DNA encod	933	29	76.3	34	5	ABG46381	AbG46381	Human pep
861	30	78.9	213	6	AAO29886	Aao29886	LM5 fusio	934	29	76.3	42	4	AAU21420	AAU21420	Human nov
862	30	78.9	213	6	AAO29878	Aao29878	LM2 fusio	935	29	76.3	51	4	ABG28064	AbG28064	Novel hum
863	30	78.9	213	6	AAO29884	Aao29884	LM3 fusio	936	29	76.3	66	4	AAU48022	AAU48022	Proptonib
864	30	78.9	213	6	AAO29887	Aao29887	LM6 fusio	937	29	76.3	66	6	ABM44541	AbM44541	Proptonib
865	30	78.9	213	7	AAO29885	Aao29885	LM4 fusio	938	29	76.3	68	5	ABB97819	AbB97819	Human sec
866	30	78.9	213	7	ADU79838	AdU79838	LM4-type	939	29	76.3	72	8	ADU04135	AdU04135	Murine im
867	30	78.9	213	7	ADU79837	AdU79837	LM3-type	940	29	76.3	75	2	AAW26702	AAW26702	Secreted
868	30	78.9	213	7	ADU79810	AdU79810	Humanized	941	29	76.3	84	7	ABO77080	AbO77080	Pseudomon
869	30	78.9	213	7	ADU79839	AdU79839	LM5-type	942	29	76.3	85	4	AAU61714	AAU61714	Proptonib
870	30	78.9	213	7	ADU79840	AdU79840	LM6-type	943	29	76.3	85	6	ABM58233	AbM58233	Proptonib
871	30	78.9	223	1	AAU40031	AAU40031	Kappa ant	944	29	76.3	90	4	AAU41550	AAU41550	Proptonib
872	30	78.9	223	1	AAU68009	AAU68009	Mouse ant	945	29	76.3	90	6	ABM38069	AbM38069	Proptonib
873	30	78.9	233	5	AAU72802	AAU72802	TRA-8 lig	946	29	76.3	97	2	AAU59994	AAU59994	Human end
874	30	78.9	234	6	AAO29870	AAO29870	Mouse ant	947	29	76.3	99	4	AAU43953	AAU43953	Proptonib
875	30	78.9	234	7	ADU79788	AdU79788	TRA-8 ant	948	29	76.3	99	6	ABM40472	AbM40472	Proptonib
876	30	78.9	245	9	ADU52285	AdU52285	Single ch	949	29	76.3	102	4	AAU52423	AAU52423	Proptonib
877	30	78.9	247	1	AAU80156	AAU80156	Frs and C	950	29	76.3	102	6	ABM48942	AbM48942	Proptonib
878	30	78.9	247	1	AAU80155	AAU80155	Bioeynte	951	29	76.3	103	7	ABO81913	AbO81913	Pseudomon
879	30	78.9	256	6	ABU38350	AbU38350	Protein e	952	29	76.3	108	8	ADO90772	AdO90772	Deimmunis
880	30	78.9	260	8	ADU09618	AdU09618	Human pro	953	29	76.3	109	8	ADO32156	AdO32156	Mouse ant
881	30	78.9	262	8	ADU93227	AdU93227	Plant ful	954	29	76.3	112	5	ABG70739	AbG70739	Variable
882	30	78.9	310	5	ABE91336	AbE91336	Herbicide	955	29	76.3	120	7	ABO75415	AbO75415	Pseudomon
883	30	78.9	348	7	ABO81304	AbO81304	Pseudomon	956	29	76.3	137	7	ABO82246	AbO82246	Pseudomon
884	30	78.9	349	3	AAU85691	AAU85691	Murine Sa	957	29	76.3	141	2	AAU52823	AAU52823	Treponea
885	30	78.9	349	4	AAU49332	AAU49332	Murine SL	958	29	76.3	141	2	AAU52826	AAU52826	Treponea
886	30	78.9	349	5	AAE23393	AAE23393	Human int	959	29	76.3	142	2	AAU4967	AAU4967	Myobacte
887	30	78.9	349	7	ADU53780	AdU53780	Human pro	960	29	76.3	143	2	AAU52825	AAU52825	Treponea
888	30	78.9	349	7	ADU53780	AdU53780	Human nov	961	29	76.3	146	2	AAU52822	AAU52822	Treponea
889	30	78.9	442	2	ABO76511	AbO76511	Pseudomon	962	29	76.3	149	3	AAU34886	AAU34886	Arabirops
890	30	78.9	453	2	AAU97049	AAU97049	Protein e	963	29	76.3	156	3	AAU34820	AAU34820	Arabirops
891	30	78.9	453	4	AAU89244	AAU89244	Spllingomo	964	29	76.3	162	7	ABO83514	AbO83514	Pseudomon
892	30	78.9	453	4	AAU02432	AAU02432	Spllingomo	965	29	76.3	164	3	AAU34885	AAU34885	Arabirops
893	30	78.9	453	6	ABU25249	AbU25249	Protein e	966	29	76.3	169	3	AAU42685	AAU42685	Arabirops
894	30	78.9	469	8	ADU25910	AdU25910	Bacterial	967	29	76.3	170	6	ABM39204	AbM39204	Proptonib
895	30	78.9	469	8	ADU25910	AdU25910	Bacterial	968	29	76.3	173	3	AAU348419	AAU348419	Arabirops
896	30	78.9	469	8	ADU25910	AdU25910	Bacterial	969	29	76.3	175	3	AAU348418	AAU348418	Arabirops
897	30	78.9	497	2	AAU94843	AAU94843	Heat-resi	970	29	76.3	199	7	ABO71484	AbO71484	Pseudomon
898	30	78.9	497	8	ADN47768	AdN47768	Thermococ	971	29	76.3	206	7	ABO69597	AbO69597	Pseudomon
899	30	78.9	671	8	ADN25099	AdN25099	Bacterial	972	29	76.3	227	8	ADY13080	AdY13080	Plant ful
900	30	78.9	770	8	ADN20899	AdN20899	Bacterial	973	29	76.3	227	8	ADY13080	AdY13080	Plant ful

974	29	76.3	237	7	ADM05850	Adm05850 Human pro
975	29	76.3	238	5	ABG70744	ABG70744 Mouse/hum
976	29	76.3	243	6	ABU46838	ABU46838 Protein e
977	29	76.3	249	8	ABO59739	ABO59739 Human gen
978	29	76.3	257	8	ADX76447	ADX76447 Plant ful
979	29	76.3	260	7	ABO72865	ABO72865 Pseudomon
980	29	76.3	276	8	ADX75118	ADX75118 Plant ful
981	29	76.3	285	8	ADX76234	ADX76234 Plant ful
982	29	76.3	296	2	AAV00029	AAV00029 Enterococ
983	29	76.3	296	5	ABP43248	ABP43248 E. faecali
984	29	76.3	296	6	ABU88276	ABU88276 E. faecali
985	29	76.3	296	6	ABU13527	ABU13527 Enterococ
986	29	76.3	296	6	ADY38774	ADY38774 Novel Ent
987	29	76.3	308	8	ADX76540	ADX76540 Plant ful
988	29	76.3	309	8	ADX74447	ADX74447 Plant ful
989	29	76.3	314	8	ADX74506	ADX74506 Plant ful
990	29	76.3	317	2	AAV00028	AAV00028 Enterococ
991	29	76.3	317	4	AAU35312	AAU35312 Enterococ
992	29	76.3	317	5	ABP43247	ABP43247 E. faecali
993	29	76.3	317	6	ABU88275	ABU88275 E. faecali
994	29	76.3	317	6	ABU13526	ABU13526 Enterococ
995	29	76.3	317	9	ADY16763	ADY16763 E. faecali
996	29	76.3	317	9	ADY38772	ADY38772 Novel Ent
997	29	76.3	327	7	ADH86457	ADH86457 Enterococ
998	29	76.3	328	3	AAU28931	AAU28931 Arabidops
999	29	76.3	337	3	AAU28930	AAU28930 Arabidops
1000	29	76.3	338	3	AAU33324	AAU33324 Zea mays

ALIGNMENTS

RESULT 1
AAR30157
ID AAR30157 standard; protein; 7 AA.

AC AAR30157;
XX
XX
XX 25-MAR-2003 (revised)
DT 06-MAY-1993 (first entry)
XX
XX
XX MAB GAH variable region of light chain.
DE
XX Monoclonal antibody; hybridoma; PCR; variable region; constant region;
KW heavy chain; light chain.
XX
XX Synthetic.
OS
XX
XX EP520499-A1.
PN
XX
XX 30-DEC-1992.
PD
XX
XX 26-JUN-1992; 92EP-00110841.
PF
XX
XX 28-JUN-1991; 91JP-00158859.
PR
XX 28-JUN-1991; 91JP-00158860.
PR
XX 28-JUN-1991; 91JP-00158861.
XX
XX (MITU) MITSUBISHI KASEI CORP.
PA
XX Hosokawa S, Tagawa T, Hirakawa Y, Ito N, Nagaike K;
PI
XX WPI; 1993-001328/01.
DR N-PSDB; AAQ3044.
XX
XX Human monoclonal antibody specific for a cancer cell membrane surface
PT antigen - prepd. from a hybridoma obtd. by cell fusion between human
PT lymphocytes derived from cancer patients and mouse myeloma cells.
XX
XX Claim 3; Page 30 + 23; 37pp; English.
PS
XX
XX The sequence is described is the specification as having 27 bases. A
CC human Mab specifically binding to a surface antigen of cancer cell

CC membrane comprises variable regions of the heavy and light chains having
CC the amino acid sequences of AAR30153-55 and AAR30156-58 respectively,
CC encoded by DNA sequences AAQ3040-42 and AAQ3043-45 respectively. The
CC antibody is obtained from a hybridoma producing human antibody GAH.
CC (Updated on 25-MAR-2003 to correct PN field.)

SO Sequence 7 AA;

Query Match 100.0%; Score 38; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

Oy 1 WASTRES 7
Db 1 WASTRES 7

RESULT 2

AAR57966
ID AAR57966 standard; protein; 7 AA.

AC AAR57966;
XX

DT 25-MAR-2003 (revised)
DT 05-OCT-1994 (first entry)
XX

DE MAB NFS2 light chain variable region CDR2 (modified).

KW Monoclonal antibody; Plasmodium falciparum; CDR;
KW complementarity determining region; fusion protein; murine; variable;
KW light; heavy; chain; malaria.

OS Synthetic.

PN WO9405690-A1.

PD 17-MAR-1994.

PF 08-SEP-1993; 93WO-US008435.

PR 09-SEP-1992; 92US-00941654.

PA (SMTK) SMITHKLINE BEECHAM CORP.

PA (USNA) US SEC OF NAVY.

PI (USCA) US SEC OF ARMY.

PI Gross MS, Rosenberg M, Sadoff JC, Hoffman S, Sylvester DR;
PI Charoenvit Y, Hurlle M;

DR WPI; 1994-101115/12.
DR N-PSDB; AAQ44839.

PT New engineered antibodies and fusion proteins for preventing Plasmodium
PT infection - contg. murine antibody CDR sequences, and corresp. nucleic
PT acid, vectors and transformed cells.

PS Disclosure; Page 69; 98pp; English.

XX Naturally-occurring (AAQ44841-42) and synthetic (AAQ44825-28) variable
CC light chain and variable heavy chain sequences derived from murine mab
CC NFS2 are provided. Murine mab NFS2, its variable chain peptides, CDRs, of
CC functional fragments, Fab fragments, and analogs are useful in prodn. of
CC fusion proteins, esp. engineered antibodies. These prods. are used to
CC protect humans against Plasmodium infections. (Updated on 25-MAR-2003 to
CC correct PN field.)

SO Sequence 7 AA;

Query Match 100.0%; Score 38; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

Oy 1 WASTRES 7

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Db          |||||
            1 WASTRES 7

RESULT 3
AAR50317
ID AAR50317 standard; protein; 7 AA.
XX
XX AAR50317;
AC
XX
XX 25-MAR-2003 (revised)
DT 05-OCT-1994 (first entry)
XX
XX MAB NFS2 light chain variable region CDR2 (modified).
DE
XX Monoclonal antibody; Plasmodium falciparum; CDR;
KW complementarity determining region; fusion protein; murine; variable;
KM light; heavy; chain; malaria.
XX
XX Synthetic.
OS
XX WO9405690-A1.
XX
XX 17-MAR-1994.
PD
XX
XX 08-SEP-1993; 93WO-US008435.
XX
XX 09-SEP-1992; 92US-00941654.
XX
XX (SMITK ) SMITHKLINE BEECHAM CORP.
PA (USNA ) US SEC OF NAVY.
XX (USNA ) US SEC OF ARMY.
XX
XX Gross MS, Rosenberg M, Sadoff JC, Hoffman S, Sylvester DR;
PI Charoenvic Y, Hurlle M;
XX WPI; 1994-101115/12.
DR N-PSDB; AAQ44833.
XX
XX New engineered antibodies and fusion proteins for preventing Plasmodium
PT infection - contg. murine antibody CDR sequences, and corresp. nucleic
PT acid, vectors and transformed cells.
XX
XX Claim 16; Page 83; 98pp; English.
PS
XX Naturally-occurring (AAQ44841-42) and synthetic (AAQ44825-28) variable
CC light chain and variable heavy chain sequences derived from murine mab
CC NFS2 are provided. Murine mab NFS2, its variable chain peptides, CDRs,
CC functional fragments, Fab fragments, and analogs are useful in prodn. of
CC fusion proteins, esp. engineered antibodies. These prods. are used to
CC protect humans against Plasmodium infections. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
XX Sequence 7 AA;
SQ

Query Match          100.0%; Score 38; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
   |||||
   1 WASTRES 7
Db

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DE MAB NFS2 light chain variable region CDR2.
XX Monoclonal antibody; Plasmodium falciparum; CDR;
KW complementarity determining region; fusion protein; murine; variable;
KM light; heavy; chain; malaria.
XX
XX Plasmodium falciparum.
OS
XX WO9405690-A1.
XX
XX 17-MAR-1994.
PD
XX
XX 08-SEP-1993; 93WO-US008435.
XX
XX 09-SEP-1992; 92US-00941654.
XX
XX (SMITK ) SMITHKLINE BEECHAM CORP.
PA (USNA ) US SEC OF NAVY.
XX (USNA ) US SEC OF ARMY.
XX
XX Gross MS, Rosenberg M, Sadoff JC, Hoffman S, Sylvester DR;
PI Charoenvic Y, Hurlle M;
XX WPI; 1994-101115/12.
DR N-PSDB; AAQ44837.
XX
XX New engineered antibodies and fusion proteins for preventing Plasmodium
PT infection - contg. murine antibody CDR sequences, and corresp. nucleic
PT acid, vectors and transformed cells.
XX
XX Disclosure; Page 68; 98pp; English.
PS
XX Naturally-occurring (AAQ44841-42) and synthetic (AAQ44825-28) variable
CC light chain and variable heavy chain sequences derived from murine mab
CC NFS2 are provided. Murine mab NFS2, its variable chain peptides, CDRs,
CC functional fragments, Fab fragments, and analogs are useful in prodn. of
CC fusion proteins, esp. engineered antibodies. These prods. are used to
CC protect humans against Plasmodium infections. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
XX Sequence 7 AA;
SQ

Query Match          100.0%; Score 38; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
   |||||
   1 WASTRES 7
Db

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RESULT 5
AAV08713
ID AAV08713 standard; protein; 7 AA.
XX
XX AAV08713;
AC
XX
XX 10-AUG-1999 (first entry)
DT
XX
XX Human milk fat globule antigen binding fragment 5.
DE
XX Immunoglobulin; immunospecific; variable domain; CDR; cancer antigen;
KW complementarity determining region; infectious disease agent antigen;
KW cellular receptor; infectious agent; chemotherapeutic agent; vaccine;
KW cancer; infectious disease; autoimmune disease; rheumatoid arthritis;
KW ulcerative colitis; psoriasis; allergy; immunoassay reagent; diagnosis;
KW veterinary medicine; antibody; immunisation; antibody; immune tolerance;
KW human milk fat globule antigen; cryptic expression;
XX anti-idiotypic immune response.
XX
XX Homo sapiens.
OS
XX
XX WO9925378-A1.
PN

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XX 27-MAY-1999.
 PD 13-NOV-1998; 98WO-US024302.
 XX PF
 XX 14-NOV-1997; 97US-0065716P.
 PR 10-APR-1998; 98US-0081403P.
 XX PA (EURO-) EUROCELLTIGUE SA.
 XX PI Burch RM;
 XX WPI; 1999-357555/30.
 DR Modified immunoglobulins including engineered binding site.
 PT
 XX Claim 9; Page 76; 123pp; English.
 PS
 XX This invention describes a novel modified immunoglobulin (mIg), or its
 CC fragment, that binds immunospecifically to one member (M1) of a binding
 CC pair comprising a variable domain (V) having at least one CDR
 CC (complementarily determining region) that contains a portion of the
 CC second member (M2) of the pair. This portion is not present in the
 CC natural CDR and M1 is a cancer antigen, infectious disease agent antigen,
 CC a cellular receptor for an infectious agent (provided the binding site is
 CC not NAMP or NNDP) or a member of a receptor-ligand pair. mIg (also
 CC related molecules containing the same V region), optionally coupled to a
 CC chemotherapeutic agent, are used in the same V region, optionally coupled to a
 CC compositions, or vaccines, against cancers, infectious or autoimmune
 CC diseases (rheumatoid arthritis, ulcerative colitis or psoriasis) or
 CC allergies. They can also be used as immunoassay reagents for diagnosing
 CC these conditions. mIg can be used in human or veterinary medicine. mIg
 CC have higher affinity or specificity than native antibodies. Manipulation
 CC of CDR ensures binding specificity and avoids the unpredictable
 CC immunization and screening procedures currently used. It is now possible
 CC to generate antibodies against antigens that are inaccessible, by virtue
 CC of immune tolerance or cryptic expression. mIg neutralize antigens
 CC directly or they induce an anti-idiotypic immune response. This sequence
 CC represents a fragment of modified immunoglobulin that immunospecifically
 CC binds to a binding pair in which the first member is the human milk fat
 CC globule antigen
 CC
 SQ Sequence 7 AA:
 Query Match 100.0%; Score 38; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 WASTRES 7
 DB 1 WASTRES 7
 ID AAY95234 standard; peptide; 7 AA.
 XX AAY95234;
 AC AAY95234;
 XX
 DT 29-AUG-2000 (first entry)
 XX
 DE Human monoclonal antibody LEN VL CDR2.
 XX
 KW Human; monoclonal antibody; LEN; humanised antibody; CC49; HuCC49; CDR;
 KW complementarity determining region; colon cancer;
 KW tumor associated glycoprotein-72; TAG-72; tumour marker; carcinoma;
 KW diagnosis; therapy.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 1..6
 /note="specificity determining region"

XX WO200026394-A1.
 EN 11-MAY-2000.
 XX PD
 XX 29-OCT-1999; 99WO-US025552.
 PF
 XX 31-OCT-1998; 98US-0106534P.
 PR 02-NOV-1998; 98US-0106757P.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PI Kaashmali SVS, Padlan EA, Schlom J;
 XX WPI; 2000-365637/31.
 DR
 XX Chimeric variants of CC49 monoclonal antibodies useful for detecting and
 PT treating cancers associated with the expression of the pancreaticoma tumor
 PT -associated antigen TAG-72.
 PS
 XX Disclosure; Fig 2; 76pp; English.
 CC
 XX The present sequence is that of complementarity determining region 2 (L-
 CC CDR2) of the light chain variable region (VL) of human monoclonal
 CC antibody LEN. The invention is directed toward mouse-human chimeric
 CC variants of CC49 Mabs with minimal murine content, to methods of making
 CC such variants, and to their therapeutic application. Variants are
 CC provided of huCC49, a humanised Mab formed by grafting hypervariable
 CC regions from murine CC49 into VL and VH frameworks of human Mabs LEN and
 CC 21/28' CL, respectively, while retaining murine framework residues
 CC required for integrity of the antigen combining site structure. HuCC49
 CC binds to the human pancreaticoma tumor associated glycoprotein-72 (TAG-
 CC 72), which is found on the surface of certain human tumours. Novel
 CC variants of huCC49 of the invention have fewer than all 6 CDRs of CC49
 CC present. Also provided are specificity determining region (SDR) variants
 CC of huCC49 in which only SDRs of at least 1 CDR from CC49 are present.
 CC Particular variants of huCC49 have either L-CDR1 and/or L-CDR2 from human
 CC Mab LEN. These variants have the same or 2-fold lower affinity constant
 CC than huCC49. They are used in claimed methods of treating cancer and for
 CC detecting cancer cells that express TAG-72
 CC
 SQ Sequence 7 AA:
 Query Match 100.0%; Score 38; DB 3; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 WASTRES 7
 DB 1 WASTRES 7
 ID AAY32227 standard; peptide; 7 AA.
 XX AAY32227;
 AC AAY32227;
 XX
 DT 15-FEB-2000 (first entry)
 XX
 DE G-CSF agonist antibody mab163-93 light chain variable region CDR2.
 XX
 KW Granulocyte colony stimulating factor receptor; G-CSF; mouse;
 KW monoclonal antibody; agonist; screening; neutropenia; therapy;
 KW complementarity determining region; CDR; mab163-93.
 XX
 OS Mus musculus.
 XX
 PN MO9955735-A1.
 XX
 PD 04-NOV-1999.
 XX
 PF 30-APR-1999; 99WO-US009466.

XX 30-APR-1998; 98US-0083575P.
XX (TANO-) TANOX INC.
XX Ni B, Sun BNC, Sun CRX;
XX WPI; 2000-052805/04.
XX
XX Treatment of neutropenia by stimulating proliferation of neutrophilic
XX cell lineage progenitors.
XX
XX Claim 13; Page 30; 64pp; English.
XX
XX The present sequence represents complementarity determining region 2
XX (CDR2) of the light chain variable region of murine monoclonal antibody
XX mAb163-93. This antibody is an example of an agonist molecule that
XX specifically binds to or interacts with human granulocyte colony
XX stimulating factor (G-CSF) receptor to stimulate cell proliferation and
XX differentiation, especially by dimerizing the receptor or activating
XX phosphorylation of kinases associated with the receptor. Agonist
XX antibodies can be used to stimulate proliferation of G-CSF-dependent
XX cells, e.g. to differentiate leading to a repopulation of neutrophilic
XX granulocyte lineage cells, especially to treat neutropenia (claimed).
XX They can also be used to detect human G-CSF receptor immunologically.
XX
XX Sequence 7 AA:

Query Match 100.0%; Score 38; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7
1 |||||
Db 1 WASTRES 7

RESULT 8
AAB07952
ID AAB07952 standard; peptide; 7 AA.
XX
XX AAB07952;
XX
XX 14-NOV-2000 (first entry)
XX
XX CDR2 sequence from an antibody with affinity for B7 molecules.
XX
XX Complementarity determining region; CDR; antibody; B7 molecule; B7-1;
XX B7-2; humanised immunoglobulin; autoimmune disease; infectious disease;
XX inflammatory disorder; systemic lupus erythematosus; diabetes mellitus;
XX insulinitis; asthma; arthritis; inflammatory bowel disease; cancer;
XX inflammatory dermatitis; multiple sclerosis; transplant rejection;
XX proliferative disease; leukemia; lymphoma; anaemia; sickle-cell anaemia;
XX thalassemia; aplastic anaemia; myeloid dysplasia syndrome.
XX
XX Mus sp.
XX
XX WO200047625-A2.
XX
XX 17-AUG-2000.
XX
XX 09-FEB-2000; 2000WO-US003303.
XX
XX 12-FEB-1999; 99US-00249011.
XX 24-JUN-1999; 99US-00339596.
XX
XX (GENY) GENETICS INST INC.
XX
XX Co MS, Vazquez M, Carreno B, Gelinkner AC, Collins M, Goldman S;
XX Gray GS, Knight A, O'hara D, Rup B, Veldman GM;
XX WPI; 2000-524532/47.
XX

PT Humanized immunoglobulin having a binding specificity to B7-1 (derived
PT from ARCC PTA-263), or B7-2 (derived from ARCC CRU-12524) molecules,
PT modulates immune responses and can therefore treat e.g. autoimmune
PT diseases, infectious diseases.
XX
XX Disclosure; Page 28; 162pp; English.
XX
XX
XX The present sequence represents a complementarity determining region
XX (CDR) 2 from the light chains of a murine antibody with having a binding
XX specificity to B7-2 molecules. The sequence is used to construct
XX humanized immunoglobulins, which comprise an antigen binding region of
XX non-human origin and a portion of a human immunoglobulin. The humanized
XX immunoglobulins are useful for treating autoimmune diseases, infectious
XX diseases, inflammatory disorders, systemic lupus erythematosus, diabetes
XX mellitus, insulinitis, asthma, arthritis, inflammatory bowel disease,
XX inflammatory dermatitis, and multiple sclerosis. The immunoglobulins are
XX also useful for treating a transplant recipient or preventing transplant
XX rejection in a transplant recipient, and treating proliferative disease
XX (leukemia, lymphoma and cancer), anaemia (sickle-cell anaemia,
XX thalassemia and aplastic anaemia), inborn errors of metabolism,
XX congenital immunodeficiency diseases, and myeloid dysplasia syndrome
XX
XX Sequence 7 AA:

Query Match 100.0%; Score 38; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7
1 |||||
Db 1 WASTRES 7

RESULT 9
AAU81257
ID AAU81257 standard; peptide; 7 AA.
XX
XX AAU81257;
XX
XX 09-APR-2002 (first entry)
XX
XX Human trkC antibody light chain CDR2 of variable region #2.
XX
XX Human; mouse; anti-trkC agonist monoclonal antibody; trkC; antibody;
XX trkA; trkB; cisplatin-induced neuropathy; pyridoxine-induced neuropathy;
XX peripheral neuropathy; diabetic neuropathy; neurodegenerative disease;
XX large-fibre sensory neuropathy; amyotrophic lateral sclerosis; tumour;
XX nerve cell injury; blood cell disorder; leukopaenia; eosinopaenia; wound;
XX haemopaenia; lymphopaenia; monocytopenia; neutropenia; cancer; ulcer;
XX Alzheimer's disease; Parkinson's disease; Huntington's disease; diabetes;
XX sickle cell disease; cardiac ischaemia; cerebrovascular disorder;
XX cellular degeneration; gene therapy.
XX
XX Homo sapiens.
XX
XX WO200198361-A2.
XX
XX 27-DEC-2001.
XX
XX 22-JUN-2001; 2001WO-US020153.
XX
XX 22-JUN-2000; 2000US-0213141P.
XX 05-OCT-2000; 2000US-0238319P.
XX
XX (GERTH) GENENTECH INC.
XX
XX Devaux B, Hongo JS, Presta LG, Shelton DL;
XX WPI; 2002-130790/17.
XX
XX Novel anti-trkC agonist monoclonal antibody useful for treating
XX neurodegenerative disease, shows no significant cross-reactivity with
XX trkA/trkB, and recognizes epitope in domain 5 of trkC.
XX

XX Claim 13; Fig 11, 121pp; English.
PS
XX
CC The invention relates to an anti-tyrk agonist monoclonal antibody which
CC shows no significant cross-reactivity with tyrk or tyrkB, and recognizes
CC an epitope in domain 5 of tyrk. The antibodies of the invention are
CC effective in the treatment of cleft-lip- or pyridoxine-induced
CC neuropathy, peripheral neuropathy, diabetic neuropathy and large-fibre
CC sensory neuropathy, neurodegenerative disease including amyotrophic
CC lateral sclerosis, nerve cell injuries, disorders of insufficient blood
CC cells such as leukopenia, including eosinopenia, basopenia,
CC lymphopenia, monocytopenia, neutropenia, Alzheimer's disease,
CC Parkinson's disease, Huntington's disease and tumours. The sequences are
CC also useful for inducing angiogenesis for treating wounds, ulcers and
CC diabetic complications of sickle cell disease, for treating cardiac
CC ischaemia and cerebrovascular disorders and in the diagnosis of diseases
CC involving cellular degeneration. Sequences AA61229-AA61284 represent
CC human and mouse anti-tyrk agonist monoclonal antibodies and antibody
CC fragments of the invention
XX
SQ Sequence 7 AA;
Query Match 100.0%; Score 38; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 WASTRES 7
| | | | |
Db 1 WASTRES 7
RESULT 10
ABP62361
ID ABP62361 standard; peptide; 7 AA.
XX
AC ABP62361;
XX
DT 10-OCT-2002 (first entry)
XX
DE Human immunopeptide to HCV E2 glycoprotein light chain CDR #8.
XX
KM Virucide; human; immunopolypeptide; immunopeptide; envelope glycoprotein;
XX nonstructural protein; hepatitis C virus; HCV; E2 glycoprotein;
XX NS3 protein; viral infection.
XX
OS Homo sapiens.
XX
PN WO200259340-A1.
XX
PD 01-AUG-2002.
XX
PF 25-JAN-2002; 2002WO-US002303.
XX
PR 26-JAN-2001; 2001US-0264451P.
XX
PA (SCRI) SCRIpps RES INST.
XX
PI Maruyama T, Jones IM, Burton DR, Fox RI;
XX WPI; 2002-599801/64.
XX
DR WPI; 2002-599801/64.
XX
PT New human immunopolypeptide with binding specificity for certain envelope
XX glycoproteins and nonstructural proteins of hepatitis C virus (HCV), for
XX diagnosing or treating patients having or suspected of having HCV
XX infection.
XX
PS Claim 1; Fig 17; 308pp; English.
XX
CC The present invention relates to human immunopolypeptides, produced by a
CC phage transfect cell library. The present sequence is one such
CC immunopolypeptide. The immunopolypeptides have binding specificity for
CC envelope glycoprotein E2 and nonstructural protein NS3 of hepatitis C
CC virus (HCV). E2 glycoprotein is believed to be responsible for target

CC cell binding and contains neutralising epitopes, while NS3 is thought to
CC be involved in the replication of HCV. The immunopolypeptides are useful
CC for diagnosing and treating a patient having or suspected to be having
CC HCV infection
XX
SQ Sequence 7 AA;
Query Match 100.0%; Score 38; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 WASTRES 7
| | | | |
Db 1 WASTRES 7
RESULT 11
AAE29275
ID AAE29275 standard; peptide; 7 AA.
XX
AC AAE29275;
XX
DT 27-JAN-2003 (first entry)
XX
DE Anti-C1fa monoclonal antibody variable light chain CDR2.
XX
KM Clumping factor A; C1fa; fibrinogen; fibrin; C1f40; C1f33; N3 protein;
XX immunological; staphylococcal infection; impetigo; pneumonia; furuncle;
XX septic arthritis; sepsis; endocarditis; antibacterial; wound; therapy;
XX complementarity determining region; CDR.
XX
OS Unidentified.
XX
PN WO200272600-A2.
XX
PD 19-SEP-2002.
XX
PF 28-JAN-2002; 2002WO-US002296.
XX
PR 26-JAN-2001; 2001US-0264072P.
XX 12-MAR-2001; 2001US-0274611P.
XX 18-JUN-2001; 2001US-0298413P.
XX 30-JUL-2001; 2001US-0308116P.
XX
PA (INH-) INHIBITEX INC.
XX
PI Patil JM, Hutchins JT, Domaneki P, Patel P, Hall A;
XX WPI; 2002-759834/82.
XX
DR WPI; 2002-759834/82.
XX
PT New anti-clumping factor A (C1fa) monoclonal antibody, useful for
XX treating or preventing Staphylococcus aureus infection e.g. wound
XX infections, impetigo, furuncles, pneumonia, septic arthritis or sepsis in
XX a human or animal.
XX
PS Claim 30; Page 55; 80pp; English.
XX
XX The invention relates to monoclonal antibody which binds the clumping
XX factor A (C1fa) protein from Staphylococcus aureus. The anti-C1fa
XX monoclonal antibody is useful for treating or preventing S. aureus
XX infection in a human or animal, and for inhibiting the binding of
XX staphylococcal bacteria to fibrinogen or fibrin. The immunogenic fragment
XX S. aureus C1f40 protein, S. aureus C1f33 protein, or the S. aureus N3
XX protein is useful for inducing an immunological response in a human or
XX animal. These staphylococcal infections include wound infections, sepsis,
XX impetigo, furuncles, pneumonia, septic arthritis or endocarditis. The
XX present sequence is an anti-C1fa monoclonal antibody variable light chain
XX complementarity determining region (CDR)
XX
SQ Sequence 7 AA;
Query Match 100.0%; Score 38; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 WASTRES 7
|||||
1 WASTRES 7

Db 1 WASTRES 7

RESULT 12
ABG68854
ID ABG68854 standard; peptide; 7 AA.
XX
AC ABG68854;
XX
DT 07-OCT-2002 (first entry)
XX
DE CDR2 VL peptide.
XX
KW Cytostatic; virucide; hepatotropic; antiinflammatory; neuroprotective;
KW immunosuppressive; antithyroid; cytokine receptor; interferon; IFN;
KW cancer; haematological malignancy; viral infection; hepatitis; human;
KW multiple sclerosis; autoimmune disease; arthritis.
XX
OS Synthetic.
XX
PN WO200244197-A2.
XX
PD 06-JUN-2002.
XX
PF 30-NOV-2001; 2001WO-CA001701.
XX
PR 01-DEC-2000; 2000US-00727388.
XX
PA (FISH/) FISH E N.
XX
PI Fish EN;
XX
DR WPI; 2002-547689/58.
XX
DR N-PSDB; ABR97817.

PT Cytokine receptor binding peptide construct, in particular interferon
PT receptor binding peptide construct for use as an interferon mimetic,
PT comprises a cytokine receptor binding domain incorporated in a molecular
PT scaffold.

PS Example 8; Page 50; 105pp; English.

XX This invention relates to a novel cytokine receptor binding peptide
CC construct comprising a cytokine receptor binding domain incorporated in a
CC suitable molecular scaffold so that the scaffold maintains the binding
CC domain in a configuration suitable for binding to the cytokine receptor.
CC The peptides of the invention may have cytosstatic, virucide,
CC hepatotropic, antiinflammatory, neuroprotective, immunosuppressive and
CC antithyroidic activities. A new interferon receptor binding peptide
CC construct is useful in the manufacture of a medicament as an interferon
CC (IFN) mimetic. A peptide that mimics the effect of IFN is useful in
CC medical therapies for cancer, haematological malignancies, viral
CC infections (hepatitis B or C), multiple sclerosis and autoimmune diseases
CC such as arthritis, to detect modulators of IFN action, in screening
CC assays to compare the activity and/or interaction with another molecule
CC or potential IFN modulator and also in the diagnosis of IFN activity
CC related disorders. A nucleic acid encoding the peptide of the invention
CC or is useful for the treatment and therapy of the mentioned medical
CC conditions. The peptide of the invention has less side effect than those
CC of native cytokines. The present sequence represents an interferon
CC receptor binding peptide of the invention
XX

SQ Sequence 7 AA;

Query Match 100.0%; Score 38; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 WASTRES 7

Db 1 WASTRES 7
|||||
1 WASTRES 7

RESULT 13
AAU70347
ID AAU70347 standard; peptide; 7 AA.
XX
AC AAU70347;
XX
DT 14-FEB-2002 (first entry)
XX
DE Mouse Kappa I light chain CDR2.
XX
KW Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;
KW complementarity determining region; framework region; IGBP;
KW transgenic plant; immunoglobulin binding protein array; IGM; IGG; IGA;
KW IGD; IGB; IGY; IGV; IGM; Kappa; Lambda; CHBP.
XX
OS Mus musculus.
XX
PN WO200183806-A1.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US014349.
XX
PR 02-MAY-2000; 2000US-00563222.
XX
PA (EPIC-) EPICYTE PHARM INC.
XX
PI Hiatt AC, Hein MB;
XX
DR WPI; 2002-055482/07.

PT Preparing immunoglobulin binding protein array in plant cells by
PT transforming the cells with different polynucleotides encoding binding
PT protein polypeptides specific to ligand, selecting plant cells for
PT preparing array.

PS Disclosure; Page 14; 129pp; English.

XX The invention relates to transforming a population of cells (e.g. plant
CC cells), comprising using a library of two different polynucleotides
CC encoding different immunoglobulin binding protein (IGBP) polypeptides
CC that specifically bind to a ligand or form one or more disulphide bonds
CC with polypeptides in transfected cells, to generate an IGBP that binds to
CC a ligand, and transformed plant cells are selected, and preparing an IGBP
CC array in plant cells. At least one peptide sequence has at least 75%
CC sequence identity to a framework region (FR) of a native IGM, IGG, IGA,
CC IGD, IGB, IGY, kappa or lambda immunoglobulin molecule. The method is
CC useful for preparing an immunoglobulin binding protein array, preferably
CC heavy chain binding protein (CHBP) array in eukaryotic cells especially
CC plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic
CC cells (e.g. insect cells or mammalian cells). The CHBP is useful for
CC discovery of e.g. screening assays of IGBPs having desired
CC characteristics. The present sequence is a mammalian immunoglobulin
CC derived peptide that may be incorporated into an IGBP of the invention
XX

SQ Sequence 7 AA;

Query Match 100.0%; Score 38; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 WASTRES 7
|||||
1 WASTRES 7

Db 1 WASTRES 7

RESULT 14
AAU70335
ID AAU70335 standard; peptide; 7 AA.

```
XX AC AAU70335;
XX AC 14-FEB-2002 (first entry)
XX DE Human Kappa IV light chain CDR2.
XX XX Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;
XX KW complementarity determining region; framework region; IgB;
XX KW transgenic plant; immunoglobulin binding protein array; IGM; IGF; IGA;
XX KW IGF; IGF; IGM; kappa; lambda; CHBP.
XX OS Homo sapiens;
XX PN WO200183806-A1.
XX PD 08-NOV-2001.
XX PF 02-MAY-2001; 2001WO-US014349.
XX PR 02-MAY-2000; 2000US-00563222.
XX PA (EPIC-) EPICYTE PHARM INC.
XX PI Hiact AC, Hein MB;
XX DR WPI; 2002-055482/07.
XX PT Preparing immunoglobulin binding protein array in plant cells by
XX PT transforming the cells with different polynucleotides encoding binding
XX PT protein polypeptides specific to ligand, selecting plant cells for
XX PT preparing array.
XX PS Disclosure; Page 14; 129pp; English.
XX CC The invention relates to transforming a population of cells (e.g. plant
XX CC cells), comprising using a library of two different polynucleotides
XX CC encoding different immunoglobulin binding protein (IGBP) polypeptides
XX CC that specifically bind to a ligand or form one or more disulphide bonds
XX CC with polypeptides in transfected cells, to generate an IGBP that binds to
XX CC a ligand, and transformed plant cells are selected, and preparing an IGBP
XX CC array in plant cells. At least one peptide sequence has at least 75%
XX CC sequence identity to a framework region (FR) of a native IGM, IGF, IGA,
XX CC IGD, IGE, IGY, kappa or lambda immunoglobulin molecule. The method is
XX CC useful for preparing an immunoglobulin binding protein array, preferably
XX CC heavy chain binding protein (CHBP) array in eukaryotic cells especially
XX CC plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic
XX CC cells (e.g. insect cells or mammalian cells). The CHBP is useful for
XX CC discovery of e.g. screening assays of IGBPs having desired
XX CC characteristics. The present sequence is a mammalian immunoglobulin
XX CC derived peptide that may be incorporated into an IGBP of the invention
XX CC
XX SQ Sequence 7 AA;
XX
XX Query Match 100.0%; Score 38; DB 5; Length 7;
XX Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 WASTRES 7
XX |||||
XX 1 WASTRES 7
XX
XX Db 1 WASTRES 7
XX
XX RESULT 15
XX ID AAE34369 standard; peptide; 7 AA.
XX AC AAE34369;
XX AC 14-MAY-2003 (first entry)
XX DT Becherichia coli light chain variable region CDR2.
XX DE
```

```
KW S-surface antigen; Hepatitis B virus; HBV; therapy; infection; virucide;
KW hepatotropic; complementarity determining region; CDR.
XX OS Escherichia coli.
XX PN WO200292819-A1.
XX PD 21-NOV-2002.
XX PF 15-MAY-2002; 2002WO-KR000905.
XX PR 16-MAY-2001; 2001KR-00026634.
XX PA (YUHA-) YUHAN CORP.
XX PI Lee JW, Ko IY, Kang HK, Song MY, Song TH, Kim CS;
XX DR WPI; 2003-140281/13.
XX PT New light and heavy chain variable regions of a monoclonal antibody
XX PT against the S-surface antigen of the hepatitis B virus (HBV), useful for
XX PT neutralizing or removing HBV, or for preventing or treating HBV
XX PT infection.
XX PS Claim 11; Page 17; 20pp; English.
XX CC The invention relates to light and heavy chain variable regions of a
XX CC monoclonal antibody against S-surface antigen of the hepatitis B virus
XX CC (HBV). The variable regions of the antibodies are useful against HBV S-
XX CC surface antigens, e.g. adr, adw, ayr or ayw, particularly for
XX CC neutralising or removing HBV. They may also be employed to treat or
XX CC prevent HBV infection. The present sequence is Escherichia coli light
XX CC chain variable region complementarity determining region (CDR)
XX CC
XX SQ Sequence 7 AA;
XX
XX Query Match 100.0%; Score 38; DB 6; Length 7;
XX Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 WASTRES 7
XX |||||
XX 1 WASTRES 7
XX
XX Db 1 WASTRES 7
XX
XX RESULT 16
XX ID ABP98689 standard; peptide; 7 AA.
XX AC ABP98689;
XX AC 30-MAY-2003 (first entry)
XX DT Human GAN antibody light chain hypervariable region #2.
XX DE Human; antibody; hypervariable region; diagnosis; cancer therapy;
XX KW light chain; antitumour; cytostatic; stomach; colon.
XX OS Homo sapiens.
XX PN WO2003009870-A1.
XX PD 06-FEB-2003.
XX PF 25-JUL-2002; 2002WO-IP007548.
XX PR 25-JUL-2001; 2001JP-00224596.
XX PA (MITS-) MITSUBISHI PHARMA CORP.
XX PI Hosokawa S, Niki H;
XX DR WPI; 2003-239397/23.
```


XX Tissue-specific remedies for mammary cancer containing human monoclonal
PT antibody associated with antitumor substance for bonding to liposome and
PT encapsulation.
XX
XX Claim 1, Page 24, 30pp; Japanese.
XX
XX This sequence represents the hypervariable region #2 of the human GAN
CC antibody light chain (ABP98692). The antibody or its peptide derivative
CC can be conjugated with an antitumor substance and used for cancer
CC therapy. The method can also be used for treating stomach or colon cancer
XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 38; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

QY 1 WASTRES 7
Db 1 WASTRES 7

RESULT 17
ABP98681
ID ABP98681 standard; peptide; 7 AA.
XX
XX ABP98681;
AC
XX
XX 30-MAY-2003 (first entry)
DT
XX
XX Human GAN antibody light chain hypervariable region #2.
DE
XX human; antibody; epitope; cytostatic; diagnosis; fluorescence wavelength;
KW GAN antibody light chain; hypervariable region; cancer therapy.
XX
XX Homo sapiens.
OS
XX WO2003010542-A1.
PN
XX 06-FEB-2003.
PD
XX
XX 25-JUL-2002; 2002WO-JP007547.
PF
XX 25-JUL-2001; 2001JP-00224054.
PR
XX
XX (MITS-) MITSUBISHI PHARMA CORP.
PA
XX
XX Niki H, Tagawa T, Hosokawa S;
PI
XX
XX WPI; 2003-229648/22.
DR
XX
XX Cancer diagnostics based on peptide or protein recognizing part of tissue
PT slice for staining and detection, also applicable in selecting remedies
PT for cancer therapy and analysis of expression or behavior of protein.
XX
XX
XX Claim 8; Page 46; 52pp; Japanese.
PS
XX The invention relates to diagnostic agents comprising a peptide or a
CC protein capable of recognizing at least a part of a tissue slice and a
CC fluorescent substance characterized by: (a) having a fluorescence
CC wavelength not close to the wavelength region of a non-specific
CC autofluorescence of the tissue slice at a definite excitation wavelength;
CC and (b) allowing simultaneous observation of image of the peptide or
CC protein and that of the tissue slice. This peptide is an example of a
CC peptide used in the method of the invention and represents the
CC hypervariable region #2 from the human GAN antibody light chain. The
CC diagnostic agents are for the detection of cancer, which are also
CC applicable in selecting remedies for cancer therapy and analysis of
CC expression and/or behaviour of proteins
XX
SQ Sequence 7 AA;

XX Query Match 100.0%; Score 38; DB 6; Length 7;
PT Best Local Similarity 100.0%; Pred. No. 2e+06;
PT Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX
XX Claim 1, Page 24, 30pp; Japanese.
XX
XX This sequence represents the hypervariable region #2 of the human GAN
CC antibody light chain (ABP98692). The antibody or its peptide derivative
CC can be conjugated with an antitumor substance and used for cancer
CC therapy. The method can also be used for treating stomach or colon cancer
XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 38; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

QY 1 WASTRES 7
Db 1 WASTRES 7

RESULT 18
ABG71653
ID ABG71653 standard; peptide; 7 AA.
XX
XX ABG71653;
AC
XX
XX 17-JAN-2003 (first entry)
DT
XX
XX CDR2 of HMFg-1 light chain variable region (VL).
DE
XX
XX Human; immunoglobulin variable domain; CDR2; framework region;
KW complementarity determining region 2; anti-MUC-1; HMFg-1;
KW anti-mucin-1 monoclonal antibody; human milk fat globule-1; cancer;
KW tumour cell; mucin-like glycoprotein; neoplasm; carcinoma; breast cancer;
KW ovarian cancer; gastrointestinal cancer; epithelial-derived tumour;
KW light chain variable region; VL; cytostatic.
XX
XX Homo sapiens.
OS
XX WO200278613-A2.
PN
XX 10-OCT-2002.
PD
XX
XX 02-APR-2002; 2002WO-US010304.
PF
XX 02-APR-2001; 2001US-0281182P.
PR
XX
XX (PURD) PURDUE PHARMA LP.
PA
XX
XX Solis DA, Burch RM, Shukla R;
PI
XX
XX WPI; 2003-040616/03.
DR
XX
XX New variant of an immunoglobulin variable domain comprising a
PT complementarity determining region (CDR) and framework regions flanking
PT the CDR, useful for treating or preventing e.g. breast cancer.
XX
XX
XX Disclosure; Page 11; 75pp; English.
PS
XX
XX The present invention relates to a variant of an immunoglobulin variable
CC domain comprising at least one complementarity determining region (CDR)
CC and framework regions flanking the CDR, where the variant also comprises
CC a CDR region to which at least one binding sequence is added or
CC substituted, and flanking framework regions, where the binding sequence
CC is heterologous to the CDR and is an antigenic sequence from a mucin-1
CC (MUC-1) binding sequence. The variant immunoglobulin variable domain is
CC preferably a variant of the variable region of an anti-mucin monoclonal
CC antibody such as the anti-MUC-1 monoclonal antibody HMFg-1 (human milk
CC fat globule-1). Compositions comprising the variant immunoglobulin and
CC the methods of the present invention are useful for treating cancer by
CC eliciting an anti-idiotypic response targeted to tumour cells that bear
CC mucin-like glycoproteins on neoplasms of epithelial origin, including
CC carcinomas of the breast, ovary and gastrointestinal tract. A vaccine
CC based on the sequence of the HMFg-1 monoclonal antibody may be used in
CC the treatment and prevention of breast cancer and other epithelial-
CC derived tumours. The present sequence represents a CDR contained in the
CC light chain variable region of HMFg-1
XX
SQ Sequence 7 AA;

QY 1 WASTRES 7
 |||||
 Db 1 WASTRES 7

RESULT 19

AAE38110
 ID AAE38110 standard; peptide; 7 AA.

XX AAE38110;

XX 06-NOV-2003 (first entry)

DE Human COU-1 antibody VL CDR2 peptide #3.

XX Human; cancer-associated epitope; cytokeratin K8; cytokeratin K18; VL;
 KM adenocarcinoma; therapy; cancer; antibody; light chain variable region;
 KM complementarity determining region; CDR.

XX Homo sapiens.

OS WO2003057168-A2.

PN 17-JUL-2003.

XX 03-JAN-2003; 2003WO-US000297.

XX 03-JAN-2002; 2002US-0345208P.

XX (SCRI) SCRIPPS RES INST.

XX Ditzel H, Jensenius JC;

XX WPI; 2003-598315/56.

PT Novel isolated cancer-associated epitope comprising two separate
 PT polypeptides, a cytokeratin 8 polypeptide and a cytokeratin 18
 PT polypeptide, useful as component of vaccine for preventing or treating
 PT adenocarcinoma.

PS Claim 15; Page 36; 155pp; English.

XX The invention provides a cancer-associated epitope comprising two
 CC separate polypeptides, a cytokeratin 8 polypeptide and a cytokeratin 18
 CC polypeptide. Vaccine composition of the invention is useful for treating
 CC or preventing colon adenocarcinoma, ovarian adenocarcinoma, renal
 CC adenocarcinoma, mammary adenocarcinoma, lung adenocarcinoma, pancreatic
 CC adenocarcinoma or non-renal adenocarcinoma. The invention is also
 CC useful for preparing a medicament for treating or preventing cancer in a
 CC mammal. The present sequence is human COU-1 cancer-associated epitope
 CC antibody VL (light chain variable region) CDR (complementarity
 CC determining region) peptide

XX Sequence 7 AA;

Query Match 100.0%; Score 38; DB 6; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
 |||||
 Db 1 WASTRES 7

RESULT 20

ABO33872
 ID ABO33872 standard; peptide; 7 AA.

XX ABO33872;

XX 18-SEP-2003 (first entry)

DE Anti-GPI-antibody light chain complementarity determining region #11.

XX Human; anti-glucose-6-phosphate isomerase-antibody; immunopolypeptide;
 KM anti-GPI-antibody; GPI; glucose-6-phosphate isomerase; immunopolypeptide;
 KM autoimmune disease; rheumatoid arthritis; light chain variable region;
 KM VL; complementarity determining region; CDR.

OS Homo sapiens.

PN US2002146753-A1.

XX 10-OCT-2002.

XX 06-APR-2001; 2001US-00828708.

XX 06-APR-2001; 2001US-00828708.

XX (DITZEL) DITZEL H.
 PA (BURTON) BURTON D R.
 PA (SCHALLER) SCHALLER M.

XX Ditzel H, Burton DR, Schaller M;

XX WPI; 2003-521517/49.

PT Immunopolypeptide for diagnosis and treatment of human autoimmune
 PT disease, e.g., human rheumatoid arthritis, comprises a polypeptide that
 PT binds to human glucose-6-phosphate isomerase.

XX Claim 3; Fig 4A; 47pp; English.

XX The invention describes an immunopolypeptide comprising a polypeptide
 CC that binds to human glucose-6-phosphate isomerase (GPI). The methods and
 CC compositions are used for diagnosis and treatment of human autoimmune
 CC disease, e.g., human rheumatoid arthritis. This is the amino acid
 CC sequence of human anti-GPI-antibody light chain variable region
 CC complementarity determining region

XX Sequence 7 AA;

Query Match 100.0%; Score 38; DB 7; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
 |||||
 Db 1 WASTRES 7

RESULT 21

ABO33869
 ID ABO33869 standard; peptide; 7 AA.

XX ABO33869;

XX 18-SEP-2003 (first entry)

DE Anti-GPI-antibody light chain complementarity determining region #8.

XX Human; anti-glucose-6-phosphate isomerase-antibody; immunopolypeptide;
 KM anti-GPI-antibody; GPI; glucose-6-phosphate isomerase;
 KM autoimmune disease; rheumatoid arthritis; light chain variable region;
 KM VL; complementarity determining region; CDR.

OS Homo sapiens.

PN US2002146753-A1.

XX 10-OCT-2002.

XX 06-APR-2001; 2001US-00828708.

XX 06-APR-2001; 2001US-00828708.

XX

PA (DITZ/) DITZEL H.
 PA (BURT/) BURTON D R.
 PA (SCHA/) SCHALLER M.
 XX
 PI Ditzel H, Burton DR, Schaller M;
 XX
 DR WPI; 2003-521517/49.
 XX
 PT Immunopolypeptide for diagnosis and treatment of human autoimmune
 PT disease, e.g., human rheumatoid arthritis, comprises a polypeptide that
 PT binds to human glucose-6-phosphate isomerase.
 XX
 PS Claim 3; Fig 4A; 47pp; English.
 XX
 CC The invention describes an immunopolypeptide comprising a polypeptide
 CC that binds to human glucose-6-phosphate isomerase (GPI). The methods and
 CC compositions are used for diagnosis and treatment of human autoimmune
 CC disease, e.g., human rheumatoid arthritis. This is the amino acid
 CC sequence of human anti-GPI-antibody light chain variable region
 CC complementarity determining region
 XX
 SQ Sequence 7 AA;

Query Match 100.0%; Score 38; DB 7; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
 |||||
 DB 1 WASTRES 7

RESULT 22

ID ADC97709 standard; peptide; 7 AA.
 XX
 AC ADC97709;

DT 01-JAN-2004 (first entry)
 XX

DE Mouse monoclonal antibody LL2 VKappa CDR2.
 XX

XX Mouse; monoclonal antibody; LL2; Kappa chain variable region; VKappa;
 KW cytostatic; complementarity determining region; CDR; B-lymphoma;
 KW leukemia; humanised antibody.
 XX

OS Mus sp.
 XX

PN US2003103979-A1.
 XX

PD 05-JUN-2003.
 XX

PF 16-NOV-2001; 2001US-00988013.
 XX

PR 16-NOV-2001; 2001US-00988013.
 XX

PA (LEUNG/) LEUNG S.
 PA (HANS/) HANSEN H.
 XX

PI Leung S, Hansen H;
 XX

DR WPI; 2003-801218/75.
 XX

PT Novel LL2 monoclonal antibody useful for diagnosing and treating B-cell
 PT lymphoma or leukemia.
 XX

PS Claim 7; Page 11; 30pp; English.
 XX

CC The invention relates to an isolated polynucleotide comprising a DNA
 CC sequence encoding the amino acid sequence of light chain (kappa) variable
 CC (VK) region or heavy chain variable (VH) region of LL2 monoclonal
 CC antibody (mab), and hLL2 VK domain or hLL2 VH domain. Also included are a
 CC protein encoded by the DNAs listed above, an isolated complementarity

CC determining region-1 (CDRL1, CDR2 or CDR3) polypeptide of the VK or VH
 CC region of the LL2 mab, a cll2 mab (comprising the light chain and heavy
 CC chains of the LL2 mab linked to the human kappa and human IgG 1 constant
 CC regions, respectively), an hLL2 mab (comprising a light chain and a heavy
 CC chain CDR of a mLL2 mab joined to a framework sequence of a human VK and
 CC human VH region, respectively, linked to human kappa and IgG 1 constant
 CC region domains, respectively, such that the hLL2 mab retains
 CC substantially the B-lymphoma cell and leukemia cell targeting cell
 CC internalisation characteristics of the parent mLL2 antibody) and a
 CC conjugate comprising a cll2 or hll2 antibody or its fragment covalently
 CC bound to a diagnostic or therapeutic reagent. The conjugate is useful for
 CC treating and diagnosing a B-cell lymphoma or leukemia in a subject. The
 CC present sequence represents mouse LL2 VKappa CDR2.
 XX

SQ Sequence 7 AA;

Query Match 100.0%; Score 38; DB 7; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
 |||||
 DB 1 WASTRES 7

RESULT 23
 ID ADG43867 standard; peptide; 7 AA.
 XX
 AC ADG43867;

DT 26-FEB-2004 (first entry)
 XX

DE Human peptide of the invention SEQ ID NO.5.
 XX

KW human; free cysteine; monoclonal antibody.
 XX

OS Homo sapiens.
 XX

PN MO2003048357-A1.
 XX

PD 12-JUN-2003.
 XX

PF 04-DEC-2002; 2002WO-JP012701.
 XX

PR 04-DEC-2001; 2001JP-00370541.
 XX

PA (MITS-) MITSUBISHI PHARMA CORP.
 XX

PI Kouno T, Katsumura Y;
 XX

DR WPI; 2003-505293/47.
 XX

PT Producing activated protein containing free Cys such as human monoclonal
 PT antibody.
 XX

PS Claim 14; SEQ ID NO 5; 63pp; Japanese.
 XX

CC The invention relates to a novel method for producing protein containing
 CC free cysteine in its activated form. The method of the invention is
 CC useful for preparation of activated protein containing free Cys,
 CC preferably human monoclonal antibody. The present sequence is used in the
 CC exemplification of the invention.
 XX

SQ Sequence 7 AA;

Query Match 100.0%; Score 38; DB 7; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
 |||||
 DB 1 WASTRES 7

RESULT 24	
ADL23027	
ID ADL23027 standard; peptide; 7 AA.	
XX	
AC ADL23027;	
DT 20-MAY-2004 (first entry)	
DE Myelin associated glycoprotein MAG binding antibody light chain CDR L2.	
KX antibody; MAG; myelin associated glycoprotein; light chain; CDR; stroke;	
KW neurodegenerative disorder; gene therapy; vaccine.	
XX	
OS Unidentified.	
XX	
FN WO2004014953-A2.	
PD 19-FEB-2004.	
PF 05-AUG-2003; 2003WO-EP008749.	
PR 06-AUG-2002; 2002GB-00018229.	
PR 06-AUG-2002; 2002GB-00018230.	
PR 06-AUG-2002; 2002GB-00018232.	
XX 06-AUG-2002; 2002GB-00018234.	
PA (GLAXO) GLAXO GROUP LTD.	
PI Ellis JH, Germaschewski V;	
DR WPI; 2004-180641/17.	
DR N-PsDB; ADL23032.	
PT New altered antibody that binds to and neutralizes myelin associated	
PT glycoprotein (MAG), useful for preparing a composition for treating or	
PT preventing stroke or other neurodegenerative disorders e.g., Alzheimer's	
PT disease.	
XX	
PS Claim 1; Page 53; 67pp; English.	
CC The present invention relates to a new altered antibody or its functional	
CC fragment, which binds to and neutralizes myelin associated glycoprotein	
CC (MAG) and comprises a light chain variable domain (VL) comprising	
CC complementary determining region light 1 (CDRL1), CDRL2 or CDRJ3 and/or a	
CC heavy chain variable domain (VH) comprising CDRH1, CDRH2 or CDRH3. The	
CC antibody is useful for preparing a composition for treating or preventing	
CC stroke or other neurodegenerative disorders in a human, e.g., traumatic	
CC brain injury, Alzheimer's disease, dementia, peripheral neuropathy,	
CC Parkinson's disease, Huntington's disease and multiple sclerosis. The	
CC present sequence is the anti-MAG antibody light chain CDR L2 of the	
CC invention.	
XX	
SO Sequence 7 AA;	
OY Query Match 100.0%; Score 38; DB 8; Length 7;	
Best Local Similarity 100.0%; Pred. No. 2e+06;	
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Db 1 MASTRS 7	
1 WASTRES 7	
RESULT 25	
ADO32089	
ID ADO32089 standard; peptide; 7 AA.	
XX	
AC ADO32089;	
XX	
DT 12-AUG-2004 (first entry)	

DE Mouse anti-CD33 antibody My9-6 light chain CDR2 SEQ ID NO:5.
XX
XX anti-CD33 antibody; epitope-binding fragment;
XX complementarity-determining region; CDR; immunconjugate; cytostatic;
KW antibody; myelodysplastic syndrome; acute myeloid leukaemia;
KW chronic myeloid leukaemia; pro-myelocytic leukaemia; mouse; My9-6;
KW light chain.
XX
XX Mus musculus.
OS
PN WO2004043344-A2.
PD
PD 27-MAY-2004.
XX
XX 05-NOV-2003; 2003WO-US032737.
PF
PR 07-NOV-2002; 2002US-0424332P.
XX
XX (IMMU-) IMMUNOGEN INC.
PA
PI Hoffee MG, Tavares D, Lutz RJ;
XX
XX WPI; 2004-411619/38.
DR
PT New antibodies that bind to CD33, useful for treating a disease
PT associated with CD33 expression, such as myelodysplastic syndrome, acute
PT or chronic myeloid leukemia.
PS
PS Claim 1; SEQ ID NO 5; 124pp; English.
XX
XX The present invention describes an isolated anti-CD33 antibody or its
CC epitope-binding fragment comprising: (a) at least one complementarity-
CC determining region (CDR); or (b) at least heavy chain variable region
CC comprising 3 CDRs, and at least one light chain variable region, where
CC the CDR has the ability to bind CD33. Also described: (1) an
CC immunconjugate comprising the antibody or its epitope-binding fragment
CC linked to a drug or prodrug; (2) a composition comprising the antibody or
CC epitope-binding fragment and a drug or prodrug; (3) a pharmaceutical
CC composition comprising the immunconjugate, composition or the antibody
CC defined above, or its epitope-binding fragment, and a pharmaceutical
CC agent; (4) a diagnostic reagent comprising the antibody defined above,
CC where the antibody or antibody fragment is labelled; (5) inhibiting the
CC growth of a cell expressing CD33 by contacting the cell with the above
CC defined antibody or its epitope-binding fragment, immunconjugate, or
CC (pharmaceutical) composition; (6) determining whether a biological sample
CC contains a myelogenous cancer cell; (7) an improved antibody or its
CC epitope-binding fragment that specifically binds to CD33; (8) an isolated
CC polynucleotide encoding the antibody or its epitope-binding fragment
CC defined above; (9) an isolated polynucleotide encoding a light or heavy
CC chain of the antibody defined above or its epitope-binding fragment; (10)
CC a recombinant vector comprising the polynucleotide; (11) a host cell
CC transformed with the recombinant vector; (12) producing an antibody or
CC its epitope-binding fragment having the ability to bind CD33; and (13)
CC obtaining CD33 from a biological material. The anti-CD33 antibody has
CC cytostatic activity. The antibody or its epitope-binding fragment,
CC immunconjugate, composition can be used for treating a subject having a
CC disease where CD33 is expressed, such as myelodysplastic syndrome, acute
CC myeloid leukaemia, chronic myeloid leukaemia or pro-myelocytic leukaemia.
CC It can also be used for inhibiting the growth of cells expressing CD33,
CC and for in vivo imaging or as affinity purification agents. The present
CC sequence represents the mouse anti-CD33 antibody My9-6 light chain CDR2,
CC which is used in an example from the present invention.
XX
XX
SQ Sequence 7 AA;
Query Match 100.0%; Score 38; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 WASTRES 7
|||||
1 WASTRES 7

RESULT 26
AD058066
ID ADO58066 standard; peptide; 7 AA.
XX
AC ADO58066;
XX
DT 12-AUG-2004 (first entry)
XX
XX
DE S2 cell derived human scFvL-VH CDR peptide, SEQ ID 66.
XX
XX
KW B cell; surface immunoglobulin; Ig; binding site; antigen; human CD28;
KW closed system; detection laser-beam; catcher tube;
KW electrochemical device; fluorescence activated cell sorter; FACS;
KW antibody variable region; human.
XX
XX
OS Homo sapiens.
XX
XX
PN WO2004044584-A1.
XX
PD 27-MAY-2004.
XX
XX
PF 12-NOV-2003; 2003WO-EP012664.
XX
XX
PR 13-NOV-2002; 2002EP-00025335.
XX
XX
PA (MICR-) MICROMET AG.
XX
XX
PI Baewerle P, Hoffmann P, Weinberger S, Kischel R;
XX
XX
DR WPI; 2004-449579/42.
XX
XX
DR N-PSDB; ADO58067.
XX
XX
PT Identifying a B cell carrying a surface immunoglobulin molecule having a
PT binding site for an antigen of interest, useful for constructing
PT therapeutic antibodies, comprises contacting a sample with the antigen
PT and a receptor.
XX
XX
PS Example 6; SEQ ID NO 66; 156pp; English.
XX
XX
CC The invention relates to a novel method for identifying a B cell carrying
CC a surface immunoglobulin (Ig) molecule having a binding site for an
CC antigen of interest. The method comprises contacting a sample putatively
CC containing the B cell with the antigen of interest and with a receptor
CC specifically binding to the Ig molecule, and assessing the presence of
CC the detectable signal. The invention further comprises: an antibody
CC generated by the method above which is specific for human CD28 or
CC comprising an amino acid(s) sequence(s) given in the specification,
CC and/or are encoded by a nucleic acid sequence(s) also given in the
CC specification; and a device for assessing the presence of a detectable
CC signal defined above, where the device comprises a closed system for the
CC detection laser-beam and a catcher tube, and where the B cell of interest
CC can be collected as a single cell by means of an electrochemical device,
CC which is triggered by an electric signal generated by the fluorescence
CC activated cell sorter (FACS) device, where the electrochemical device
CC moves the nozzle of the steady catcher tube liquid stream for a
CC programmed time over a collecting tube, microtiter plate or other
CC container after a B cell is sorted. The method is useful for identifying
CC a B cell carrying a surface Ig molecule having a binding site for an
CC antigen of interest. The method is also useful for cloning of antibody
CC variable regions from the identified B cells, which may subsequently be
CC employed in the construction of proteins such as antibodies or its
CC fragments or derivatives useful in therapeutic approaches. The method is
CC useful as an alternative to phage display for the gain of antibodies or
CC its fragments. This sequence represents an S2 cell derived human
CC polypeptide of the invention.
XX
XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 38; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7
|||||
Db 1 WASTRES 7

RESULT 27
ADP47268
ID ADP47268 standard; peptide; 7 AA.
XX
AC ADP47268;
XX
DT 09-SEP-2004 (first entry)
XX
XX
DE Human phospholipase A2-specific mAb light chain peptide #38.
XX
XX
KW human; monoclonal antibody; phospholipase A2; PLA2;
KW inflammatory disorder; degenerative disorder;
KW joint inflammatory reaction; skin inflammatory reaction;
KW blood vessels inflammatory reaction; arthritis; psoriasis; asthma;
KW Alzheimer's disease; atherosclerosis; restenosis; light chain.
XX
XX
OS Homo sapiens.
XX
XX
PN WO2004050850-A2.
XX
XX
PD 17-JUN-2004.
XX
XX
PF 02-DEC-2003; 2003WO-US038234.
XX
XX
PR 02-DEC-2002; 2002US-0430724P.
XX
XX
PA (ABGE-) ABGENIX INC.
XX
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
XX
PI Landes GM, Haak-Frendescho M, Chen L, Lee YR, Liang ML, Feng X,
PI Jia X, Nocerini MR;
XX
XX
DR WPI; 2004-46119/43.
XX
XX
PT New human monoclonal antibody that binds to phospholipase A2 (PLA2),
PT useful for treating inflammatory conditions, e.g. arthritis, psoriasis,
PT asthma, Alzheimer's disease, atherosclerosis, or restenosis.
XX
XX
PS Example 5; SEQ ID NO 183; 128pp; English.
XX
XX
CC The invention comprises a human monoclonal antibody that binds to
CC phospholipase A2 (PLA2). The monoclonal antibody of the invention is
CC useful in the preparation of a medicament for the treatment of
CC inflammatory and degenerative disorders stemming from inflammatory
CC reactions in the joints, skin, and blood vessels, arthritis, psoriasis,
CC asthma, Alzheimer's disease, atherosclerosis, and restenosis. The present
CC amino acid sequence represents a human PLA2-specific monoclonal antibody
CC light chain peptide.
XX
XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 38; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7
|||||
Db 1 WASTRES 7

RESULT 28
ADP47250
ID ADP47250 standard; peptide; 7 AA.
XX
AC ADP47250;
XX
DT 09-SEP-2004 (first entry)
XX

DE Human phospholipase A2-specific mAb light chain peptide #20.
XX human; monoclonal antibody; phospholipase A2; PLA2;
KW inflammatory disorder; degenerative disorder;
KW joint inflammatory reaction; skin inflammatory reaction;
KW blood vessels inflammatory reaction; arthritis; psoriasis; asthma;
KW Alzheimer's disease; atherosclerosis; restenosis; light chain.
XX Homo sapiens.
OS
PN WO2004050850-A2.
XX
PD 17-JUN-2004.
XX
PF 02-DEC-2003; 2003WO-US038234.
XX
PR 02-DEC-2002; 2002US-0430724P.
XX
PA (ABGE-) ABGENIX INC.
XX (LEXI-) LEXICON GENETICS INC.
XX
PI Landes GM, Haak-Frendscho M, Chen L, Lee YR, Liang ML, Feng X;
XX dia X, Nocerini MR;
XX WPI; 2004-461119/43.
XX
PT New human monoclonal antibody that binds to phospholipase A2 (PLA2),
PT useful for treating inflammatory conditions, e.g. arthritis, psoriasis,
PT asthma, Alzheimer's disease, atherosclerosis, or restenosis.
XX
PS Example 5; SEQ ID NO 165; 128bp; English.
XX
CC The invention comprises a human monoclonal antibody that binds to
CC phospholipase A2 (PLA2). The monoclonal antibody of the invention is
CC useful in the preparation of a medicament for the treatment of
CC inflammatory and degenerative disorders stemming from inflammatory
CC reactions in the joints, skin, and blood vessels, arthritis, psoriasis,
CC asthma, Alzheimer's disease, atherosclerosis, and restenosis. The present
CC amino acid sequence represents a human PLA2-specific monoclonal antibody
CC light chain peptide.
XX
SQ Sequence 7 AA;
XX
Query Match 100.0%; Score 38; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WASTRES 7
DB 1 WASTRES 7
XX
RESULT 29
ADP47241
ID ADP47241 standard; peptide; 7 AA.
XX
AC ADP47241;
XX
DT 09-SEP-2004 (first entry)
XX
DE Human phospholipase A2-specific mAb light chain peptide #11.
XX
KW human; monoclonal antibody; phospholipase A2; PLA2;
KW inflammatory disorder; degenerative disorder;
KW joint inflammatory reaction; skin inflammatory reaction;
KW blood vessels inflammatory reaction; arthritis; psoriasis; asthma;
KW Alzheimer's disease; atherosclerosis; restenosis; light chain.
XX
XX Homo sapiens.
OS
PN WO2004050850-A2.
XX
PD 17-JUN-2004.

XX
PF 02-DEC-2003; 2003WO-US038234.
XX
PR 02-DEC-2002; 2002US-0430724P.
XX
PA (ABGE-) ABGENIX INC.
XX (LEXI-) LEXICON GENETICS INC.
XX
PI Landes GM, Haak-Frendscho M, Chen L, Lee YR, Liang ML, Feng X;
XX dia X, Nocerini MR;
XX WPI; 2004-461119/43.
XX
PT New human monoclonal antibody that binds to phospholipase A2 (PLA2),
PT useful for treating inflammatory conditions, e.g. arthritis, psoriasis,
PT asthma, Alzheimer's disease, atherosclerosis, or restenosis.
XX
PS Example 5; SEQ ID NO 156; 128bp; English.
XX
CC The invention comprises a human monoclonal antibody that binds to
CC phospholipase A2 (PLA2). The monoclonal antibody of the invention is
CC useful in the preparation of a medicament for the treatment of
CC inflammatory and degenerative disorders stemming from inflammatory
CC reactions in the joints, skin, and blood vessels, arthritis, psoriasis,
CC asthma, Alzheimer's disease, atherosclerosis, and restenosis. The present
CC amino acid sequence represents a human PLA2-specific monoclonal antibody
CC light chain peptide.
XX
SQ Sequence 7 AA;
XX
Query Match 100.0%; Score 38; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WASTRES 7
DB 1 WASTRES 7
XX
RESULT 30
ADP47271
ID ADP47271 standard; peptide; 7 AA.
XX
AC ADP47271;
XX
DT 09-SEP-2004 (first entry)
XX
DE Human phospholipase A2-specific mAb light chain peptide #1.
XX
KW human; monoclonal antibody; phospholipase A2; PLA2;
KW inflammatory disorder; degenerative disorder;
KW joint inflammatory reaction; skin inflammatory reaction;
KW blood vessels inflammatory reaction; arthritis; psoriasis; asthma;
KW Alzheimer's disease; atherosclerosis; restenosis; light chain.
XX
XX Homo sapiens.
OS
PN WO2004050850-A2.
XX
PD 17-JUN-2004.
XX
PF 02-DEC-2003; 2003WO-US038234.
XX
PR 02-DEC-2002; 2002US-0430724P.
XX
PA (ABGE-) ABGENIX INC.
XX (LEXI-) LEXICON GENETICS INC.
XX
PI Landes GM, Haak-Frendscho M, Chen L, Lee YR, Liang ML, Feng X;
XX dia X, Nocerini MR;
XX WPI; 2004-461119/43.
XX

PT New human monoclonal antibody that binds to phospholipase A2 (PLA2),
PT useful for treating inflammatory conditions, e.g. arthritis, psoriasis,
PT asthma, Alzheimer's disease, atherosclerosis, or restenosis.
XX
PS Example 5; SEQ ID NO 186; 128bp; English.
XX
CC The invention comprises a human monoclonal antibody that binds to
CC phospholipase A2 (PLA2). The monoclonal antibody of the invention is
CC useful in the preparation of a medicament for the treatment of
CC inflammatory and degenerative disorders stemming from inflammatory
CC reactions in the joints, skin, and blood vessels, arthritis, psoriasis,
CC asthma, Alzheimer's disease, atherosclerosis, and restenosis. The present
CC amino acid sequence represents a human PLA2-specific monoclonal antibody
CC light chain peptide.
XX
SQ Sequence 7 AA;
XX
Query Match 100.0%; Score 38; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WASTRES 7
DB 1 WASTRES 7
XX
RESULT 31
ADP47286
ID ADP47286 standard; peptide; 7 AA.
XX
AC ADP47286;
XX
DT 09-SEP-2004 (first entry)
XX
DE Human phospholipase A2-specific mab light chain peptide #56.
XX
KW human; monoclonal antibody; phospholipase A2; PLA2;
KW inflammatory disorder; degenerative disorder;
KW joint inflammatory reaction; skin inflammatory reaction;
KW blood vessels inflammatory reaction; arthritis; psoriasis; asthma;
KW Alzheimer's disease; atherosclerosis; restenosis; light chain.
XX
OS Homo sapiens.
XX
PN WO2004050850-A2.
XX
PD 17-JUN-2004.
XX
PF 02-DEC-2003; 2003WO-US038234.
XX
PR 02-DEC-2002; 2002US-0430724P.
XX
PA (ABGE-) ABGENIX INC.
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Landes GM, Haak-Frendescho M, Chen L, Lee YR, Liang ML, Feng X;
PI Jia X, Nocerini MR;
XX
DR WPI; 2004-461119/43.
XX
PT New human monoclonal antibody that binds to phospholipase A2 (PLA2),
PT useful for treating inflammatory conditions, e.g. arthritis, psoriasis,
PT asthma, Alzheimer's disease, atherosclerosis, or restenosis.
XX
PS Example 5; SEQ ID NO 201; 128bp; English.
XX
CC The invention comprises a human monoclonal antibody that binds to
CC phospholipase A2 (PLA2). The monoclonal antibody of the invention is
CC useful in the preparation of a medicament for the treatment of
CC inflammatory and degenerative disorders stemming from inflammatory
CC reactions in the joints, skin, and blood vessels, arthritis, psoriasis,
CC asthma, Alzheimer's disease, atherosclerosis, and restenosis. The present
CC amino acid sequence represents a human PLA2-specific monoclonal antibody

* CC light chain peptide.
XX
SQ Sequence 7 AA;
XX
Query Match 100.0%; Score 38; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WASTRES 7
DB 1 WASTRES 7
XX
RESULT 32
ADQ28264
ID ADQ28264 standard; peptide; 7 AA.
XX
AC ADQ28264;
XX
DT 23-SEP-2004 (first entry)
XX
DE Method of protecting thiol groups in proteins peptide #5.
XX
KW thiol group; free cysteine residue; disulfide bond.
XX
OS Homo sapiens.
XX
PN WO2004056872-A1.
XX
PD 08-JUL-2004.
XX
PF 19-DEC-2003; 2003WO-JP016362.
XX
PR 20-DEC-2002; 2002JP-00370822.
XX
PA (MTS-) MITSUBISHI PHARMA CORP.
XX
PI Sasaki K, Katsunuma Y;
XX
DR WPI; 2004-507699/48.
XX
PT Protecting thiol group of protein by suppressing, inhibiting
PT polymerization reaction through thiol group and inhibiting exchange
PT reaction of protein, by adding compound having disulfide bond and free
PT cysteine residue.
XX
PS Claim 16; SEQ ID NO 5; 45bp; Japanese.
XX
CC The present invention relates to a method of protecting thiol groups in
CC proteins having a free cysteine residue. This involves adding a compound
CC which has a disulfide bond in the molecule and exerts substantially no
CC influence on the activity of the protein. The present sequence is a
CC peptide used in the exemplification of the invention.
XX
SQ Sequence 7 AA;
XX
Query Match 100.0%; Score 38; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WASTRES 7
DB 1 WASTRES 7
XX
RESULT 33
ADS88787
ID ADS88787 standard; peptide; 7 AA.
XX
AC ADS88787;
XX
DT 16-DEC-2004 (first entry)
XX

```

DE      Light chain CDR L2 of an anti-MAG antibody.
XX
XX      oligodendrocyte; stroke; neurological disease;
KW      myelin-associated glycoprotein; MAG; anti-MAG antibody;
RW      Alzheimer's disease; multiple sclerosis;
KW      chain complementarity determining region; CDR.
XX
OS      unidentified.
PN      WO200408363-A2.
PD      30-SEP-2004.
XX
PF      02-FEB-2004; 2004WO-EP001016.
PR      19-MAR-2003; 2003GB-00006309.
PA      (GLAX ) GLAXO GROUP LTD.
PI      Vinson M, Irving EA;
XX
DR      WPI: 2004-691029/67.
PT      Promoting oligodendrocyte survival in humans with neurological diseases,
PR      such as Alzheimer's disease, multiple sclerosis and/or stroke, using an
PS      anti-myelin-associated glycoprotein (MAG) antibody.
XX
XX      Claim 6; SEQ ID NO 2; 45pp; English.
CC      The specification describes a method for promoting oligodendrocyte
CC      survival in a human suffering or at risk of developing stroke or another
CC      neurological diseases. The method comprises administering to the human an
CC      anti-myelin-associated glycoprotein (MAG) antibody or its functional
CC      fragment. The anti-MAG antibody or its functional fragment is useful in
CC      the manufacture of a medicament for the promotion of oligodendrocyte
CC      survival in a human suffering from or at risk of developing stroke or
CC      another neurological disease. They can also be used in treating
CC      neurological diseases, such as Alzheimer's disease, multiple sclerosis
CC      and/or stroke, by promoting oligodendrocyte survival. AD588786-AD588788
CC      represent the light chain complementarity determining regions (CDRs) of
CC      an anti-MAG antibody which can be used in the method of the invention.
XX
XX
SQ      Sequence 7 AA;
QY      Query Match          100.0%; Score 38; DB 8; Length 7;
       Best Local Similarity 100.0%; Pred.No. 2e+06; Indels 0; Gaps 0;
       Matches 7; Conservative 0; Mismatches 0;
Db      1 WASTRES 7
       1 WASTRES 7
DE      RESULT 34
ID      ADT50351 standard; peptide; 7 AA.
AC      ADT50351;
XX
DT      13-JAN-2005 (first entry)
DE      Human monoclonal antibody light chain hypervariable region peptide Seq 5.
XX      antibody; GH; tumour; cancer; cytoskeletal; myosin;
KW      non-muscular type myosin heavy-chain type A; cytosstatic.
XX
OS      Homo sapiens.
PN      WO2004089984-A1.
PD      21-OCT-2004.
XX
PF      03-OCT-2003; 2003WO-JP012732.

```

PR	04-OCT-2002; 2002JP-00291953.
XX	(MITS-) MITSUBISHI PHARMA CORP.
XX	Hirakawa Y, Niki H, Oike S, Tagawa T, Hosokawa S, Yoshiyama Y;
PI	WPI; 2004-757952/74.
DR	New non-muscular type myosin heavy chain type A antigen expressed on cell
PT	surface of tumor mass, useful as target in treatment of cancer such as
PT	stomach cancer.
PS	Claim 18; SEQ ID NO 5; 60pp; Japanese.
XX	This invention relates to a novel antigen expressed on the surface of a
CC	cell during formation of a tumour mass. Specifically, it refers to a
CC	labelled ligand that is capable of recognising this antigen and a
CC	pharmaceutical composition derived thereof useful for treating a cancer
CC	patient. The present invention describes the antigen as a cytoskeletal
CC	protein such as myosin or its variant and preferably it is a non-muscular
CC	type myosin heavy-chain type A protein. Accordingly, the pharmaceutical
CC	compositions developed thereof exhibit cytostatic activity and are useful
CC	as anticancer agents in patients expressing this antigen and where the
CC	cancer is chosen from stomach, breast, colon or oesophageal cancer.
CC	Furthermore, the ligand is a monoclonal antibody, preferably a humanised
CC	monoclonal antibody that has cancer reactive properties and as such can
CC	specifically target the cancerous tissue or cell. This peptide sequence
CC	is from the human monoclonal antibody (GAH) light chain, hypervariable
CC	region, given in an exemplification of the invention.
SQ	Sequence 7 AA:
Query Match	100.0%; Score 38; DB 8; Length 7;
Best Local Similarity	100.0%; Pred. No. 2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Gy	1 WASTRES 7 1 WASTRES 7
Db	
RESULT 35	
ADV21417	
ID ADV21417 standard; peptide; 7 AA.	
XX AC ADV21417;	
XX DT 24-FEB-2005 (first entry)	
XX DE Human antibody VL domain CDR2 SEQ ID No1126.	
XX Antibody engineering; binding molecule; antibody; humanized antibody;	
KW proliferative disorder; tumor; inflammation; immune disorder;	
KW autoimmune disease; infectious disease; viral infection; cytotoxic;	
KW allergy; parasitic reaction; graft versus host disease; cytotoxic;	
KW antiinflammatory; immunosuppressive; antimicrobial; virulence;	
KW antiallergic; antiparasitic; light chain variable region; VL;	
XX complementarity determining region; CDR.	
OS Homo sapiens.	
XX WO2004106380-A2.	
PV 09-DEC-2004.	
PF 26-MAY-2004; 2004WO-EP005684.	
XX 31-MAY-2003; 2003EP-00012132.	
XX (MICR-) MICROMET AG.	
PA Kufer P, Raum T, Berry M, Kischel R, Mangold S, Krinner E;	
XX	

PI Kohleisen B, Zeman S, Itin C, Baerle P;
 XX WPI; 2005-021269/02.
 DR N-PSDB; ADV21416.
 XX
 PT Preparing human binding molecule specifically binding to human CD3
 PT complex, comprises selecting molecules specifically binding to
 PT extracellular domain of recombinant epsilon-chain and preparing
 PT identified selected binding molecule.
 XX
 PS Claim 27; SEQ ID NO 126; 350pp; English.
 XX
 CC The invention relates to a method of preparing a human binding molecule,
 CC fragment or its derivative which specifically binds to the human CD3
 CC complex. The method comprises selecting molecules specifically binding to
 CC or interacting with the extracellular domain of recombinant epsilon-chain
 CC expressed independent of the human CD3 complex in the absence of other
 CC members of the CD3 complex, from a population of candidate polypeptides
 CC encoded by a library, selecting molecules from a population identified in
 CC the above step for binding to the human CD3 complex, and preparing the
 CC selected binding molecule. The binding molecule is an antibody molecule,
 CC antibody fragment or its derivative or an antibody construct. Also
 CC disclosed is a nucleic acid sequence encoding a human binding molecule, a
 CC vector comprising such a nucleic acid, a host transformed or transfected
 CC with such a vector, a composition comprising a human binding molecule,
 CC and optionally a proteinaceous compound capable of providing an
 CC activation signal for immune effector cells, and a kit comprising a human
 CC binding molecule. The method further involves recombinant expression of
 CC the binding molecule, fragment or its derivative encoded by a nucleic
 CC acid sequence chosen from the identified nucleic acid sequence, a nucleic
 CC acid sequence hybridizing with the complementary strand of the identified
 CC nucleic acid sequence under stringent hybridization conditions, and a
 CC nucleic acid sequence which is degenerate as a result of the genetic code
 CC to the above mentioned nucleotide sequences. The antibody molecule,
 CC antibody fragment or its derivative or construct comprises a further
 CC antigen-interaction-site and/or a further effector domain, and is
 CC humanized and/or deluminized in an additional step. The further antigen-
 CC interaction-site is specific for one or more cell surface molecule such
 CC as a tumor specific marker. The antigen-interaction-site is further scFv,
 CC which specifically binds to or interacts with an antigen chosen from
 CC EpCAM, CCR5, CD19, EphA2, HER-2 neu, HER-3, HER-4, EGFR, PSMA, CEA, MUC-1
 CC (mucin), MUC2, MUC3, MUC4, MUC5AC, MUC5B, MUC7, betaHCG, Lewis X, CD20,
 CC CD33, CD30, ganglioside GD3, 9-O-Acetyl-GD3, GM2, Globo H, fucoseyl GM1,
 CC Poly SA, GD2, carboxypeptidase IX (NM/CA IX), CD44v6, Sonic hedgehog (Shh),
 CC Wue-1, plasma cell antigen, (membrane-bound) IGF, melanoma chondroitin
 CC sulfate proteoglycan (MSP), CCR8, TNF-alpha precursor, STEAP,
 CC mesothelin, A33 antigen, prostate stem cell antigen (PSCA), Ly-6,
 CC desmoglein 4, E-cadherin neoptope, fetal acetylcholine receptor, CD25,
 CC CA19-9 marker, CA-125 marker and muellerian inhibitory substance (MIS),
 CC receptor type II, sTn (staiylated Tn antigen, TAG-72), PAP (fibroblast
 CC activated antigen), endostatin, EGFRvIII, LG, SAS and CD63. In a human
 CC binding molecule, the antibody molecule, antibody fragment or its
 CC derivative or an antibody construct, comprises a heavy chain variable
 CC (VH) region, a light chain variable (VL) region, complementarity
 CC determining regions 1-3 (CDR1-3) of a VH-region, and CDR1-3 of a VL-
 CC region. The method is useful for preparing a human binding molecule,
 CC fragment or its derivative which specifically binds to the human CD3
 CC complex. The human binding molecule polypeptide sequences, and the
 CC polynucleotide sequences encoding them are useful for the prevention,
 CC treatment or amelioration of proliferative disease, tumorous disease,
 CC inflammatory disease, immunological disorder, autoimmune disease,
 CC infectious disease, viral disease, allergic reactions, parasitic
 CC reactions, graft-versus-host diseases or host-versus-graft diseases, or
 CC for preparation of a pharmaceutical composition for the prevention,
 CC treatment or amelioration of the above mentioned diseases. This sequence
 CC represents a CDR region of a human antibody.
 CC
 XX Sequence 7 AA;

Query Match 100.0%; Score 38; DB 9; Length 7;
 Best Local Similarity 100.0%; Pred. NO. 2e+06; Mismatches 0; Gaps 0;
 Matches 7; Conservative 0; Indels 0;

QY, 1 WASTRES 7
 |||||
 Db 1 WASTRES 7

RESULT 36
 ID ADW47139
 ID ADW47139 standard; peptide; 7 AA.
 XX
 AC ADW47139;
 XX
 DT 24-MAR-2005 (first entry)
 XX
 DE Anti-CD20 monoclonal antibody light chain MB20-01 CDR 2.
 XX
 KW CD20; monoclonal antibody; rheumatoid arthritis; antiarthritis;
 KW antirheumatic; immune disorder; inflammation; musculoskeletal disease;
 KW idiopathic thrombocytopenic purpura; hemostatic; hemolytic anemia.
 XX
 OS Mus musculus.
 XX
 PN W0200500901-A2.
 XX
 PD 06-JAN-2005.
 XX
 PF 07-MAY-2004; 2004WO-US014326.
 XX
 PR 09-MAY-2003; 2003US-0469451P.
 XX
 PA (UYDU-) UNIV DUKE.
 XX
 PI Tedder TF, Uchida J, Hamaguchi Y, Poe JC;
 DR WPI; 2005-066556/07.
 XX
 PT Novel monoclonal antibody (mAb) binding to CD20 or mouse CD20, in which
 PT density of binding of mAb to B cells is two-fold higher than density of
 PT binding of mAb1F5 to B cells, useful for depleting B cells, and treating
 PT B cell disorder.
 XX
 PS Example 1; SEQ ID NO 98; 205pp; English.
 XX
 CC The invention relates to a monoclonal antibody (mAb) or its antigen-
 CC binding fragment that specifically binds to human CD20 or mouse CD20,
 CC where the density of binding of mAb or antigen-binding fragment to B
 CC cells is at least two-fold higher than the density of binding of mAb 1F5
 CC to B cells. Also included are a pharmaceutical composition comprising mAb
 CC in a carrier, a pharmaceutical composition (comprising mAb or its antigen
 CC binding fragment which specifically binds to the same antigenic
 CC determinant as a monoclonal antibody chosen from HB20-1, HB20-3, HB20-4
 CC and HB20-25 in a carrier), a cell line producing the mAb, producing the
 CC mAb, an antigen binding fragment of the mAb, an isolated nucleic acid
 CC encoding a heavy chain or light chain comprising a variable region
 CC (comprising CDR3, or CDR1, CDR2 and CDR3 regions from mAb chosen from
 CC HB20-1, HB20-3, HB20-4, HB20-5, HB20-25, HB20-11, MB20-1, MB20-2,
 CC MB20-8, MB20-10, MB20-11, MB20-14, MB20-16 and MB20-18), a vector
 CC comprising the nucleic acid, a cell comprising the nucleic acid or
 CC vector, and depleting B cells in a mammalian subject (involving
 CC administering the mAb and anti-CD22 or anti-CD19 antibody). The anti-CD20
 CC mAb, compositions and cells are useful for depleting B cells in a
 CC mammalian subject and for treating a B cell disorder. The B cell disorder
 CC is B cell malignancy or autoimmune disease e.g. rheumatoid arthritis,
 CC idiopathic thrombocytopenic purpura or hemolytic anemia. The mammalian
 CC subject is resistant to anti-CD20 mAb therapy or resistant to therapy
 CC with mAb C2B8. The mammalian subject has been or is currently treated
 CC with chemotherapy. The mammalian subject had a relapse in a B cell
 CC disorder. The mammalian subject is immunocompromised. The present
 CC sequence represents a CDR (complementarity determining region) from anti-
 CC CD20 monoclonal antibody.
 CC
 XX Sequence 7 AA;

Query Match 100.0%; Score 38; DB 9; Length 7;

Best Local Similarity 100.0%; Pred. No. 2e+06; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

OY 1 WASTRES 7
| | | | |
Db 1 WASTRES 7

RESULT 37
ADM77439
ID ADM77439 standard; peptide; 7 AA.

AC ADM77439;

DT 07-APR-2005 (first entry)

XX Human platelet membrane glycoprotein VI associated CDR SEQ ID NO 110.

KM Antiarteriosclerotic; Thrombolytic; Anticoagulant; Antidiabetic;

KM Ophthalmological; Immunosuppressive; Vasotropic; antibody;

KM platelet membrane glycoprotein VI; diabetic retinopathy;

KM cardiovascular disease; ocular disease; graft versus host disease;

XX immune disorder.

OS Homo sapiens.

XX WO2005007800-A2.

PD 27-JAN-2005.

PF 20-JUL-2004; 2004WO-JP010596.

XX 18-JUL-2003; 2003JP-00199192.

PA (MOCH) MOCHIDA PHARM CO LTD.

XX Takayama H, Shirakawa K, Yamakawa T, Kawahara T;

XX WPI; 2005-152077/16.

PT Novel human antibody or its active fragment capable of binding

PT specifically with human platelet membrane glycoprotein VI and not

PT inducing human platelet aggregation by itself, useful for treatment or

PT prevention of thrombosis.

PS Example 8; SEQ ID NO 110; 124pp; Japanese.

XX The invention relates to a human antibody or its active fragment capable

XX of binding specifically with human platelet membrane glycoprotein VI and

XX not inducing human platelet aggregation by itself. The antibody is useful

XX in treatment or prevention of thrombosis, embolism or arteriosclerosis.

XX The antibody is useful in diagnosis of the disease by detecting or

XX determining glycoprotein VI. The antibody is useful in the prevention

XX and/or treatment of vascular endothelium failure, vascular endothelium

XX hyper trophy, blood vessel restenosis, disseminated intravascular

XX coagulation (DIC), diabetic retinopathy, graft-versus-host disease, etc.

XX The antibody exhibits high specificity with respect to glycoprotein VI,

XX and can be obtained easily. The present sequence represents the amino

XX acid sequence of a human platelet membrane glycoprotein VI associated

ADM77433
ID ADM77433 standard; peptide; 7 AA.
XX
XX ADM77433;
XX
XX 07-APR-2005 (first entry)
XX
XX Human platelet membrane glycoprotein VI associated CDR SEQ ID NO 104.
XX
XX Antiarteriosclerotic; Thrombolytic; Anticoagulant; Antidiabetic;
XX Ophthalmological; Immunosuppressive; Vasotropic; antibody;
XX platelet membrane glycoprotein VI; diabetic retinopathy;
XX cardiovascular disease; ocular disease; graft versus host disease;
XX immune disorder.
XX
XX Homo sapiens.
XX
XX WO2005007800-A2.
XX
XX 27-JAN-2005.
XX
XX 20-JUL-2004; 2004WO-JP010596.
XX
XX 18-JUL-2003; 2003JP-00199192.
XX
XX (MOCH) MOCHIDA PHARM CO LTD.
XX
XX Takayama H, Shirakawa K, Yamakawa T, Kawahara T;
XX
XX WPI; 2005-152077/16.
XX
XX Novel human antibody or its active fragment capable of binding
XX specifically with human platelet membrane glycoprotein VI and not
XX inducing human platelet aggregation by itself, useful for treatment or
XX prevention of thrombosis.
XX
XX Example 8; SEQ ID NO 104; 124pp; Japanese.
XX
XX The invention relates to a human antibody or its active fragment capable
XX of binding specifically with human platelet membrane glycoprotein VI and
XX not inducing human platelet aggregation by itself. The antibody is useful
XX in treatment or prevention of thrombosis, embolism or arteriosclerosis.
XX The antibody is useful in diagnosis of the disease by detecting or
XX determining glycoprotein VI. The antibody is useful in the prevention
XX and/or treatment of vascular endothelium failure, vascular endothelium
XX hyper trophy, blood vessel restenosis, disseminated intravascular
XX coagulation (DIC), diabetic retinopathy, graft-versus-host disease, etc.
XX The antibody exhibits high specificity with respect to glycoprotein VI,
XX and can be obtained easily. The present sequence represents the amino
XX acid sequence of a human platelet membrane glycoprotein VI associated

XX CDR.

XX Sequence 7 AA;

Query Match 100.0%; Score 38; DB 9; Length 7;

Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7
| | | | |
Db 1 WASTRES 7

RESULT 39

ADM98304
ID ADM98304 standard; peptide; 7 AA.

XX ADM98304;

DT 05-MAY-2005 (first entry)

XX Human anti-HGF antibody light chain variable region CDR2 peptide -SEQ 76.

KW	antibody; cytostatic; cancer; neoplasm; solid tumor;	
KW	hepatocyte growth factor; HGF; light chain variable region.	
XX		
OS	Homo sapiens.	
PN	WO2005017107-A2.	
XX		
PD	24-FEB-2005.	
XX		
PF	16-JUL-2004; 2004WO-US018936.	
PR	18-JUL-2003; 2003US-048681P.	
XX		
PA	(AMGE-) AMGEN INC.	
XX	(ABGE-) ABGENIX INC.	
PI	Burgess TL, Coxon A, Green LJ, Zhang K;	
DR	WPI, 2005-182350/19.	
XX		
PT	New polypeptide comprising a complementarity determining region (CDR)	
PT	consisting of CDRa, CDR2a, CDR3a, CDR1b, CDR2b or CDR3b and capable of	
PT	binding hepatocyte growth factor, useful in preparing a composition for	
PT	treating cancer.	
PS	Claim 4; SEQ ID NO 76; 301pp; English.	
CC		
CC	The invention relates to a novel isolated polypeptide comprising at least	
CC	one complementarity-determining region (CDR) consisting of CDR1a, CDR2a	
CC	or CDR1b, or CDR1b, CDR2b or CDR3b. The polypeptide, in association with	
CC	an antibody heavy or light chain, is capable of binding hepatocyte growth	
CC	factor (HGF). HGF, also known as scatter factor (SF), has been identified	
CC	as a potent mitogen for hepatocytes and also as a secretory protein of	
CC	fibroblasts and smooth muscles that acts to induce motility of epithelial	
CC	cells. The polypeptide demonstrates cytostatic activity and may be useful	
CC	in preparing a composition for treating cancer or a solid tumor. The	
CC	current sequence is that of the human anti-HGF antibody light chain	
CC	variable region CDR2 peptide -SEQ 76 of the invention.	
XX		
SQ	Sequence 7 AA;	
	Query Match 100.0%; Score 38; DB 9; Length 7;	
	Best Local Similarity 100.0%; Pred. NO. 2e+06; Indels 0; Gaps 0	
	Matches 7; Conservative 0; Mismatches 0;	
OY	1 WASTRES 7	
DB	1 WASTRES 7	
RESULT 40		
ID	ADX98299	
XX	ADX98299 standard; peptide; 7 AA.	
CC	ADX98299;	
DT	05-MAY-2005 (first entry)	
XX		
XX	Human anti-HGF antibody light chain variable region CDR2 peptide -SEQ 71.	
KW	antibody; cytostatic; cancer; neoplasm; solid tumor;	
KW	hepatocyte growth factor; HGF; light chain variable region.	
XX		
OS	Homo sapiens.	
PN	WO2005017107-A2.	
XX		
PD	24-FEB-2005.	
XX		
PF	16-JUL-2004; 2004WO-US018936.	
PR	18-JUL-2003; 2003US-048681P.	

PA	(AMGE-) AMGEN INC.
PA	(ABGE-) ABGENIX INC.
XX	
PI	Burgess TL, Coxon A, Green LL, Zhang K,
XX	
DR	WPI, 2005-182350/19.
XX	
PT	New polypeptide comprising a complementarity determining region (CDR)
PT	consisting of CDR1a, CDR2a, CDR3a, CDR1b, CDR2b or CDR3b and capable of
PT	binding hepatocyte growth factor, useful in preparing a composition for
PT	treating cancer.
XX	
PS	Claim 4; SEQ ID NO 71; 301pp; English.
XX	
CC	The invention relates to a novel isolated polypeptide comprising at least
CC	one complementarity-determining region (CDR) consisting of CDR1a, CDR2a
CC	or CDR1b, CDR2b or CDR3b. The polypeptide, in association with
CC	an antibody heavy or light chain, is capable of binding hepatocyte growth
CC	factor (HGF). HGF, also known as scatter factor (SF), has been identified
CC	as a potent mitogen for hepatocytes and also as a secretory protein of
CC	fibroblasts and smooth muscles that acts to induce motility of epithelial
CC	cells. The polypeptide demonstrates cytostatic activity and may be useful
CC	in preparing a composition for treating cancer or a solid tumor. The
CC	current sequence is that of the human anti-HGF antibody light chain
CC	variable region CDR2 peptide -SEQ 71 of the invention.
XX	
SEQ	Sequence 7 A;
Query Match	100.0%; Score 38; DB 9; Length 7;
Best Local Similarity	100.0%; Pred. No. 2e+06;
Matches	7; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Oy	1 WASTRES 7
Db	1 WASTRES 7
RESULT 41	
ID	ADY59130
ADY59130	ADY59130 standard; peptide; 7 AA.
XX	
AC	ADY59130;
XX	
DT	19-MAY-2005 (first entry)
XX	
DE	Anti-Tag-72 humanized antibody HuCC49V10 light chain CDR2.
XX	
KW	Tumor-associated antigen; Tag-72; humanized antibody;
KW	antibody engineering; monoclonal antibody; cancer; neoplasia;
KW	antibody therapy; diagnosis; cytostatic; light chain.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
XX	WO2005021594-A2.
XX	
XX	10-MAR-2005.
XX	
XX	27-AUG-2004; 2004WO-US028004.
XX	
XX	29-AUG-2003; 2003US-0498903P.
XX	
PA	(USNA) US SEC OF NAVY.
XX	
XX	Kashmiri SVS, Schlom J, Padian EA;
XX	
XX	WPI, 2005-223157/23.
XX	
PT	New humanized anti-TAG-72 CC49 monoclonal antibody comprising a light and
PT	heavy chain, and a light and heavy chain framework region from HuCC49V10,
PT	useful for treating or diagnosing a tumor, such as a carcinoma,
PT	expressing TAG-72.
XX	

PS Claim 8; SEQ ID NO 10; 86pp; English.

XX The invention provides humanized anti-TAG-72 CC49 monoclonal antibodies.

CC The antibodies include a light chain complementarity determining region L

CC -CDR1, H-CDR2 and L-CDR3 and a heavy chain complementarity determining

CC -CDR1, L-CDR2 and L-CDR3 from humanized antibody HuCC49V10. The L

CC region that includes the corresponding amino acid from human monoclonal

CC antibody LEN at position 5, 19, 21 and 106 in the light chain. The H-

CC CDR1, H-CDR2 and H-CDR3 are within a heavy chain HuCC49V10 framework

CC comprising a human monoclonal antibody 21/28' CL residue at positions 20,

CC 38, 48, 66, 67, 69 and 80 in the heavy chain. The humanized CC49

CC antibodies retain binding affinity for tumor-associated glycoprotein TAG-

CC 72 and have reduced immunogenicity as compared to a parental HuCC49V10

CC antibody. Methods are disclosed for using these antibodies in the

CC treatment or diagnosis of a tumor, such as a carcinoma, expressing TAG-

CC 20. The present sequence is the amino acid sequence of L-CDR2 of

CC HuCC49V10. In a claimed monoclonal antibody, L-CDR2 comprises this

CC sequence.

CC

XX

SQ Sequence 7 AA;

Query Match 100.0%; Score 38; DB 9; Length 7;

Best Local Similarity 100.0%; Pred. No. 2e+06; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 0;

OY 1 WASTRES 7

DB 1 WASTRES 7

RESULT 42

ADY59136

ID ADY59136 standard; peptide; 7 AA.

XX

AC ADY59136;

DT 19-MAY-2005 (first entry)

XX

DE Human monoclonal antibody LEN light chain CDR2.

XX

KW Tumor-associated antigen; Tag-72; humanized antibody;

KW antibody engineering; monoclonal antibody; cancer; neoplasm;

KW antibody therapy; diagnosis; cytostatic; light chain.

XX

OS Homo sapiens.

OS

PN WO2005021594-A2.

PD 10-MAR-2005.

PF 27-AUG-2004; 2004WO-US028004.

XX

PR 29-AUG-2003; 2003US-0498903P.

XX

PA (USNA) US SEC OF NAVY.

XX

PI Kashmiri SVS, Schlom J, Padian EA;

XX

DR WPI; 2005-223157/23.

XX

PT New humanized anti-TAG-72 CC49 monoclonal antibody comprising a light and

PT heavy chain, and a light and heavy chain framework region from HuCC49V10,

PT useful for treating or diagnosing a tumor, such as a carcinoma,

PT expressing TAG-72.

XX

PS Disclosure; SEQ ID NO 16; 86pp; English.

XX

CC The invention provides humanized anti-TAG-72 CC49 monoclonal antibodies.

CC The antibodies include a light chain complementarity determining region L

CC -CDR1, L-CDR2 and L-CDR3 and a heavy chain complementarity determining

CC region H-CDR1, H-CDR2 and H-CDR3 from humanized antibody HuCC49V10. The L

CC -CDR1, L-CDR2 and L-CDR3 are within a HuCC49V10 light chain framework

CC region that includes the corresponding amino acid from human monoclonal

CC antibody LEN at position 5, 19, 21 and 106 in the light chain. The H-

CC CDR1, H-CDR2 and H-CDR3 are within a heavy chain HuCC49V10 framework

CC comprising a human monoclonal antibody 21/28' CL residue at positions 20,

CC 38, 48, 66, 67, 69 and 80 in the heavy chain. The humanized CC49

CC antibodies retain binding affinity for tumor-associated glycoprotein TAG-

CC 72 and have reduced immunogenicity as compared to a parental HuCC49V10

CC antibody. Methods are disclosed for using these antibodies in the

CC treatment or diagnosis of a tumor, such as a carcinoma, expressing TAG-

CC 20. The present sequence is the amino acid sequence of L-CDR2 of LEN.

XX

SQ Sequence 7 AA;

Query Match 100.0%; Score 38; DB 9; Length 7;

Best Local Similarity 100.0%; Pred. No. 2e+06; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 0;

OY 1 WASTRES 7

DB 1 WASTRES 7

RESULT 43

ADY58494

ID ADY58494 standard; peptide; 7 AA.

XX

AC ADY58494;

DT 19-MAY-2005 (first entry)

XX

DE Peptide used in antibody engineering.

XX

KW Antibody engineering; humanized antibody; antibody therapy; cancer;

KW cytostatic; infection; cytostatic; antimicrobial; immunosuppressive;

KW antineumatic; antidiabetic; antiinflammatory; dermatological;

KW anticancer; gastrointestinal-gen.; antiproliferative; antiallergic; virucide;

KW anti-HIV; antibacterial; protozoacide.

XX

OS Homo sapiens.

OS

PN WO2005021595-A1.

PD 10-MAR-2005.

PF 27-AUG-2004; 2004WO-US028023.

XX

PR 28-AUG-2003; 2003US-0499314P.

XX

PA (EURO-) EUROCELLTQUE SA.

XX

PI Kyle DJ, Brogle KC, Soltis DA;

XX

DR WPI; 2005-202740/21.

XX

PT New modified antibody having human/humanized heavy and light chain

PT variable regions and comprising a heterologous peptide contained entirely

PT within an antibody display region (ADR), useful for treating e.g.,

PT cancer.

XX

PS Disclosure; SEQ ID NO 7; 132pp; English.

XX

CC The invention relates to methods for modifying antibodies and antibody

CC fragments by following certain Antibody Display Region (ADR) rules,

CC thereby resulting in improved production of antibodies and fragments.

CC These ADR rules define certain amino acid residues within each

CC complementarity determining region (CDR) that have a higher tolerance for

CC modification. Such residues are distinguished from those that are

CC essential for antibody structure and function. In one embodiment,

CC antibodies are modified by the introduction of a heterologous binding

CC domain peptide into one or more CDRs. The resulting Synthobody (TM)

CC molecules provide improved accessibility of the heterologous binding

CC domain to its binding partner. The invention provides modified antibodies

CC and antibody fragments modified according to the ADR rules, and

CC pharmaceutical compositions containing such modified antibodies or
CC fragments. The modified antibodies or fragments are useful for treating
CC or preventing a cancer characterized by the presence of a cancer antigen
CC or an infectious disease (claimed). They are also useful for treating
CC autoimmune diseases including rheumatoid arthritis, lupus, ulcerative
CC colitis, psoriasis or allergies, as well as viral diseases such as HIV,
CC bacterial diseases, and protozoal diseases. The present sequence is that
CC of a peptide used in the production of a modified antibody according to
CC ADR rules. The modified antibody specifically binds to the human milk fat
CC globule antigen.

XX Sequence 7 AA;

Query Match 100.0%; Score 38; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7
| | | | |
Db 1 WASTRES 7

RESULT 44

ADZ45515 standard; peptide; 7 AA.

ADZ45515;

30-JUN-2005 (first entry)

Murine factor IX directed antibody CDR2 SEQ ID NO 219.

bispecific antibody; blood coagulation factor VIII; bleeding;
KW fibrinolysis; blood coagulation factor X; blood-coagulation factor IX;
KW factor VIII deficiency; von Willebrand disease; hemostatic;
KW immunostimulator; antibody engineering.

OS Mus musculus.

PN WO2005035756-A1.

21-APR-2005.

08-OCT-2004; 2004WO-JP014911.

10-OCT-2003; 2003WO-JP013062.

14-OCT-2003; 2003WO-JP013123.

(CHUS) CHUGAI SEIYAKU KK.

Hattori K, Kojima T, Miyazaki T, Soeda T;

WPI, 2005-315563/32.

Novel bispecific antibody substituting for function of cofactor that
PT enhances enzyme reaction, and recognizing both enzyme and substrates of
PT enzyme, useful for treating hemophilia A.

PS Disclosure; SEQ ID NO 219; 69pp; Japanese.

This invention describes a novel bispecific antibody which can act as a
CC cofactor to enhance an enzyme reaction and can recognize the enzyme and
CC the enzyme substrate. The antibody specifically binds to blood
CC coagulation factor VIII. The invention also describes a composition
CC comprising the antibody and a carrier, a kit useful in preventing and/or
CC treating bleeding associated with a disorder or from a disease caused by
CC bleeding. The composition includes blood coagulation factor VIII. The
CC antibody of the invention can be a blood-coagulation fibrinolysis related
CC factor including blood-coagulation factor VIII, blood coagulation factor
CC X, or blood-coagulation factor IX. The antibody comprises a complementary
CC determining region (CDR) of anti-blood-coagulation factor IX/IXa factor
CC antibody. The novel antibody or composition is useful for preventing
CC and/or treating a disease accompanying bleeding, or the disease resulting

CC from bleeding, where the disease accompanying bleeding or the disease
CC resulting from bleeding develops and/or progresses by an active reduction
CC or deletion of the blood coagulation factor VIII. The disease the
CC develops and/or progresses by an active reduction or deletion of the

CC blood coagulation factor VIII and/or activation blood coagulation factor
CC VIII, is hemophilia A or von Willebrand disease, where the hemophilia is
CC an acquired hemophilia A. This sequence represents a fragment of the
CC antibody described in the method of the invention. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 7 AA;

Query Match 100.0%; Score 38; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7
| | | | |
Db 1 WASTRES 7

RESULT 45

ADZ45538 standard; peptide; 7 AA.

ADZ45538;

30-JUN-2005 (first entry)

Murine factor IX directed antibody CDR2 SEQ ID NO 242.

bispecific antibody; blood coagulation factor VIII; bleeding;
KW fibrinolysis; blood coagulation factor X; blood-coagulation factor IX;
KW factor VIII deficiency; von Willebrand disease; hemostatic;
KW immunostimulator; antibody engineering; ds; gene.

OS Mus musculus.

PN WO2005035756-A1.

21-APR-2005.

08-OCT-2004; 2004WO-JP014911.

10-OCT-2003; 2003WO-JP013062.

14-OCT-2003; 2003WO-JP013123.

(CHUS) CHUGAI SEIYAKU KK.

Hattori K, Kojima T, Miyazaki T, Soeda T;

WPI, 2005-315563/32.

N-PSDB; ADZ45537.

Novel bispecific antibody substituting for function of cofactor that
PT enhances enzyme reaction, and recognizing both enzyme and substrates of
PT enzyme, useful for treating hemophilia A.

PS Disclosure; SEQ ID NO 242; 69pp; Japanese.

This invention describes a novel bispecific antibody which can act as a
CC cofactor to enhance an enzyme reaction and can recognize the enzyme and
CC the enzyme substrate. The antibody specifically binds to blood
CC coagulation factor VIII. The invention also describes a composition
CC comprising the antibody and a carrier, a kit useful in preventing and/or
CC treating bleeding associated with a disorder or from a disease caused by
CC bleeding. The composition includes blood coagulation factor VIII. The
CC antibody of the invention can be a blood-coagulation fibrinolysis related
CC factor including blood-coagulation factor VIII, blood coagulation factor
CC X, or blood-coagulation factor IX. The antibody comprises a complementary
CC determining region (CDR) of anti-blood-coagulation factor IX/IXa factor

CC antibody. The novel antibody or composition is useful for preventing
CC and/or treating a disease accompanying bleeding, or the disease resulting
CC from bleeding, where the disease accompanying bleeding or the disease
CC resulting from bleeding develops and/or progresses by an active reduction
CC or deletion of the blood coagulation factor VIII. The disease the
CC develops and/or progresses by an active reduction or deletion of the
CC blood coagulation factor VIII and/or activation blood coagulation factor
CC VIII, is hemophilia A or von Willebrand disease, where the hemophilia is
CC an acquired hemophilia A. This sequence encodes a fragment of the
CC antibody described in the method of the invention. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

CC Sequence 7 AA:

Query Match 100.0%; Score 38; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7
|||
1 WASTRES 7

DB

RESULT 46
AD235818
ID AD235818 standard; peptide; 7 AA.

AC AD235818;

DT 30-JUN-2005 (first entry)

DE Anti-glucose-6-phosphate isomerase antibody light chain CDR2 #4.

XX antibody engineering; immunosuppressive; immunoglobulin; antibody;

KM glucose-6-phosphate isomerase; diagnosis; autoimmune disease;

KW light chain; complementarity determining region.

OS Homo sapiens;

PN US2005080239-A1.

PD 14-APR-2005.

PF 29-JUL-2003; 2003US-00630009.

PR 06-APR-2001; 2001US-00828708.

PA (SCRI) SCRIPPS RES INST.

PI Ditzel H, Burton DR, Schaller M;

PT WPI; 2005-305027/31.

PT New immunoglobulin antibody that specifically binds to human glucose-6-phosphate isomerase, useful in preparing a composition for diagnosing or treating autoimmune disease.

PS Claim 11; SEQ ID NO 46; 71pp; English.

XX A new isolated immunoglobulin antibody specifically binds to human
XX glucose-6-phosphate isomerase. INDEPENDENT CLAIMS are also included for:
XX an immunopolypeptide having an amino acid sequence homologous to a
XX sequence consisting of 5-116 amino acids (SEQ ID NO. 1-108); an antisense
XX oligonucleotide that specifically hybridizes with a polynucleotide
XX encoding anti-glucose-6-phosphate isomerase antibody or encoding glucose-
XX 6-phosphate isomerase; a composition comprising immobilized human glucose-
XX 6-phosphate isomerase; a pharmaceutical composition comprising the
XX NO. 109-122); a pharmaceutical composition comprising the
XX immunopolypeptide and a carrier; diagnosing autoimmune disease; and
XX treating a patient having autoimmune disease. Preferred Antibody: The
XX isolated immunoglobulin antibody specifically binds to human glucose-6-

CC phosphate isomerase. The immunopolypeptide comprises at least one CDR
CC sequence consisting of 5-23 amino acids (SEQ ID NO. 15-56) or its
CC significant homolog. The immunopolypeptide has a triplet of CDR
CC sequences. Each CDR of the triplet is separated from other CDR's by a
CC spacer amino acid sequence. The spacer amino acid sequence is a framework
CC region sequence having an amino acid sequence consisting of 11-32 amino
CC acids (SEQ ID NO. 57-108) or its significant homolog. The CDR's of the
CC triplet are selected from either a light chain group or a heavy chain
CC group. The CDR's are matched according to their Fab source. The framework
CC amino acid sequence is matched to the Fab source of the CDR triplet. The
CC amino acid sequence is a VL or VH fragment of the Fab source of the
CC matched CDR triplet and framework regions. Preferred Method: Diagnosing
CC autoimmune disease comprises determining the presence of an immune
CC complex formed by combining the blood sera of a patient with human
CC glucose-6-phosphate isomerase. Treating a patient having autoimmune
CC disease comprises administering to the patient the immunopolypeptide or
CC human glucose-6-phosphate isomerase. The method also comprises filtering
CC the patient's blood extracorporeally through a filter system containing
CC immobilized human glucose-6-phosphate isomerase. Immunosuppressive. No
CC biological data given. Gene therapy. The immunoglobulin antibody that
CC specifically binds to human glucose-6-phosphate isomerase is useful in
CC preparing a composition for diagnosing or treating autoimmune disease
CC (claimed). No relevant examples given.

CC Sequence 7 AA:

Query Match 100.0%; Score 38; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7
|||
1 WASTRES 7

DB

RESULT 47
AD235815
ID AD235815 standard; peptide; 7 AA.

AC AD235815;

DT 30-JUN-2005 (first entry)

DE Anti-glucose-6-phosphate isomerase antibody light chain CDR2 #1.

XX antibody engineering; immunosuppressive; immunoglobulin; antibody;

KM glucose-6-phosphate isomerase; diagnosis; autoimmune disease;

KW light chain; complementarity determining region.

OS Homo sapiens.

PN US2005080239-A1.

PD 14-APR-2005.

PF 29-JUL-2003; 2003US-00630009.

PR 06-APR-2001; 2001US-00828708.

PA (SCRI) SCRIPPS RES INST.

PI Ditzel H, Burton DR, Schaller M;

PT WPI; 2005-305027/31.

PT New immunoglobulin antibody that specifically binds to human glucose-6-phosphate isomerase, useful in preparing a composition for diagnosing or treating autoimmune disease.

PS Claim 11; SEQ ID NO 43; 71pp; English.

XX A new isolated immunoglobulin antibody specifically binds to human
XX glucose-6-phosphate isomerase. INDEPENDENT CLAIMS are also included for:

an immunopolypeptide having an amino acid sequence homologous to a sequence consisting of 5-116 amino acids (SEQ ID NO. 1-108); an antisense oligonucleotide that specifically hybridizes with a polynucleotide encoding anti-glucose-6-phosphate isomerase antibody or encoding glucose-6-phosphate isomerase; a nucleotide sequence comprising immobilized human glucose-6-phosphate isomerase; a pharmaceutical composition comprising the immunopolypeptide and a carrier; diagnosing autoimmune disease; and treating a patient having autoimmune disease. Preferred Antibody: The isolated immunoglobulin antibody specifically binds to human glucose-6-phosphate isomerase. The immunopolypeptide comprises at least one CDR sequence consisting of 5-23 amino acids (SEQ ID NO. 15-56) or its significant homolog. The immunopolypeptide has a triplet of CDR sequences. Each CDR of the triplet is separated from other CDR's by a spacer amino acid sequence. The spacer amino acid sequence is a framework region sequence having an amino acid sequence consisting of 11-32 amino acids (SEQ ID NO. 57-108) or its significant homolog. The CDR's of the triplet are selected from either a light chain group or a heavy chain group. The CDR's are matched according to their Fab source. The framework region sequence is matched to the Fab source of the CDR triplet. The amino acid sequence is a VL or VH fragment of the Fab source of the matched CDR triplet and framework regions. Preferred Method: Diagnosing autoimmune disease comprises determining the presence of an immune complex formed by combining the blood sera of a patient with human glucose-6-phosphate isomerase. Treating a patient having autoimmune disease comprises administering to the patient the immunopolypeptide or human glucose-6-phosphate isomerase. The method also comprises filtering the patient's blood extracorporeally through a filter system containing immobilized human glucose-6-phosphate isomerase. Immunosuppressive. No biological data given. Gene therapy. The immunoglobulin antibody that specifically binds to human glucose-6-phosphate isomerase is useful in preparing a composition for diagnosing or treating autoimmune disease (claimed). No relevant examples given.

SEQ Sequence 7 AA;

Query Match 100.0%; Score 38; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
11111111
DB 1 WASTRES 7

RESULT 48

AEA38789 standard; peptide; 7 AA.

AEA38789;
11-AUG-2005 (first entry)
Humanized antibody-related VL CDR peptide - SEQ ID 38.
Antibody; animal disease model; antibody therapy; radiation therapy; immunotherapy; light chain variable region.
Unidentified.
WO2005050200-A2.
02-JUN-2005.
04-NOV-2004; 2004WO-US036651.
13-NOV-2003; 2003US-0520398P.
31-MAR-2004; 2004US-0557951P.
(GETH) GENENTECH INC.
Filvaroff EH;
XX

WPI; 2005-41772/42.
Screening compounds useful for treating tumor metastasis involves administering a test compound to non-human animal model bearing soft tissue/bone metastasis and identifying compound that inhibits soft tissue growth/bone metastasis.

Disclosure; SEQ ID NO 38; 109pp; English.

The present invention relates to the screening of candidate molecules [anti-transforming growth factor (TGF-beta antibodies) for the treatment of tumor metastasis and treatment methods using such molecules. The screening method of the invention involves administering several test substances to a non-human syngeneic immunocompetent animal model bearing at least one soft tissue or bone metastasis optionally in presence of a primary tumor, determining the effects of these test substances on the soft tissue or bone metastasis and growth of the primary tumor and identifying a test substance inhibiting soft tissue growth or bone metastasis without adverse effect on the status of the primary tumor. The invention is useful in the diagnosis and treatment of breast cancer, colorectal cancer, liver and lung metastases, bone destruction and bone loss. The animal models of the present invention is useful to screen substances useful for the prophylaxis or treatment of soft tissue and/or bone metastases which may additionally be effective in treating the primary tumor. The present sequence is humanized antibody variable light chain (VL) complementarity determining region (CDR) peptide.

SEQ Sequence 7 AA;

Query Match 100.0%; Score 38; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
11111111
DB 1 WASTRES 7

RESULT 49

AEA38759 standard; peptide; 7 AA.

AEA38759;
11-AUG-2005 (first entry)
Humanized murine anti-TGF-beta antibody VL mutant CDR L2, SEQ ID NO: 19.
Monoclonal antibody; animal disease model; metastasis; cytostatic; neoplasm; bone metastases; breast tumor; colorectal tumor; bone disease; osteopathic; antibody therapy; radiation therapy; immunotherapy; cancer cell proliferation inhibitor; transforming growth factor-beta-antagonist; humanized antibody; chimeric antibody; light chain variable region.
Mus musculus.
Homo sapiens.
Synthetic.
Chimeric.
WO2005050200-A2.
02-JUN-2005.
04-NOV-2004; 2004WO-US036651.
13-NOV-2003; 2003US-0520398P.
31-MAR-2004; 2004US-0557951P.
(GETH) GENENTECH INC.
Filvaroff EH;
XX

DR WPI: 2005-417772/42.
 DR N-PSDB; AEA38753.
 XX
 XX Screening compounds useful for treating tumor metastasis involves
 PT administering a test compound to non-human animal model bearing soft
 PT tissue/bone metastasis and identifying compound that inhibits soft tissue
 PT growth/bone metastasis.
 XX
 XX Example 2; SEQ ID NO 19; 109pp; English.
 PS
 XX The present invention relates to the screening of candidate molecules
 CC [anti-transforming growth factor (TGF)-beta antibodies] for the treatment
 CC of tumor metastasis and treatment methods using such molecules. The
 CC screening method of the invention involves administering several test
 CC substances to a non-human syngeneic immunocompetent animal model bearing
 CC at least one soft tissue or bone metastasis optionally in presence of a
 CC primary tumor, determining the effects of these test substances on the
 CC soft tissue or bone metastasis and growth of the primary tumor and
 CC identifying a test substance inhibiting soft tissue growth or bone
 CC metastasis without adverse effect on the status of the primary tumor. The
 CC invention is useful in the diagnosis and treatment of breast cancer,
 CC colorectal cancer, liver and lung metastases, bone destruction and bone
 CC loss. The animal models of the present invention is useful to screen
 CC substances useful for the prophylaxis or treatment of soft tissue and/or
 CC bone metastases which may additionally be effective in treating the
 CC primary tumor. The present sequence is humanized murine anti-transforming
 CC growth factor-beta (anti-TGF-beta) antibody (also referred as humanized
 CC monoclonal antibody 2G7) variable light chain (VL) protein mutant
 CC complementarity determining region (CDR) peptide. Note: This sequence is
 CC wrongly designated as SEQ ID NO: 38 in the disclosure (page 34) of the
 CC specification.
 CC
 CC Sequence 7 AA:
 SQ
 Query Match 100.0%; Score 38; DB 9; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+06; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WASTRES 7
 Db 1 WASTRES 7
 RESULT 50
 AEB23167
 ID AEB23167 standard; peptide; 7 AA.
 XX
 AC AEB23167;
 XX
 XX 22-SEP-2005 (first entry)
 DT
 XX
 XX Antibody fragment light chain CDR, SEQ ID No:5.
 DE
 XX
 XX antibody; antigen; light chain; diagnosis; cancer; neoplasm;
 KW immune disorder; autoimmune disease; rheumatoid arthritis;
 KW thrombocytopenia purpura; systemic lupus erythematosus; psoriasis;
 KW Sjogren's syndrome; insulin-dependent diabetes mellitus; cytostatic;
 KW immunomodulator; immunosuppressive; anti-neumatic; antiarthritic;
 KW dermatological; hemostatic; antiinflammatory; antipsoriatic;
 KW antidiabetic; vaccine; complementarity determining region; CDR.
 XX
 XX Unidentified.
 OS
 XX
 XX WO2005063816-A2.
 PN
 XX
 XX 14-UTL-2005.
 PD
 XX
 XX 17-DEC-2004; 2004WO-US042619.
 PF
 XX 19-DEC-2003; 2003US-0531409P.
 PR
 XX
 XX (GETH) GENENTECH INC.
 PA
 XX

PI Huang AJ, Schwall RH, Yansura DG;
 XX
 XX WPI: 2005-506651/51.
 DR
 XX
 XX New monovalent antibody fragment, useful for diagnosing, treating or
 PT preventing a disease, e.g. cancer, rheumatoid arthritis, immune
 PT thrombocytopenia purpura, systemic lupus erythematosus, psoriasis, or
 PT diabetes.
 XX
 XX Disclosure; SEQ ID NO 5; 101pp; English.
 PS
 XX
 XX The invention relates to a monovalent antibody fragment comprising a
 CC single antigen binding arm and an Fc region that increases the stability
 CC of the antibody fragment compared to a Fab molecule comprising the
 CC antigen binding arm, where the Fc region comprises a complex of a first
 CC and a second Fc polypeptide, where one but not both of the Fc
 CC polypeptides is an N-terminally truncated heavy chain. Also described
 CC are: (1) a composition comprising: (a) a population of immunoglobulins
 CC where at least 75% of the immunoglobulins is the new antibody fragment,
 CC (b) two or more recombinant nucleic acids which collectively encode the
 CC new antibody fragment, or (c) the new antibody fragment and a carrier;
 CC (2) an isolated nucleic acid encoding the new antibody fragment; (3) a
 CC host cell comprising the nucleic acid; and (4) a method of preparing,
 CC making or generating the new antibody fragment. The antibody fragment,
 CC methods, and compositions of the invention are useful for diagnosing,
 CC treating or preventing a disease, e.g. cancer or an immunological
 CC disorder, such as, an autoimmune disease (e.g. rheumatoid arthritis,
 CC immune thrombocytopenia purpura, systemic lupus erythematosus, psoriasis,
 CC Sjogren's syndrome, or insulin dependent diabetes mellitus). This
 CC sequence represents a complementarity determining region (CDR) of a light
 CC chain that can be used in an antibody fragment of the invention.
 CC
 CC Sequence 7 AA:
 SQ
 Query Match 100.0%; Score 38; DB 9; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+06; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WASTRES 7
 Db 1 WASTRES 7
 Search completed: May 4, 2006, 12:58:03
 JOD time : 83.2222 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 4, 2006, 13:00:03 ; Search time 10 Seconds
(without alignments)
67.352 Million cell updates/sec

Title: US-10-700-632-5
Perfect score: 38
Sequence: 1 WASTRES 7

Scoring table: BL0SUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR 80: *
1: PIR1: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	100.0	81	2	PH1048
2	38	100.0	92	2	S37532
3	38	100.0	92	2	S37533
4	38	100.0	92	2	S37530
5	38	100.0	92	2	S37535
6	38	100.0	92	2	S37531
7	38	100.0	92	2	S37534
8	38	100.0	92	2	S37529
9	38	100.0	98	2	S19774
10	38	100.0	101	2	PH0869
11	38	100.0	101	2	PH1046
12	38	100.0	101	2	S26337
13	38	100.0	102	2	A34153
14	38	100.0	103	2	PH1047
15	38	100.0	103	2	PH1051
16	38	100.0	103	2	PH1052
17	38	100.0	103	2	PH1050
18	38	100.0	103	2	PH1054
19	38	100.0	104	2	PH1101
20	38	100.0	104	2	F38601
21	38	100.0	104	2	PH1102
22	38	100.0	104	2	PH1103
23	38	100.0	104	2	PH1104
24	38	100.0	106	2	A49138
25	38	100.0	111	2	S03304
26	38	100.0	111	2	G30502
27	38	100.0	112	2	S09970
28	38	100.0	112	2	PL0265
29	38	100.0	112	2	S43103

30	38	100.0	113	2	S34002	Ig kappa chain V r
31	38	100.0	113	2	S34003	Ig kappa chain V r
32	38	100.0	113	2	S30523	Ig kappa chain V r
33	38	100.0	113	2	PL0263	Ig kappa chain V r
34	38	100.0	114	1	K4H0LN	Ig kappa chain V-I
35	38	100.0	114	2	S44119	Ig kappa chain V-J
36	38	100.0	114	2	S44116	Ig kappa chain V-J
37	38	100.0	118	2	PT0356	Ig kappa chain V r
38	38	100.0	120	2	S51147	antibody light cha
39	38	100.0	120	2	G33932	Ig kappa chain pre
40	38	100.0	121	1	K4HU	Ig kappa chain pre
41	38	100.0	129	2	S40329	Ig kappa chain V-J
42	38	100.0	129	2	S40347	Ig kappa chain - h
43	38	100.0	133	1	K4HUT1	Ig kappa chain pre
44	38	100.0	133	2	PS0023	Ig kappa chain pre
45	38	100.0	134	2	S49531	anti-Sm antibody V
46	38	100.0	134	2	PC1214	Ig kappa chain pre
47	38	100.0	138	2	A53261	Ig kappa chain pre
48	38	100.0	145	2	S26040	Ig kappa chain pre
49	38	100.0	145	2	PL0014	Ig kappa chain pre
50	38	100.0	220	2	A31790	Ig kappa chain V r
51	35	92.1	112	2	S41393	Ig kappa chain V r
52	35	92.1	240	2	S06084	Ig kappa chain pre
53	34	89.5	96	2	G38601	Ig kappa chain V r
54	34	89.5	107	2	S36268	Ig lambda chain V
55	34	89.5	113	2	PT0408	Ig light chain V r
56	34	89.5	113	2	PT0407	Ig light chain V r
57	34	89.5	132	2	S46373	Ig kappa chain V-J
58	34	89.5	136	2	A49137	Ig kappa chain pre
59	33	86.8	113	2	A49260	antitumor monoclon
60	33	86.8	124	2	S40364	Ig kappa chain - h
61	32	84.2	102	2	B34153	Ig kappa chain V-I
62	32	84.2	113	2	S30520	Ig kappa chain V r
63	32	84.2	347	2	D83554	hypothetical prote
64	32	84.2	685	2	G82022	methionine-CNA 11
65	31	81.6	97	2	A42575	Ig kappa chain V r
66	31	81.6	184	2	JC2104	hypothetical 20.8K
67	31	81.6	382	2	S75823	threonine synthase
68	31	81.6	572	1	H95860	probable phosphoe
69	31	81.6	642	2	A11827	cyclomalodextrin
70	31	81.6	642	2	C87410	lolic protein [limp
71	30	78.9	76	2	G49164	chromogranin-B - r
72	30	78.9	117	2	S42466	Ig kappa chain V r
73	30	78.9	131	2	PL0207	anti-idiotypic ant
74	30	78.9	134	2	S21917	Ig kappa chain V r
75	30	78.9	152	2	S30751	Ig kappa chain pre
76	30	78.9	216	2	JB0241	Ig kappa chain Am3
77	30	78.9	256	2	C83474	hypothetical prote
78	30	78.9	310	2	A96569	probable oxidoredu
79	30	78.9	408	2	AC2729	conserved hypotet
80	30	78.9	409	2	D97510	hypothetical prote
81	30	78.9	489	2	AE2810	glycerol kinase 2
82	30	78.9	489	2	H97568	glycerol kinase 2
83	30	78.9	497	2	T43888	glycerol kinase (E
84	30	78.9	668	1	V0CWFC	coat protein - fel
85	30	78.9	677	1	S09078	chromogranin B pre
86	30	78.9	820	2	G75251	cytochrome-c oxida
87	30	78.9	1067	2	T06672	probable aminoacyl
88	30	78.9	1067	2	T48850	glycine-CNA ligas
89	30	78.9	1139	1	B64234	cytadherence-acces
90	30	78.9	3414	1	GNMWVE	genome polypeptein
91	29	76.3	92	2	A12362	hypothetical prote
92	29	76.3	95	2	T09855	hypothetical prote
93	29	76.3	124	2	T09855	acetyl-CoA carboxy
94	29	76.3	148	2	H95849	hypothetical prote
95	29	76.3	194	2	A10248	ribosomal-protein-
96	29	76.3	206	2	S25482	ribulose-bisphosph
97	29	76.3	227	2	G71390	H+-transporting tw
98	29	76.3	232	2	S25484	ribulose-bisphosph
99	29	76.3	300	2	G75285	hypothetical prote
100	29	76.3	335	2	G71439	hypothetical prote
101	29	76.3	368	2	T35150	probable glycosyl
102	29	76.3	384	2	B90678	cyanate transport

103	29	76.3	384	2	F85528	cyanoate transport
104	29	76.3	395	1	K1SMG	galactokinase (EC
105	29	76.3	410	2	B5523	aromatic dioxygena
106	29	76.3	413	2	S28172	ribulose-bisphosph
107	29	76.3	425	2	A23703	ribulose-bisphosph
108	29	76.3	427	2	C86311	protein F113.18 [i
109	29	76.3	430	1	HM1HMS	hemagglutinin-este
110	29	76.3	430	2	G87324	hypothetical prote
111	29	76.3	437	2	S39551	ribulose-bisphosph
112	29	76.3	439	2	S25483	ribulose-bisphosph
113	29	76.3	439	2	UQ0997	hemagglutinin-este
114	29	76.3	441	2	T10815	ribulose-bisphosph
115	29	76.3	446	2	T01003	ribulose-bisphosph
116	29	76.3	472	2	A31082	ribulose-bisphosph
117	29	76.3	474	2	T01002	ribulose-bisphosph
118	29	76.3	490	2	T48608	hypothetical prote
119	29	76.3	500	2	D83984	gluconate kinase g
120	29	76.3	536	2	T02431	acetyl-CoA carboxy
121	29	76.3	537	2	T01180	acetyl-CoA carboxy
122	29	76.3	539	2	T06279	acetyl-CoA carboxy
123	29	76.3	539	2	T07093	acetyl-CoA carboxy
124	29	76.3	566	1	E41648	protein-cytrosine-p
125	29	76.3	574	2	I66868	cdc25B - rat
126	29	76.3	665	2	T45598	hypothetical prote
127	29	76.3	685	2	A81246	methionyl-tRNA syn
128	29	76.3	1015	2	B84458	probable retroelem
129	29	76.3	1097	2	T49187	hypothetical prote
130	29	76.3	1345	2	T29080	surface layer-asso
131	29	76.3	1653	2	B91052	hypothetical prote
132	29	76.3	1653	2	F85896	hypothetical prote
133	29	76.3	1653	2	G65028	hypothetical prote
134	29	76.3	2357	2	A59249	class VII unconven
135	29	76.3	3063	2	S55505	fatty-acid synthas
136	29	76.3	3063	2	H70656	fatty-acid synthas
137	29	76.3	3076	2	A87058	fatty acid synthas
138	29	76.3	3104	2	S20473	fatty-acid synthas
139	29	76.3	79	2	S24215	ig kappa chain - m
140	28	73.7	79	2	G87186	conserved hypochet
141	28	73.7	99	2	PH1053	ig light chain V r
142	28	73.7	104	2	S26336	ig light chain V r
143	28	73.7	109	2	UC2270	PL7-6 antibody I1g
144	28	73.7	113	2	AH0217	probable exported
145	28	73.7	118	2	T30929	hypothetical prote
146	28	73.7	160	2	I39709	fixr homolog - Agr
147	28	73.7	177	2	UC5354	2-nitroethlene dio
148	28	73.7	186	2	T15549	hypothetical prote
149	28	73.7	194	2	B37329	antigen 5 - easter
150	28	73.7	204	2	A44583	venom allergen ant
151	28	73.7	204	2	B44583	venom allergen ant
152	28	73.7	204	2	C44583	venom allergen ant
153	28	73.7	204	2	AF3433	riboosomal-protein-
154	28	73.7	206	2	S68212	ig kappa chain (Ma
155	28	73.7	214	2	D87697	transaldolase faml
156	28	73.7	217	2	T26429	hypothetical prote
157	28	73.7	234	2	T14169	hypothetical prote
158	28	73.7	236	2	F89963	hypothetical prote
159	28	73.7	237	2	B86724	oxidoreductase yia
160	28	73.7	243	2	AG2962	short-chain alcoho
161	28	73.7	244	2	G98320	fixr protein homol
162	28	73.7	256	2	B95383	probable Short Cha
163	28	73.7	269	2	T38995	hypothetical prote
164	28	73.7	275	2	D97525	hypothetical prote
165	28	73.7	277	2	AD3232	lysosyme (EC 3.2.1
166	28	73.7	309	2	H72626	probable 2-oxoacid
167	28	73.7	334	2	G84327	probable ABC trans
168	28	73.7	335	2	AB3130	hypothetical prote
169	28	73.7	335	2	G98157	oligopeptide ABC t
170	28	73.7	339	2	AG0165	L-allo-threonine a
171	28	73.7	360	2	TS1419	transcription fact
172	28	73.7	396	1	TR1XB4	alpha-lytic protei
173	28	73.7	397	2	T08345	hypothetical prote
174	28	73.7	397	2	G82755	conserved hypochet
175	28	73.7	398	2		
176	28	73.7	407	2	T25011	hypothetical prote
177	28	73.7	412	2	T23385	hypothetical prote
178	28	73.7	481	2	T01850	UDP-glucose glucos
179	28	73.7	527	2	E70543	probable L-asparta
180	28	73.7	538	2	B84552	hypothetical prote
181	28	73.7	538	2	C86976	ppe-family protein
182	28	73.7	557	2	T22079	hypothetical prote
183	28	73.7	557	2	AF3091	hypothetical prote
184	28	73.7	557	2	D98195	hypothetical prote
185	28	73.7	570	2	A47266	L-ornithine N5--oxy
186	28	73.7	580	2	T46024	hypothetical prote
187	28	73.7	597	2	UC5829	alkylglycerone-pho
188	28	73.7	667	2	G89978	DNA ligase (import
189	28	73.7	700	2	S67098	probable membrane
190	28	73.7	724	2	JC4563	acyl-CoA oxidase (
191	28	73.7	776	2	T33543	hypothetical prote
192	28	73.7	780	2	G96826	hypothetical prote
193	28	73.7	929	2	T28927	hypothetical prote
194	28	73.7	1355	2	T22552	hypothetical prote
195	28	73.7	1792	2	T08878	supervillin P205 -
196	27	71.1	82	2	S69480	bombyxin A-10 prec
197	27	71.1	92	2	JQ0825	bombyxin A-9 precu
198	27	71.1	92	2	S69479	bombyxin A-5 precu
199	27	71.1	98	2	PL0034	photosystem I chal
200	27	71.1	105	2	C30535	ig kappa chain V r
201	27	71.1	107	2	F30535	ig kappa chain V r
202	27	71.1	107	2	D30535	ig kappa chain V r
203	27	71.1	107	2	G30535	ig kappa chain V r
204	27	71.1	107	2	B30535	ig kappa chain V r
205	27	71.1	107	2	B81964	conserved hypochet
206	27	71.1	108	2	F30535	ig kappa chain V r
207	27	71.1	112	2	F30538	ig kappa chain V r
208	27	71.1	112	2	E30538	ig kappa chain V r
209	27	71.1	113	2	PL0264	ig kappa chain pre
210	27	71.1	134	1	K4H017	ig kappa chain V-U
211	27	71.1	135	2	S38807	cytochrome-c oxida
212	27	71.1	142	2	S28757	hypothetical prote
213	27	71.1	151	2	C84013	probable iron accu
214	27	71.1	158	2	T40843	hypothetical prote
215	27	71.1	165	2	S35195	hypothetical prote
216	27	71.1	166	2	E90471	hypothetical prote
217	27	71.1	168	2	E90403	hypothetical prote
218	27	71.1	184	2	E90335	hypothetical prote
219	27	71.1	185	2	AB2099	hypothetical prote
220	27	71.1	187	1	AGEC2	p-aminobenzoate sy
221	27	71.1	187	2	C91155	p-aminobenzoate sy
222	27	71.1	187	2	H86000	p-aminobenzoate sy
223	27	71.1	202	2	H44583	venom allergen ant
224	27	71.1	202	2	G44583	venom allergen ant
225	27	71.1	204	2	F90483	second ORF in tran
226	27	71.1	205	2	F44583	venom allergen ant
227	27	71.1	205	2	D44583	venom allergen ant
228	27	71.1	206	2	E44583	venom allergen ant
229	27	71.1	218	2	T40118	peptidyl-terna hydr
230	27	71.1	223	2	A99386	conserved hypochet
231	27	71.1	236	2	B84718	hypothetical prote
232	27	71.1	240	2	C64152	hypothetical prote
233	27	71.1	247	2	G97363	phosphoribosylform
234	27	71.1	247	2	A12581	hypothetical prote
235	27	71.1	249	2	B84072	hypothetical prote
236	27	71.1	251	2	A70891	probable helix-tur
237	27	71.1	251	2	AG1998	peroxiredoxin 2 fa
238	27	71.1	252	2	B87558	hypothetical prote
239	27	71.1	258	2	JH0472	apolipoprotein A-I
240	27	71.1	262	2	F90298	transposase ISCl05
241	27	71.1	267	2	C90307	transposase ISCl05
242	27	71.1	268	2	C90484	hypothetical prote
243	27	71.1	286	2	A87690	hypothetical prote
244	27	71.1	287	2	C81106	conserved hypochet
245	27	71.1	287	2	H81910	hypothetical prote
246	27	71.1	293	2	G71806	hypothetical prote
247	27	71.1	299	2	E90487	transposase ISCl05
248	27	71.1	299	2	H90352	transposase ISCl05

249	27	71.1	300	2	S72914	phosphoserine phos
250	27	71.1	301	2	T01499	NADPH Hc toxin red
251	27	71.1	315	2	T17340	hypothetical prote
252	27	71.1	330	2	T37990	probable polysacch
253	27	71.1	336	2	T37874	probable mitochond
254	27	71.1	328	2	D81778	conserved hypochet
255	27	71.1	328	2	H81201	conserved hypochet
256	27	71.1	332	2	T18527	anexin homolog -
257	27	71.1	339	2	D70942	conserved pfkfb prot
258	27	71.1	341	2	E89906	conserved hypochet
259	27	71.1	344	2	AB1349	oligopeptide ABC t
260	27	71.1	344	2	AF1719	oligopeptide ABC t
261	27	71.1	347	2	H84608	probable RNA-bindi
262	27	71.1	350	2	S43772	phosphatidylcholin
263	27	71.1	350	2	AH2005	phosphatidylcholin
264	27	71.1	350	2	A86325	hypothetical prote
265	27	71.1	351	2	S25480	hypothetical prote
266	27	71.1	352	2	E70847	heat shock transcr
267	27	71.1	353	2	G86298	hypothetical prote
268	27	71.1	355	2	F72625	protein F309.16 [1
269	27	71.1	365	2	B81505	probable N-acetyl-
270	27	71.1	365	2	G86590	hypothetical prote
271	27	71.1	365	2	F72033	hypothetical prote
272	27	71.1	367	2	AE2601	conserved hypochet
273	27	71.1	367	2	F97383	hypothetical prote
274	27	71.1	408	2	S54813	probable chain len
275	27	71.1	410	2	T06213	probable aspartic
276	27	71.1	410	2	T04372	protein E8A1 - bar
277	27	71.1	418	2	E86171	hypothetical prote
278	27	71.1	427	2	E87669	conserved hypochet
279	27	71.1	446	2	G72731	probable malate ox
280	27	71.1	446	2	E82975	conserved hypochet
281	27	71.1	452	2	S75956	nitrile transport
282	27	71.1	456	2	T36912	probable periplasm
283	27	71.1	466	2	AF2374	hypothetical prote
284	27	71.1	467	2	A43357	pancreatic lipase-
285	27	71.1	469	2	E82264	probable polysacch
286	27	71.1	490	1	H70473	IMP dehydrogenase
287	27	71.1	492	2	G82498	conserved hypochet
288	27	71.1	492	2	B83020	hypothetical prote
289	27	71.1	488	2	A81635	conserved hypochet
290	27	71.1	502	2	S35158	lriticin - wheat
291	27	71.1	509	2	A84404	hypothetical prote
292	27	71.1	534	2	UC7912	amino-acid N-acety
293	27	71.1	568	2	A85642	probable terminase
294	27	71.1	568	2	D90781	probable terminase
295	27	71.1	576	2	A49933	proteinase SM tran
296	27	71.1	586	2	T48672	ABC-type transport
297	27	71.1	606	2	UC5604	ABC-transporting p
298	27	71.1	616	2	T19873	hypothetical prote
299	27	71.1	663	2	S69626	hypothetical prote
300	27	71.1	668	1	VCWMPF	coat protein - fel
301	27	71.1	668	2	TQ2354	capsid protein - f
302	27	71.1	690	2	F71239	hypothetical prote
303	27	71.1	720	2	A36526	choleline O-acetyltr
304	27	71.1	728	2	A24689	choleline O-acetyltr
305	27	71.1	821	2	T01181	hypothetical prote
306	27	71.1	835	1	A49891	outer membrane uet
307	27	71.1	860	2	JC4939	beta-glucosidase (
308	27	71.1	873	2	T50171	hypothetical prote
309	27	71.1	892	2	D64370	alanine-tRNA ligas
310	27	71.1	909	2	S32538	GMP-gated cation
311	27	71.1	962	2	C71617	SERA antigen/Dapa1
312	27	71.1	964	2	T01860	reverse transcript
313	27	71.1	967	2	G96637	hypothetical prote
314	27	71.1	986	2	S76194	hypothetical prote
315	27	71.1	1006	2	D86431	protein T518.6 [lm
316	27	71.1	1015	2	T32186	hypothetical prote
317	27	71.1	1036	2	T38734	hypothetical prote
318	27	71.1	1052	2	C64221	hypothetical 114K
319	27	71.1	1064	2	A41542	adenylate cyclase
320	27	71.1	1081	1	WZBR46	119K DNA helicase/
321	27	71.1	1196	2	T14108	SH3-containing pro
322	27	71.1	1215	2	T43916	chitinase A [impor
323	27	71.1	1330	1	VCBR55	major capsid prote
324	27	71.1	1358	2	S64356	phosphoribosylform
325	27	71.1	1364	2	T14900	condensin XCAP-D2
326	27	71.1	1375	2	T42586	major capsid prote
327	27	71.1	1376	1	VCBER6	major capsid prote
328	27	71.1	1385	2	S61236	major capsid prote
329	27	71.1	1440	2	UC6312	protein-tyrosine-p
330	27	71.1	1457	1	A48066	protein-tyrosine-p
331	27	71.1	1485	2	C88400	protein H19M22.1 (
332	27	71.1	1825	2	T32828	hypothetical prote
333	27	71.1	2802	2	F97686	cyclic beta-(1-2)
334	27	71.1	2831	2	A12911	beta (1->2) glucan
335	27	71.1	2831	2	T13734	groovin gene prote
336	27	71.1	4151	2	T11815	hypothetical prote
337	27	71.1	37	2	C49038	hypothetical prote
338	27	68.4	38	2	D84721	Ig lambda chain V
339	27	68.4	71	2	UC6167	hypothetical prote
340	27	68.4	103	2	AG2022	somatostatin-14 [p
341	27	68.4	106	2	AG2022	hypothetical prote
342	27	68.4	107	2	H72575	hypothetical prote
343	27	68.4	107	2	H72506	hypothetical prote
344	27	68.4	117	2	AB3201	conserved hypochet
345	27	68.4	125	2	E81814	hypothetical prote
346	27	68.4	144	2	B70949	hypothetical prote
347	27	68.4	152	2	G86303	hypothetical prote
348	27	68.4	157	2	S04536	embryonic abundant
349	27	68.4	157	2	S26735	hypothetical prote
350	27	68.4	172	2	JN0061	hypothetical 19.5K
351	27	68.4	173	2	B72298	hypothetical prote
352	27	68.4	179	2	A90579	dihydrofolate redu
353	27	68.4	179	2	E70573	hypothetical prote
354	27	68.4	180	2	T24069	hypothetical prote
355	27	68.4	186	2	F84058	ABC transporter [p
356	27	68.4	187	2	T01852	probable blue copp
357	27	68.4	192	2	D84293	hypothetical prote
358	27	68.4	192	2	AG2703	conserved hypochet
359	27	68.4	192	2	G97485	hypothetical prote
360	27	68.4	198	2	T41359	hypothetical prote
361	27	68.4	211	1	CYRTB3	beta-crystallin B1
362	27	68.4	212	2	T27834	hypothetical prote
363	27	68.4	214	1	JC4808	ribosomal protein
364	27	68.4	218	2	C84317	phosphoribosylant
365	27	68.4	220	2	UC5954	ribosomal protein
366	27	68.4	221	2	B86200	hypothetical prote
367	27	68.4	224	2	I37243	CMRF-35 antigen -
368	27	68.4	231	2	S12124	probable heme-bind
369	27	68.4	233	2	E82604	hypothetical prote
370	27	68.4	238	2	I62385	outer membrane pro
371	27	68.4	240	2	T33755	hypothetical prote
372	27	68.4	244	2	I62393	outer membrane pro
373	27	68.4	244	2	I62389	outer membrane pro
374	27	68.4	246	2	AG0743	conserved hypochet
375	27	68.4	246	2	C38113	yebC protein - Bsc
376	27	68.4	246	2	F90950	hypothetical prote
377	27	68.4	246	2	B85799	hypothetical prote
378	27	68.4	247	2	E86475	hypothetical prote
379	27	68.4	248	2	T44361	acetoacetyl-CoA re
380	27	68.4	249	2	A84751	probable SP16 prot
381	27	68.4	250	2	G96540	hypothetical prote
382	27	68.4	255	2	S39654	probable short-cha
383	27	68.4	255	2	A40571	testis-specific pr
384	27	68.4	257	2	T40655	hypothetical prote
385	27	68.4	259	2	S10231	nodulation protein
386	27	68.4	262	2	G95320	NodJ membrane tran
387	27	68.4	264	2	AG3950	conserved hypochet
388	27	68.4	272	2	D83154	probable permease
389	27	68.4	272	2	AD3449	glyoxylate induced
390	27	68.4	278	2	D98332	conserved hypochet
391	27	68.4	282	1	G96015	glycine betaine AB
392	27	68.4	287	2	F71322	hypothetical prote
393	27	68.4	290	2	AB2769	conserved hypochet
394	27	68.4	291	2	AE1828	hypothetical prote

395	26	68.4	295	2	S23585	carboxyphosphoen
396	26	68.4	301	2	C95872	hypothetical prote
397	26	68.4	302	1	A38097	urate oxidase (EC
398	26	68.4	308	2	B86089	pantothenate kinas
399	26	68.4	313	2	T02534	hypothetical prote
400	26	68.4	314	2	AF2930	asparaginase [impo
401	26	68.4	316	1	BVECRS	pantothenate kinas
402	26	68.4	316	2	T35006	beta-keoacetyl-acyl
403	26	68.4	316	2	AF0934	pantothenate kinas
404	26	68.4	316	2	E91241	pantothenate kinas
405	26	68.4	316	2	AF0457	pantothenate kinas
406	26	68.4	317	2	T50881	2-alpha-hydroxy et
407	26	68.4	319	2	T37130	hypothetical prote
408	26	68.4	319	2	T04500	hypothetical prote
409	26	68.4	320	2	E70900	probable lipase -
410	26	68.4	320	2	C86289	hypothetical prote
411	26	68.4	321	2	AF3307	methylytransferase
412	26	68.4	323	2	G86877	glucokinase (EC 2.
413	26	68.4	325	2	F64845	probable 2-hydroxy
414	26	68.4	325	2	B90805	probable dehydroge
415	26	68.4	325	2	G85664	probable dehydroge
416	26	68.4	328	2	H86348	hypothetical prote
417	26	68.4	329	2	G95848	probable transcrip
418	26	68.4	330	2	H98351	probable asparagin
419	26	68.4	330	2	F81656	conserved hypochet
420	26	68.4	331	2	B70837	hypothetical prote
421	26	68.4	335	2	H75029	hypothetical prote
422	26	68.4	336	2	H72303	mannose-1-phosphat
423	26	68.4	337	2	T28630	hypothetical prote
424	26	68.4	339	2	T49597	hypothetical prote
425	26	68.4	340	2	T23562	hypothetical prote
426	26	68.4	342	2	A45462	C 4.2.3.9 aristolo
427	26	68.4	344	2	C70580	integrase/recombin
428	26	68.4	344	2	T03499	low specificity L-
429	26	68.4	344	2	C97320	TPR-repeat-contain
430	26	68.4	346	2	B97014	hypothetical prote
431	26	68.4	350	2	E70678	outer membrane pro
432	26	68.4	350	2	S07222	phospho-2-dehydro-
433	26	68.4	358	2	B83426	hypothetical prote
434	26	68.4	360	2	S75350	mem-2 protein - Ca
435	26	68.4	362	2	T42049	hypothetical prote
436	26	68.4	363	2	D75423	conserved hypochet
437	26	68.4	364	2	D97549	porin precursor -
438	26	68.4	364	2	D75491	hypothetical prote
439	26	68.4	368	2	S46435	hypothetical prote
440	26	68.4	372	2	T25621	Alp2/3 complex cha
441	26	68.4	377	2	T45528	probable arp2-3 co
442	26	68.4	377	2	T39434	aminoctransterase,
443	26	68.4	379	2	D87480	poly-gamma-glutam
444	26	68.4	380	2	H70069	hypothetical prote
445	26	68.4	381	2	T34254	probable transamin
446	26	68.4	382	2	G75294	hypothetical prote
447	26	68.4	385	2	B84447	hypothetical prote
448	26	68.4	389	2	A83229	hypothetical prote
449	26	68.4	390	2	T39818	isopenicillin N ep
450	26	68.4	398	2	S30901	hypothetical prote
451	26	68.4	402	2	A84766	flagellar hook pro
452	26	68.4	405	2	E84969	probable PPE prote
453	26	68.4	408	2	G70925	chain length deter
454	26	68.4	412	2	B55587	serine/threonine k
455	26	68.4	413	2	S51667	hypothetical prote
456	26	68.4	414	2	D96751	probable pectinase
457	26	68.4	416	2	T02194	Flt2p19.7 [importe
458	26	68.4	416	2	C96683	probable beta-keto
459	26	68.4	424	1	S11975	ribulose-bisphosph
460	26	68.4	426	2	B23703	hemagglutinin-este
461	26	68.4	427	1	HMIHMH	ribulose-bisphosph
462	26	68.4	428	2	A10034	protein T23178.5 [
463	26	68.4	428	2	G86247	ribulose-bisphosph
464	26	68.4	432	2	T04160	probable gsmA prot
465	26	68.4	432	2	A70794	hypothetical prote
466	26	68.4	435	2	T48717	
467	26	68.4	435	2		
468	26	68.4	442	2	S58738	nitrate-binding pr
469	26	68.4	443	2	T02134	nitrate transport
470	26	68.4	446	2	A56733	nuclear domain 10
471	26	68.4	455	2	D81284	probable fumarate
472	26	68.4	461	2	H70899	probable cytochrom
473	26	68.4	464	2	T06176	ribulose-bisphosp
474	26	68.4	466	2	T22141	hypothetical prote
475	26	68.4	469	2	B70607	probable cysS prot
476	26	68.4	470	2	T23512	hypothetical prote
477	26	68.4	473	2	C86949	probable cysteinyl
478	26	68.4	476	2	D95318	Nife oxidoreductas
479	26	68.4	481	2	S74590	hypothetical prote
480	26	68.4	483	2	S76583	hypothetical prote
481	26	68.4	484	2	D71419	probable indole-3-
482	26	68.4	489	2	T24971	hypothetical prote
483	26	68.4	491	2	T01856	hypothetical prote
484	26	68.4	492	2	T36429	probable iron-sulf
485	26	68.4	493	2	A96197	hypothetical prote
486	26	68.4	493	2	A13089	conserved hypochet
487	26	68.4	499	2	E96969	histidine kinase (
488	26	68.4	504	2	C64398	hypothetical prote
489	26	68.4	504	2	T24729	hypothetical prote
490	26	68.4	504	2	H64775	probable membrane
491	26	68.4	504	2	B88322	protein C47D12.8 l
492	26	68.4	504	2	T19998	hypothetical prote
493	26	68.4	504	2	T04591	ferulate-5-hydroxy
494	26	68.4	504	2	H75513	probable sodium/pr
495	26	68.4	504	2	T33527	hypothetical prote
496	26	68.4	504	2	UT0531	muscarinic acetylch
497	26	68.4	504	2	UT0530	muscarinic acetylch
498	26	68.4	504	2	A38170	cytochrome d compl
499	26	68.4	504	2	A86405	unknown protein [l
500	26	68.4	504	2	D86262	F13K23.13 protein
501	26	68.4	504	2	T50742	protoporphyrin IX
502	26	68.4	504	2	S29246	urocanate hydratase
503	26	68.4	504	2	C89993	hypothetical prote
504	26	68.4	504	2	AG1412	DNA polymerase III
505	26	68.4	504	2	AF1788	DNA polymerase III
506	26	68.4	504	2	F83136	inner membrane cop
507	26	68.4	504	2	E69513	signal-transducing
508	26	68.4	504	2	B90428	conserved hypochet
509	26	68.4	504	2	T32327	hypothetical prote
510	26	68.4	504	2	S49000	hypothetical prote
511	26	68.4	504	2	A40802	protein-tyrosine k
512	26	68.4	504	2	B84461	hypothetical prote
513	26	68.4	504	2	A75069	dipeptide transpor
514	26	68.4	504	2	T12792	hypothetical prote
515	26	68.4	504	2	A83395	probable acyl-CoA
516	26	68.4	504	2	S76909	hypothetical prote
517	26	68.4	504	2	D84634	hypothetical prote
518	26	68.4	504	2	A11029	hypothetical prote
519	26	68.4	504	2	S48964	DNA ligase - Deino
520	26	68.4	504	2	G75318	DRH1 DEAD box prot
521	26	68.4	504	2	T48634	hypothetical prote
522	26	68.4	504	2	T23769	cellulase (EC 3.2.
523	26	68.4	504	2	B47093	hypothetical prote
524	26	68.4	504	2	T47806	hypothetical prote
525	26	68.4	504	2	T07693	DNA repair/recombi
526	26	68.4	504	2	A56244	hypothetical prote
527	26	68.4	504	2	781	aminopeptidase, pr
528	26	68.4	504	2	D87391	protein TIF9.12 [l
529	26	68.4	504	2	D96639	S-receptor kinase
530	26	68.4	504	2	T09349	probable receptor
531	26	68.4	504	2	AB5041	hypothetical prote
532	26	68.4	504	2	AB2020	hypothetical prote
533	26	68.4	504	2	S69700	endopeptidase C1P
534	26	68.4	504	2	D71555	glucan 1,4-beta-gl
535	26	68.4	504	2	S24325	F6A14.8 protein -
536	26	68.4	504	2	B86322	beta-glucosidase (
537	26	68.4	504	2	A45956	beta-glucosidase (
538	26	68.4	504	2	880	valyl-tRNA synthet
539	26	68.4	504	2	F84404	TonB-dependent rec
540	26	68.4	504	2	E87304	

541	26	68.4	889	2	AD2215	two-component hybr	614	25	65.8	150	2	H85586	molycopterin conv
542	26	68.4	903	2	TE0327	dynamn-related pr	615	25	65.8	150	2	S31883	molycopterin bios
543	26	68.4	903	2	TE0334	hypothetical prote	616	25	65.8	151	2	S21987	probable heme-bind
544	26	68.4	926	2	AH1034	hypothetical prote	617	25	65.8	151	2	S17326	probable heme-bind
545	26	68.4	940	2	A38149	RNA-directed RNA p	618	25	65.8	151	2	S17322	probable heme-bind
546	26	68.4	968	2	C64691	type III restructi	619	25	65.8	154	2	T08354	hypothetical prote
547	26	68.4	972	2	C71861	hypothetical prote	620	25	65.8	155	2	T52501	hypothetical prote
548	26	68.4	984	2	T00326	hypothetical prote	621	25	65.8	155	2	B83048	hypothetical prote
549	26	68.4	990	2	UC7878	fucokinase (EC 2.7	622	25	65.8	157	2	H70902	hypothetical prote
550	26	68.4	992	2	T39315	hypothetical prote	623	25	65.8	159	2	AE2657	NTF pyrophosphohyd
551	26	68.4	993	1	GNXS98	genome polypotein	624	25	65.8	159	2	B97439	hypothetical prote
552	26	68.4	1012	1	GNXS52	genome polypotein	625	25	65.8	160	2	B64225	hypothetical prote
553	26	68.4	1012	1	GNXS4V	genome polypotein	626	25	65.8	164	2	D83172	dihydrofolate redu
554	26	68.4	1012	1	GNXS4V	genome polypotein	627	25	65.8	166	2	A13403	hypothetical membr
555	26	68.4	1012	1	GNXSIR	genome polypotein	628	25	65.8	168	2	B69849	conserved hypochet
556	26	68.4	1012	1	GNXS4V	genome polypotein	629	25	65.8	170	2	G86356	hypothetical prote
557	26	68.4	1012	1	S68259	DNA polymerase gam	630	25	65.8	174	2	T49613	hypothetical prote
558	26	68.4	1013	2	S32214	hypothetical prote	631	25	65.8	175	2	S28240	NADH2 dehydrogenas
559	26	68.4	1032	2	S65341	probable membrane	632	25	65.8	183	2	C95165	acetyltransferase,
560	26	68.4	1047	2	T49425	hypothetical prote	633	25	65.8	183	2	B98031	conserved hypochet
561	26	68.4	1048	2	A27421	integrin alpha-5 c	634	25	65.8	183	2	A11820	hypothetical prote
562	26	68.4	1088	2	S50925	hypothetical prote	635	25	65.8	185	2	B84531	hypothetical prote
563	26	68.4	1111	2	A86922	probable arabinosy	636	25	65.8	187	2	H87701	MutT/nudix family
564	26	68.4	1130	2	T29089	alpha-mannosidase	637	25	65.8	191	2	A87365	transcription regu
565	26	68.4	1175	2	T20346	pyruvate carboxyla	638	25	65.8	196	2	T08288	hypothetical prote
566	26	68.4	1190	2	F86677	pyruvate-flavodoxi	639	25	65.8	198	1	B64366	thioredoxin-2 - Me
567	26	68.4	1199	2	T33337	hypothetical prote	640	25	65.8	199	2	T31317	hypothetical 22.3k
568	26	68.4	1205	2	S64819	probable membrane	641	25	65.8	203	2	T44695	bur protein [impo
569	26	68.4	1224	2	S28368	hypothetical prote	642	25	65.8	206	2	A84664	probable phytoeyan
570	26	68.4	1275	2	D38164	cobN protein - Pse	643	25	65.8	206	2	C83590	probable transcrip
571	26	68.4	1277	2	S70306	hypothetical prote	644	25	65.8	208	1	BVECB1	incB protein - pha
572	26	68.4	1374	2	S69875	hypothetical prote	645	25	65.8	212	2	C90786	probable tet opero
573	26	68.4	1383	2	S70310	hypothetical prote	646	25	65.8	212	2	A85645	probable tet opero
574	26	68.4	1383	2	T13052	guanine nucleotide	647	25	65.8	212	2	C64843	probable transcrip
575	26	68.4	1401	2	G82336	DNA-directed RNA p	648	25	65.8	216	2	T25025	hypothetical prote
576	26	68.4	1450	2	T40325	dermonecrotic toxi	649	25	65.8	220	2	T24319	hypothetical prote
577	26	68.4	1480	2	T05566	hypothetical prote	650	25	65.8	221	1	QOECW7	YecA protein - Esc
578	26	68.4	1522	2	T00028	brain-specific ang	651	25	65.8	221	2	H90955	hypothetical prote
579	26	68.4	1644	2	AC0823	probable lipoprote	652	25	65.8	221	2	B85804	hypothetical prote
580	26	68.4	1666	1	C3GP	complement C3 prec	653	25	65.8	221	2	B64305	conserved hypochet
581	26	68.4	1681	2	S59693	hypothetical prote	654	25	65.8	226	1	QJ1570	major surface anti
582	26	68.4	1758	2	S57015	probable purine nu	655	25	65.8	226	1	QJ1571	major surface anti
583	26	68.4	1796	2	S65004	probable membrane	656	25	65.8	226	1	QJ1573	major surface anti
584	26	68.4	1859	2	S63325	probable membrane	657	25	65.8	226	1	QJ1574	major surface anti
585	26	68.4	1859	2	S64633	probable membrane	658	25	65.8	226	1	QJ1576	major surface anti
586	26	68.4	1875	2	S38173	myosin-like protei	659	25	65.8	226	1	QJ1577	major surface anti
587	26	68.4	1886	2	S04921	nuclear pore prote	660	25	65.8	226	1	QJ1578	major surface anti
588	26	68.4	1891	2	T43262	calcium channel al	661	25	65.8	226	1	QJ1579	major surface anti
589	26	68.4	2175	2	A59255	myosin VIIa, long	662	25	65.8	226	1	QJ1580	major surface anti
590	26	68.4	2182	2	T28634	variant-specific s	663	25	65.8	226	1	QJ1581	major surface anti
591	26	68.4	2215	2	T30870	myosin VIIa - mous	664	25	65.8	226	1	SAVLAD	major surface anti
592	26	68.4	2327	2	T42630	aggrean - bovine	665	25	65.8	226	1	SAVLAR	major surface anti
593	26	68.4	3411	1	GNWV	genome polypotein	666	25	65.8	226	1	SAVLNI	major surface anti
594	26	68.4	3411	1	GNWVYP	genome polypotein	667	25	65.8	226	1	QJ1572	major surface anti
595	26	68.4	3421	1	WZBBE6	367K tegument prot	668	25	65.8	226	2	QJ2058	surface antigen -
596	26	68.4	3623	2	T08618	intrinsic factor-B	669	25	65.8	226	2	QJ2103	surface antigen -
597	26	68.4	5825	2	T12117	polypotein - fava	670	25	65.8	226	2	QJ2075	surface antigen -
598	26	65.8	66	2	AB0352	conserved hypochet	671	25	65.8	226	2	QJ2052	surface antigen -
599	26	65.8	86	2	S73048	hypothetical prote	672	25	65.8	226	2	QJ2225	small surface prot
600	26	65.8	102	2	S06101	hypothetical prote	673	25	65.8	226	2	QJ2073	surface antigen -
601	26	65.8	110	2	B26848	hypothetical prote	674	25	65.8	226	2	QJ2104	surface antigen -
602	26	65.8	114	2	B64000	hypothetical prote	675	25	65.8	226	2	QJ2057	surface antigen -
603	26	65.8	118	2	T07905	low-carbon dioxide	676	25	65.8	226	2	QJ2065	surface antigen -
604	26	65.8	122	2	S52840	haloalkanoic acid	677	25	65.8	226	2	QJ2113	surface antigen -
605	26	65.8	127	2	AB1063	phage immunity rep	678	25	65.8	226	2	QJ2114	surface antigen -
606	26	65.8	127	2	G72535	hypothetical prote	679	25	65.8	226	2	QJ2068	surface antigen -
607	26	65.8	129	2	G84768	hypothetical prote	680	25	65.8	226	2	QJ2094	surface antigen -
608	26	65.8	134	2	T49623	hypothetical prote	681	25	65.8	226	2	QJ2077	surface antigen -
609	26	65.8	141	2	A45731	comC-alpha protei	682	25	65.8	226	2	QJ2087	surface antigen -
610	26	65.8	146	2	S10089	beta-crystallin B3	683	25	65.8	226	2	QJ2096	surface antigen -
611	26	65.8	147	2	H87132	conserved hypochet	684	25	65.8	226	2	QJ2076	surface antigen -
612	26	65.8	147	2	UC7938	type II antifreeze	685	25	65.8	226	2	QJ2095	surface antigen -
613	26	65.8	150	2	G90736	molycopterin bios	686	25	65.8	226	2	QJ2053	surface antigen -

687	25	65.8	226	2	JQ2111	surface antigen -	760	25	65.8	292	2	T05317	hypothetical prote
688	25	65.8	226	2	JQ2089	surface antigen -	761	25	65.8	292	2	T08947	hypothetical prote
689	25	65.8	226	2	JQ2050	surface antigen -	762	25	65.8	293	2	T49564	hypothetical prote
690	25	65.8	226	2	JQ2085	surface antigen -	763	25	65.8	296	2	AD1040	putative methyltra
691	25	65.8	226	2	JQ2119	surface antigen -	764	25	65.8	299	2	T52444	hypothetical prote
692	25	65.8	226	2	JQ2108	surface antigen -	765	25	65.8	300	2	T42343	hypothetical prote
693	25	65.8	226	2	JQ2105	surface antigen -	766	25	65.8	301	2	AD3578	glycine betaine/1-
694	25	65.8	226	2	JQ2072	surface antigen -	767	25	65.8	302	2	T42598	gene 55 protein -
695	25	65.8	226	2	JQ2092	surface antigen -	768	25	65.8	305	2	A81144	hypothetical prote
696	25	65.8	226	2	JQ2101	surface antigen -	769	25	65.8	305	2	T24736	hypothetical prote
697	25	65.8	226	2	JQ2047	surface antigen -	770	25	65.8	306	2	AC1835	hypothetical prote
698	25	65.8	226	2	JQ2066	surface antigen -	771	25	65.8	307	2	AF3239	conserved hypochet
699	25	65.8	226	2	JQ2098	surface antigen -	772	25	65.8	312	2	A83112	Bira difunctional
700	25	65.8	226	2	JQ2061	surface antigen -	773	25	65.8	313	2	S73033	probable metalloth
701	25	65.8	226	2	JQ2069	surface antigen -	774	25	65.8	313	2	D96616	hypothetical prote
702	25	65.8	226	2	JQ2115	surface antigen -	775	25	65.8	317	2	G89044	protein B0238.11 [
703	25	65.8	226	2	JQ2116	surface antigen -	776	25	65.8	321	2	B70421	conserved 38.2k hy
704	25	65.8	226	2	JQ2048	surface antigen -	777	25	65.8	328	2	D82411	conserved hypochet
705	25	65.8	226	2	JQ2081	surface antigen -	778	25	65.8	331	2	A54295	interferon alpha/b
706	25	65.8	226	2	JQ2070	surface antigen -	779	25	65.8	331	2	S59501	interferon recepto
707	25	65.8	226	2	JQ2060	surface antigen -	780	25	65.8	334	2	B81372	probable sugar nuc
708	25	65.8	226	2	JQ2055	surface antigen -	781	25	65.8	334	2	S25785	hypothetical prote
709	25	65.8	226	2	JQ2078	surface antigen -	782	25	65.8	338	2	E72636	probable nodulario
710	25	65.8	226	2	JQ2051	surface antigen -	783	25	65.8	340	2	AG2712	pyridoxal phosphat
711	25	65.8	226	2	JQ2046	surface antigen -	784	25	65.8	342	2	S57814	oxidase like prote
712	25	65.8	226	2	JQ2112	surface antigen -	785	25	65.8	343	2	G95300	hypothetical prote
713	25	65.8	226	2	JQ2080	surface antigen -	786	25	65.8	345	2	T48758	hypothetical prote
714	25	65.8	226	2	JQ2090	surface antigen -	787	25	65.8	347	2	T06371	probable udp-glucu
715	25	65.8	226	2	JQ2091	surface antigen -	788	25	65.8	348	2	E97494	pyridoxal phosphat
716	25	65.8	226	2	JQ2122	surface antigen -	789	25	65.8	349	2	S54822	cbrc protein - Brw
717	25	65.8	226	2	JQ2045	surface antigen -	790	25	65.8	352	2	T49396	hypothetical prote
718	25	65.8	226	2	JQ2121	surface antigen -	791	25	65.8	354	1	T070433	probable X-Pro dip
719	25	65.8	226	2	JQ2097	surface antigen -	792	25	65.8	354	2	E84645	hypothetical prote
720	25	65.8	226	2	JQ2079	surface antigen -	793	25	65.8	356	2	JC6558	outer membrane pro
721	25	65.8	226	2	JQ2067	surface antigen -	794	25	65.8	359	2	JC5382	hereditary hemochr
722	25	65.8	226	2	JQ2083	surface antigen -	795	25	65.8	360	2	G83831	spore germination
723	25	65.8	226	2	JQ2120	surface antigen -	796	25	65.8	362	2	T02057	fructose-bisphosph
724	25	65.8	226	2	JQ2106	surface antigen -	797	25	65.8	363	2	S74814	hypothetical prote
725	25	65.8	226	2	JQ2102	surface antigen -	798	25	65.8	372	2	A83714	iron (III) transpo
726	25	65.8	226	2	JQ2056	surface antigen -	799	25	65.8	378	2	S41870	surface antigen -
727	25	65.8	226	2	JQ2054	surface antigen -	800	25	65.8	378	2	S41869	surface antigen -
728	25	65.8	226	2	JQ2063	surface antigen -	801	25	65.8	382	2	C86230	hypothetical prote
729	25	65.8	226	2	JQ2088	surface antigen -	802	25	65.8	382	2	T13474	large surface anti
730	25	65.8	226	2	JQ2110	surface antigen -	803	25	65.8	384	2	T13469	large surface anti
731	25	65.8	226	2	JQ2099	surface antigen -	804	25	65.8	384	2	B87427	hypothetical prote
732	25	65.8	226	2	JQ2062	surface antigen -	805	25	65.8	384	2	T21929	hypothetical prote
733	25	65.8	226	2	JQ2059	surface antigen -	806	25	65.8	385	2	T12980	hypothetical prote
734	25	65.8	226	2	JQ2100	surface antigen -	807	25	65.8	388	2	T03679	probable fructose-
735	25	65.8	229	2	T06346	chloroplast envelo	808	25	65.8	388	2	AE2641	aspartate aminotra
736	25	65.8	229	2	T04857	hypothetical prote	809	25	65.8	388	2	T31705	hypothetical prote
737	25	65.8	230	2	S05118	hypothetical prote	810	25	65.8	389	1	SAVLAI	large surface anti
738	25	65.8	230	2	S58553	cema protein EC 3.4.2	811	25	65.8	389	1	SAVLAI	large surface anti
739	25	65.8	235	2	D42696	trypsin (EC 3.4.21	812	25	65.8	389	1	SAVLAI	large surface anti
740	25	65.8	242	2	S49489	hypothetical prote	813	25	65.8	389	1	SAVLAI	large surface anti
741	25	65.8	242	2	H72512	outer membrane pro	814	25	65.8	389	1	SAVLAI	large surface anti
742	25	65.8	243	2	I62386	phosphoglucanase d	815	25	65.8	389	1	SAVLJ2	large surface anti
743	25	65.8	249	2	A48325	H+-transporting tw	816	25	65.8	389	1	SAVLJ3	large surface anti
744	25	65.8	255	2	S65032	glutamine cyclotra	817	25	65.8	389	1	SAVLVE	large surface anti
745	25	65.8	260	1	B87577	carbonate dehydrat	818	25	65.8	389	1	S36654	surface antigen -
746	25	65.8	261	1	JN0836	carbonate dehydrat	819	25	65.8	389	2	S20745	surface antigen -
747	25	65.8	261	2	JN0835	nitrate ABC transp	820	25	65.8	389	2	S47407	surface antigen -
748	25	65.8	261	2	AB7325	antihemagglutinin	821	25	65.8	389	2	S67506	large surface anti
749	25	65.8	261	2	AB7325	antihemagglutinin	822	25	65.8	389	2	S47407	large surface anti
750	25	65.8	263	2	A75565	hypothetical prote	823	25	65.8	389	2	S20753	surface antigen -
751	25	65.8	267	2	AB2997	hypothetical prote	824	25	65.8	389	2	S20749	surface antigen -
752	25	65.8	271	2	AD2212	hypothetical prote	825	25	65.8	389	2	S41871	surface antigen -
753	25	65.8	273	2	G69521	probable short-cha	826	25	65.8	389	2	S32202	large surface anti
754	25	65.8	276	2	B83161	hypothetical prote	827	25	65.8	390	2	H86253	hypothetical prote
755	25	65.8	279	2	S64007	hypothetical prote	828	25	65.8	391	2	G97423	probable aspartate
756	25	65.8	281	2	JQ2226	middle surface pro	829	25	65.8	391	2	A97633	hypothetical prote
757	25	65.8	286	2	G83433	spermidine synthas	830	25	65.8	391	2	AD2856	conserved hypochet
758	25	65.8	286	2	G75489	hypothetical prote	831	25	65.8	392	2	AB0980	xylose operon regu
759	25	65.8	290	2	JX0175	lectin precursor -	832	25	65.8	392	2	D91185	probable regulator

833	25	65.8	392	2	B86032	906	25	65.8	493	2	C64847	ymdc protein - Esc
834	25	65.8	392	2	S47790	907	25	65.8	493	2	H90806	probable synthase
835	25	65.8	393	2	JU0334	908	25	65.8	493	2	D85666	probable synthase
836	25	65.8	400	1	J01575	909	25	65.8	493	2	JA0089	11s globulin seed
837	25	65.8	400	1	SAVLA	910	25	65.8	494	2	T51529	hypothetical prote
838	25	65.8	400	1	SAVLKS	911	25	65.8	495	2	A73608	aldenhyde dehydroge
839	25	65.8	400	1	SAVLVD	912	25	65.8	495	2	AE0636	conserved hypochet
840	25	65.8	400	1	SAV528	913	25	65.8	498	2	T13462	hypothetical prote
841	25	65.8	401	2	JQ2230	914	25	65.8	499	2	A46039	steroid 11beta-mon
842	25	65.8	401	2	I50679	915	25	65.8	500	2	I56601	cytochrome P450 al
843	25	65.8	403	2	AB0640	916	25	65.8	500	2	B41552	steroid 11beta-mon
844	25	65.8	403	2	SI0365	917	25	65.8	500	2	B41552	aldosterone syntha
845	25	65.8	408	2	T32237	918	25	65.8	501	2	A11031	probable membrane
846	25	65.8	410	2	S41188	919	25	65.8	504	2	T37164	probable monooxyge
847	25	65.8	410	2	C84176	920	25	65.8	505	1	KICRGP	phosphoglycerate k
848	25	65.8	412	2	F88978	921	25	65.8	506	2	JN0615	steroid 11beta-mon
849	25	65.8	412	2	AB2471	922	25	65.8	507	2	T08337	hypothetical prote
850	25	65.8	416	2	S75321	923	25	65.8	515	2	I39073	interferon alpha-b
851	25	65.8	419	1	WJFFH2	924	25	65.8	517	2	T18636	hypothetical prote
852	25	65.8	420	2	E69461	925	25	65.8	519	2	H86897	glucosyltransferase (EC
853	25	65.8	426	2	A49892	926	25	65.8	521	2	T04791	hypothetical prote
854	25	65.8	426	2	F71220	927	25	65.8	523	2	A31948	carliline octanoyl
855	25	65.8	426	2	G75187	928	25	65.8	527	2	T37055	probable oxidoredu
856	25	65.8	430	2	C95300	929	25	65.8	529	2	T51214	related to trichod
857	25	65.8	430	2	AC3037	930	25	65.8	530	2	S38092	hypothetical prote
858	25	65.8	435	2	D72379	931	25	65.8	536	2	AB1327	genee protein limp
859	25	65.8	435	2	B86266	932	25	65.8	536	2	AB3123	hypothetical prote
860	25	65.8	437	1	S73806	933	25	65.8	548	2	E98164	probable transfera
861	25	65.8	439	2	C96003	934	25	65.8	553	2	C81024	hypothetical prote
862	25	65.8	440	2	C82410	935	25	65.8	555	2	B87003	probable DNA methy
863	25	65.8	441	2	T42694	936	25	65.8	555	2	F69312	heterodisulfide re
864	25	65.8	442	2	T42342	937	25	65.8	558	2	F81967	probable inner mem
865	25	65.8	445	2	S43492	938	25	65.8	559	2	T23571	hypothetical prote
866	25	65.8	446	2	S77389	939	25	65.8	560	2	C90065	conserved hypochet
867	25	65.8	447	2	T12978	940	25	65.8	567	2	S69779	adhesin AP65-2 pre
868	25	65.8	448	1	S24756	941	25	65.8	567	2	S69778	adhesin AP65-1 pre
869	25	65.8	449	2	T45605	942	25	65.8	570	1	A34354	sulfite reductase
870	25	65.8	449	2	F72762	943	25	65.8	570	1	RDRC5H	sulfite reductase
871	25	65.8	450	2	D86356	944	25	65.8	570	2	AF0858	sulfite reductase
872	25	65.8	450	2	I50631	945	25	65.8	570	2	B91081	sulfite reductase
873	25	65.8	451	2	T45604	946	25	65.8	570	2	C85926	sulfite reductase,
874	25	65.8	452	2	T12981	947	25	65.8	570	2	S70400	zona pellucida gly
875	25	65.8	452	2	A57217	948	25	65.8	571	2	I37405	polypeptide N-acet
876	25	65.8	452	2	T05689	949	25	65.8	582	2	B84721	probable calcium-d
877	25	65.8	452	2	T40634	950	25	65.8	585	1	S14732	H+-transporting tw
878	25	65.8	453	2	T45603	951	25	65.8	591	2	S65588	ABC-transporter St
879	25	65.8	453	2	E83517	952	25	65.8	593	2	T44479	conserved hypochet
880	25	65.8	454	2	T49300	953	25	65.8	597	2	AB0721	hydrogenase-1 larg
881	25	65.8	455	2	B64860	954	25	65.8	597	2	C87627	hypothetical prote
882	25	65.8	456	2	C71402	955	25	65.8	611	2	T44560	hypothetical prote
883	25	65.8	458	2	C71420	956	25	65.8	612	2	JC7101	carliline O-octano
884	25	65.8	460	2	T47709	957	25	65.8	612	2	S60025	carliline octanoyl
885	25	65.8	462	2	T01732	958	25	65.8	612	2	T15485	hypothetical prote
886	25	65.8	462	2	B86262	959	25	65.8	616	2	T14235	NADHr dehydrogenas
887	25	65.8	467	2	T02238	960	25	65.8	626	2	B42094	bwl protein - smut
888	25	65.8	469	2	D86144	961	25	65.8	631	2	B86233	hypothetical prote
889	25	65.8	471	1	GBBYAG	962	25	65.8	639	2	C95342	nitrous-oxide redu
890	25	65.8	471	2	S50312	963	25	65.8	640	2	T45824	protein kinase-lik
891	25	65.8	471	2	S50311	964	25	65.8	641	2	S64064	probable membrane
892	25	65.8	471	2	S50310	965	25	65.8	643	2	T03631	oxygenase, patnoge
893	25	65.8	472	2	H98248	966	25	65.8	643	2	T19549	hypothetical prote
894	25	65.8	472	2	S39507	967	25	65.8	646	2	E82133	ATP-dependent heli
895	25	65.8	474	2	D83995	968	25	65.8	650	2	T44660	nitrous-oxide redu
896	25	65.8	477	2	H75026	969	25	65.8	652	1	S39409	nitrous-oxide redu
897	25	65.8	478	2	B72543	970	25	65.8	653	2	A49722	endoglin precursor
898	25	65.8	479	2	F86356	971	25	65.8	658	2	D84669	probable receptor
899	25	65.8	479	2	G86207	972	25	65.8	664	2	E70770	probable atp-depen
900	25	65.8	480	2	B85014	973	25	65.8	665	2	T30481	occlusion-derived
901	25	65.8	481	2	B86356	974	25	65.8	665	2	T00015	unc-14 protein - C
902	25	65.8	487	2	C86356	975	25	65.8	670	2	F84540	hypothetical prote
903	25	65.8	488	2	G81295	976	25	65.8	676	1	A39379	hatching-supprese
904	25	65.8	488	2	S31916	977	25	65.8	676	1	S67136	hypothetical prote
905	25	65.8	490	2	T35948	978	25	65.8	681	2	AD3045	conserved hypochet

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979      25      65.8      684      2      D83645      glycy1-cRNA synthe
980      25      65.8      686      2      H98240      hypochetrical prote
981      25      65.8      688      2      AB2352      ribonuclease II [i
982      25      65.8      688      2      T18263      S-layer protein -
983      25      65.8      699      2      D96767      unknown protein F2
984      25      65.8      711      2      S66261      X-pro dipeptidyl-P
985      25      65.8      712      2      T27165      hypochetrical prote
986      25      65.8      716      2      A86181      hypochetrical prote
987      25      65.8      719      2      A10769      protein-tyrosine k
988      25      65.8      731      2      AE1945      hypochetrical prote
989      25      65.8      739      2      T29407      hypochetrical prote
990      25      65.8      762      2      D70407      DNA mismatch repai
991      25      65.8      773      1      JH0609      protein-tyrosine-P
992      25      65.8      774      2      F96639      protein T1p9.8 [im
993      25      65.8      775      2      S55345      protein-tyrosine-P
994      25      65.8      778      2      B70667      hypochetrical prote
995      25      65.8      802      2      G96640      hypochetrical prote
996      25      65.8      807      1      MMAD15      late 100K protein
997      25      65.8      807      2      T24110      hypochetrical prote
998      25      65.8      809      2      T32899      probable leukotrie
999      25      65.8      817      2      A96640      protein T1p9.2 [im
1000     25      65.8      817      2      D87350      tonB-dependent rec

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ALIGNMENTS

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RESULT 1
PHI048
Ig light chain V region (clone 165.49) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 15-Jun-1996
C/Accession: PH1048
R/Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A/Title: Both Igm and IgG anti-DNA antibodies are the products of clonally selective B c
A/Reference number: PH0971; MUID:92381444; PMID:1512540
A/Accession: PH1048
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-81 <TIL>
A/Cross-references: UNIPARC:UPI0000176AA9
A/Experimental source: B cell, strain [NZB x NZW]F1
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: immunoglobulin

Query Match      100.0%; Score 38; DB 2; Length 81;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 WASTRES 7
Db      35 WASTRES 41

RESULT 2
S37532
Ig kappa chain V region (V-kappa 4) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C/Accession: S37532
R/Klein, U.; Kupepers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A/Description: Human Igm(+) Igd(+) cells, the major B cell subset in the peripheral blood
A/Reference number: S37501
A/Accession: S37532
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-92 <KLB>
A/Cross-references: UNIPARC:UPI000011658C; EMBL:Z26628; NID:G405706; PIDN:CAA81381.1; PI
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin

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Query Match      100.0%; Score 38; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY      1 WASTRES 7
Db      34 WASTRES 40

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RESULT 3
S37533
Ig kappa chain V region (V-kappa 4) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C/Accession: S37533
R/Klein, U.; Kupepers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A/Description: Human Igm(+) Igd(+) cells, the major B cell subset in the peripheral blood,
A/Reference number: S37501
A/Accession: S37533
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-92 <KLB>
A/Cross-references: UNIPARC:UPI000011658B; EMBL:Z26627; NID:G405708; PIDN:CAA81380.1; PI
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin

```

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Query Match      100.0%; Score 38; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY      1 WASTRES 7
Db      34 WASTRES 40

```

```

RESULT 4
S37530
Ig kappa chain V region (V-kappa 4) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C/Accession: S37530
R/Klein, U.; Kupepers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A/Description: Human Igm(+) Igd(+) cells, the major B cell subset in the peripheral blood,
A/Reference number: S37501
A/Accession: S37530
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-92 <KLB>
A/Cross-references: UNIPARC:UPI000011658E; EMBL:Z26630; NID:G405702; PIDN:CAA81383.1; PI
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin

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Query Match      100.0%; Score 38; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY      1 WASTRES 7
Db      34 WASTRES 40

```

```

RESULT 5
S37535
Ig kappa chain V region (V-kappa 4) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C/Accession: S37535
R/Klein, U.; Kupepers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A/Description: Human Igm(+) Igd(+) cells, the major B cell subset in the peripheral blood,
A/Reference number: S37501

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A:Accession: S37535
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-92 <KLE>
A:Cross-references: UNIPARC:UPI0000116589; EMBL:Z26625; NID:9405712; PIDN:CAA61378.1; PIR
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 38; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7
|||||
34 WASTRES 40

RESULT 6
S37531
Ig kappa chain V region (V-kappa 4) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37531
R:Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A:Description: Human IGM(+) IGD(+) cells, the major B cell subset in the peripheral blood
A:Reference number: S37501
A:Accession: S37531
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-92 <KLE>
A:Cross-references: UNIPARC:UPI0000116589; EMBL:Z26629; NID:9405704; PIDN:CAA61382.1; PIR
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 38; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7
|||||
34 WASTRES 40

RESULT 7
S37534
Ig kappa chain V region (V-kappa 4) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37534
R:Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A:Description: Human IGM(+) IGD(+) cells, the major B cell subset in the peripheral blood
A:Reference number: S37501
A:Accession: S37534
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-92 <KLE>
A:Cross-references: UNIPARC:UPI0000116589; EMBL:Z26626; NID:9405710; PIDN:CAA61379.1; PIR
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 38; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7
|||||
34 WASTRES 40

RESULT 8
S37529

Ig kappa chain V region (V-kappa 4) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37529
R:Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A:Description: Human IGM(+) IGD(+) cells, the major B cell subset in the peripheral blood
A:Reference number: S37501
A:Accession: S37529
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-92 <KLE>
A:Cross-references: UNIPARC:UPI0000116589; EMBL:Z26631; NID:9405700; PIDN:CAA61384.1; PIR
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 38; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7
|||||
34 WASTRES 40

RESULT 9
S19974
Ig kappa chain V region (M-T406) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C:Accession: S19974
R:Wissenhorn, W.; Rietmueller, G.; Weiss, E.M.; Rieber, E.P.
submitted to the EMBL Data Library, March 1992
A:Description: Structural characterization of CD4 mAb.
A:Reference number: S19963
A:Accession: S19974
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-98 <MEI>
A:Cross-references: UNIPARC:UPI0000116034; EMBL:X65096; NID:952294; PIDN:CAA6224.1; PIR
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-80/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 38; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7
|||||
40 WASTRES 46

RESULT 10
PH0869
Ig kappa chain V region (anti-DNA, H2F) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 21-Jan-2000
C:Accession: PH0869
R:Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghosesein, C.; Smith, A.; Diamond, B.
J. Exp. Med. 174, 1639-1652, 1991
A:Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype
A:Reference number: PH0862; MUID:92078875; PMID:1660528
A:Accession: PH0869
A:Molecule type: DNA
A:Residues: 1-101 <MAN>
A:Cross-references: UNIPARC:UPI0000176AE1
A:Note: residues 28-33 were obtained from Figure 4
C:Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that bears
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-23/Region: framework 1
F:16-96/Domain: immunoglobulin homology <IMM>

F;24-40/Region: complementarity-determining 1
F;41-55/Region: framework 2
F;56-62/Region: complementarity-determining 2
F;63-94/Region: framework 3
F;95-101/Region: complementarity-determining 3

Query Match 100.0%; Score 38; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7
|||||
Db 56 WASTRES 62

RESULT 11

PH1046
Ig light chain V region (clone 202.9) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C/Accession: PH1046
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IGM and IGG anti-DNA antibodies are the products of clonally selective B c
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH1046
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-101 <TIL>
A;Cross-references: UNIPARC:UPI0000176AA8
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;16-96/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 38; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7
|||||
Db 56 WASTRES 62

RESULT 12

S26337
Ig light chain V region - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 20-Jun-2000
C/Accession: S26337; S78449
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protein e
A;Reference number: S26309; MUID:91341421; PMID:1908510
A;Accession: S26337
A;Molecule type: mRNA
A;Residues: 1-101 <STRA>
A;Cross-references: UNIPARC:UPI00001769B0; EMBL:X59193
R;Caton, A.J.
submitted to the EMBL Data Library, April 1991
A;Reference number: S78447
A;Accession: S78449
A;Molecule type: mRNA
A;Residues: 1-60, 'T', 62-91, 'S', 93-101 <CAT>
A;Cross-references: UNIPARC:UPI000015F7F; EMBL:X59193; NID:G52323; PIDN:CAA41903.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;8-68/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 38; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7
|||||
Db 48 WASTRES 54

RESULT 13

A34153
Ig kappa chain V-IV region (Dep) - human
C/Species: Homo sapiens (man)
C/Date: 11-Apr-1990 #sequence_revision 11-Apr-1990 #text_change 21-Jan-2000
C/Accession: A34153
R;Mhaesco, E.; Ayadi, H.; Congy, N.; Gendron, M.C.; Roy, J.P.; Heyermann, H.; Frangione,
J. Biol. Chem. 264, 21481-21485, 1989
A;Title: Multiple mutations in the variable region of the kappa light chains of three mor
A;Reference number: A34153; MUID:9094313; PMID:2480953
A;Accession: A34153
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-102 <MIH>
A;Cross-references: UNIPARC:UPI0000176AE5
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-96/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 38; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7
|||||
Db 56 WASTRES 62

RESULT 14

PH1047
Ig light chain V region (clones 165.45 and 163-cl) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C/Accession: PH1047; PH1049
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IGM and IGG anti-DNA antibodies are the products of clonally selective B c
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH1047
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-103 <TIL>
A;Cross-references: UNIPARC:UPI0000176AD0
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;16-96/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 38; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7
|||||
Db 56 WASTRES 62

RESULT 15

PH1051
Ig light chain V region (clone 165.3) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C/Accession: PH1051
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IGM and IGG anti-DNA antibodies are the products of clonally selective B c
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH1051

A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-103 <TIL>
A;Cross-references: UNIPARC:UPI0000176AAB
C;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;16-96/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 38; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
|||||
Db 56 WASTRES 62

RESULT 16
PH1052
Ig light chain V region (clone 165.5) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1052
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both Igm and IgG anti-DNA antibodies are the products of clonally selective B
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH1052
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-103 <TIL>
A;Cross-references: UNIPARC:UPI0000176AAC
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;16-96/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 38; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
|||||
Db 56 WASTRES 62

RESULT 17
PH1050
Ig light chain V region (clone 111-c1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1050
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both Igm and IgG anti-DNA antibodies are the products of clonally selective B
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH1050
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-103 <TIL>
A;Cross-references: UNIPARC:UPI0000176AAA
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;16-96/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 38; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
|||||
Db 56 WASTRES 62

Db 56 WASTRES 62

RESULT 18
PH1054
Ig light chain V region (clone 202.135) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1054
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both Igm and IgG anti-DNA antibodies are the products of clonally selective B
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH1054
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-103 <TIL>
A;Cross-references: UNIPARC:UPI0000176AAE
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;16-96/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 38; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
|||||
Db 56 WASTRES 62

RESULT 19
PH1101
Ig light chain V region (clone 111.19) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1101
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both Igm and IgG anti-DNA antibodies are the products of clonally selective B
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH1101
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-104 <TIL>
A;Cross-references: UNIPARC:UPI0000176AC3
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;16-96/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 38; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
|||||
Db 56 WASTRES 62

RESULT 20
F38601
Ig kappa chain V region (2F8) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 21-Jan-2000
C;Accession: F38601
R;Goshorn, S.C.; Retzel, E.; Jermerson, R.
J. Biol. Chem. 266, 2134-2142, 1991
A;Title: Common structural features among monoclonal antibodies binding the same antigen
A;Reference number: A38601; MUID:9115823; PMID:1703527
A;Accession: F38601
A;Status: preliminary

A:Molecule type: mRNA
A:Residues: 1-104 <QOS>
A:Cross-references: UNIPARC:UPI000011517A; GB:M57983; NID:G196412; PIDN:AAA63364.1; PID:
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: PH1102
R:Titman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both Igm and IgG anti-DNA antibodies are the products of clonally selective B c
A:Reference number: PH0971; MUID:92381444; PMID:1512540
A:Accession: PH1102
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-104 <TTL>
A:Cross-references: UNIPARC:UPI0000176AC4
A:Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>
Query Match 100.0%; Score 38; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 WASTRES 7
Db 48 WASTRES 54
RESULT 21
PH1102
Ig light chain V region (clone 111.61) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: PH1102
R:Titman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both Igm and IgG anti-DNA antibodies are the products of clonally selective B c
A:Reference number: PH0971; MUID:92381444; PMID:1512540
A:Accession: PH1102
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-104 <TTL>
A:Cross-references: UNIPARC:UPI0000176AC5
A:Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>
Query Match 100.0%; Score 38; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 WASTRES 7
Db 56 WASTRES 62
RESULT 22
PH1103
Ig light chain V region (clone 111.109) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: PH1103
R:Titman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both Igm and IgG anti-DNA antibodies are the products of clonally selective B c
A:Reference number: PH0971; MUID:92381444; PMID:1512540
A:Accession: PH1103
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-104 <TTL>
A:Cross-references: UNIPARC:UPI0000176AC5
A:Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>
Query Match 100.0%; Score 38; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 WASTRES 7
Db 56 WASTRES 62

RESULT 23
PH1104
Ig light chain V region (clone 111.100) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: PH1104
R:Titman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both Igm and IgG anti-DNA antibodies are the products of clonally selective B c
A:Reference number: PH0971; MUID:92381444; PMID:1512540
A:Accession: PH1104
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-104 <TTL>
A:Cross-references: UNIPARC:UPI0000176AC6
A:Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>
Query Match 100.0%; Score 38; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 WASTRES 7
Db 56 WASTRES 62
RESULT 24
A49138
IGA kappa rheumatoid factor variable - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: A49138
R:Gause, A.; Kuppers, R.; Mierau, R.
Clin. Exp. Immunol. 88, 430-434, 1992
A:Title: A somatically mutated V kappa IV gene encoding a human rheumatoid factor light c
A:Reference number: A49138; MUID:92298590; PMID:1606727
A:Accession: A49138
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-106 <GAU>
A:Cross-references: UNIPARC:UPI0000176B10; GB:S37926; NID:G298207; PIDN:AA823366.1; PID:
A:Note: sequence inconsistent with the nucleotide translation
A:Superfamily: immunoglobulin V region; immunoglobulin homology
F:20-99/Domain: immunoglobulin homology <IMM>
Query Match 100.0%; Score 38; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 0.44;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 WASTRES 7
Db 59 WASTRES 65
RESULT 25
S03304
Ig kappa chain V region (61B8) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 21-Jan-2000
C:Accession: S03304; J10043
R:Van Cleave, V.H.; Naeye, C.W.; Metzger, D.W.
J. Exp. Med. 167, 1841-1848, 1988
A:Title: Do antibodies recognize amino acid side chains of protein antigens independently
A:Reference number: J10043; MUID:88258372; PMID:2455014
A:Accession: S03304
A:Molecule type: mRNA
A:Residues: 1-111 <VAN>
A:Cross-references: UNIPARC:UPI0000115DB2; EMBL:X12380; NID:G52341; PIDN:CAA30938.1; PID:

A;Note: the authors translated the codon GAT for residue 76 as Asn
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;16-96/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 38; DB 2; Length 111;
 Best Local Similarity 100.0%; Pred. No. 0.46;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
 Db 56 WASTRES 62

RESULT 26

Ig kappa chain V region (A52) - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 03-Nov-1988 #sequence_revision 03-Nov-1988 #text_change 21-Jan-2000
 C;Accession: G30502
 R;Eilat, D.; Webster, D.M.; Rees, A.R.

J. Immunol. 141, 1745-1753, 1988
 A;Title: V region sequences of anti-DNA and anti-RNA autoantibodies from NZB/NZW F-1 m/c
 A;Reference number: A30502; MUID:88315787; PMID:2457627

A;Accession: G30502
 A;Status: preliminary
 A;Molecule type: mRNA

A;Cross-references: UNIPARC:UPI0000176AF0
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;16-96/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 38; DB 2; Length 111;
 Best Local Similarity 100.0%; Pred. No. 0.46;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
 Db 56 WASTRES 62

RESULT 27

S09970

Ig kappa chain V-D region (4C8) - mouse (fragment)

C;Species: Mus musculus (house mouse)
 C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 21-Jan-2000
 C;Accession: S09970
 R;Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.

Eur. J. Immunol. 20, 771-777, 1990
 A;Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodies
 A;Reference number: S09955; MUID:90263328; PMID:2347362

A;Accession: S09970
 A;Molecule type: mRNA

A;Residues: 1-112 <REI>

A;Cross-references: UNIPARC:UPI0000115E69; EMBL:X51858; NID:955406; PIDN:CAA36151.1; PII
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;16-96/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 38; DB 2; Length 112;
 Best Local Similarity 100.0%; Pred. No. 0.47;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
 Db 56 WASTRES 62

RESULT 28

PL0265
 Ig kappa chain V region (anti-DNA, DP13VK and DP18VK) - mouse (fragment)
 C;Species: Mus musculus (house mouse)

C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
 C;Accession: PL0265
 R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
 J. Exp. Med. 171, 265-287, 1990

A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
 A;Reference number: PL0231; MUID:90111618; PMID:2104919

A;Accession: PL0265
 A;Molecule type: mRNA
 A;Residues: 1-112 <SHL>

A;Cross-references: UNIPARC:UPI0000176AF3
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin

F;1-23/Region: framework 1

F;16-96/Domain: immunoglobulin homology <IMM>

F;24-40/Region: complementarity-determining 1

F;41-55/Region: framework 2

F;56-62/Region: complementarity-determining 2

F;63-94/Region: framework 3

F;95-102/Region: complementarity-determining 3

F;103-112/Region: framework 4

Query Match 100.0%; Score 38; DB 2; Length 112;
 Best Local Similarity 100.0%; Pred. No. 0.47;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
 Db 56 WASTRES 62

RESULT 29

S43103

Ig kappa chain V-J region (4B1 VL) - mouse (fragment)

C;Species: Mus musculus (house mouse)
 C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 24-May-2001
 C;Accession: S43103
 R;Gilbert, D.; Brard, F.; Margalit, C.; Delpech, A.; Tron, F.

submitted to the EMBL Data Library, March 1994

A;Description: An idotype D23-bearing polyspecific, murine anti-DNA monoclonal antibody

A;Reference number: S42484

A;Accession: S43103

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-112 <GIL>

A;Cross-references: UNIPARC:UPI0000116626; EMBL:Z31353; NID:9467574; PIDN:CAA83231.1; PII
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;16-96/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 38; DB 2; Length 112;
 Best Local Similarity 100.0%; Pred. No. 0.47;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
 Db 56 WASTRES 62

RESULT 30

S34002

Ig kappa chain V region - human

C;Species: Homo sapiens (man)
 C;Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
 C;Accession: S34002; S30522
 R;Marlette, X.; Tsapis, A.; Broquet, J.C.

Eur. J. Immunol. 23, 846-851, 1993

A;Title: Nucleotide sequence analysis of the variable domains of four human monoclonal J

A;Reference number: S34001; MUID:93209281; PMID:7681398

A;Accession: S34002

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-113 <MAR>

A;Cross-references: UNIPARC:UPI0000176D32; EMBL:Z18328

C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;16-96/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 100.0%; Score 38; DB 2; Length 113;
Pred. No. 0.47;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
|||||

Db 56 WASTRES 62

RESULT 31

Ig kappa chain V region - human

C:Species: Homo sapiens (man)

C:Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C:Accession: S34003

R:Marlette, X.; Tzapis, A.; Brouet, J.C.

Eur. J. Immunol. 23, 846-851, 1993

A:Title: Nucleotide sequence analysis of the variable domains of four human monoclonal

A:Reference number: S34001; MUID:93209281; PMID:7681398

A:Accession: S34003

A>Status: preliminary

A:Molecule type: mRNA

A:Cross-references: UNIPARC:UPI0000176CCA

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F;16-96/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 100.0%; Score 38; DB 2; Length 113;
Pred. No. 0.47;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
|||||

Db 56 WASTRES 62

RESULT 32

Ig kappa chain V region - human

C:Species: Homo sapiens (man)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000

C:Accession: S30523

R:Marlette, X.

submitted to the EMBL Data Library, October 1992

A:Reference number: S30520

A:Accession: S30523

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-113 <MAR>

A:Cross-references: UNIPARC:UPI0000176AE2; EMBL:Z16329

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F;16-96/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 100.0%; Score 38; DB 2; Length 113;
Pred. No. 0.47;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
|||||

Db 56 WASTRES 62

RESULT 33

Ig kappa chain V region (anti-DNA, S5TVK, S41VK, S54VK, S7VK and S204VK) - mouse (fragment)

C:Accession: P10263

R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisercky, D.; Marshak-Rothstein, A.

J. Exp. Med. 171, 265-297, 1990

A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic n

A:Reference number: P10231; MUID:90111618; PMID:2104919

A:Accession: P10263

A:Molecule type: mRNA

A:Residues: 1-113 <SHL>

A:Cross-references: UNIPARC:UPI0000176AF7

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F;1-23/Region: framework 1

F;16-96/Domain: immunoglobulin homology <IMM>

F;24-40/Region: complementarity-determining 1

F;41-55/Region: framework 2

F;56-62/Region: complementarity-determining 2

F;63-94/Region: framework 3

F;95-103/Region: complementarity-determining 3

F;104-113/Region: framework 4

Query Match 100.0%; Score 38; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.47;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
|||||

Db 56 WASTRES 62

RESULT 34

Ig kappa chain V-IV region (Len) - human

C:Species: Homo sapiens (man)

C:Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 01-Dec-2000

C:Accession: A01903; F61458

R:Schneider, M.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 356, 507-557, 1975

A:Title: Die Primärstruktur einer monoklonalen Immunoglobulin-L-Kette der Subgruppe IV v

A:Reference number: A01903; MUID:76004342; PMID:50995

A:Accession: A01903

A:Molecule type: protein

A:Residues: 1-114 <SCH>

A:Cross-references: UNIPARC:UPI0000173708

A:Note: this is the first completely sequenced V region of a new kappa chain subgroup, de

A:Note: the C region of this chain has the Inv (3) marker

R:Brouet, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.

J. Exp. Med. 170, 1551-1558, 1989

A:Title: Expression of a public idiotype by human monoclonal IgM directed to myelin-assoc

A:Reference number: A61458; MUID:90039128; PMID:2478651

A:Accession: F61458

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-13 <BRD>

A:Cross-references: UNIPARC:UPI0000173709

C:Comment: This is a Bence Jones protein.

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F;16-96/Domain: immunoglobulin homology <IMM>

F;23-94/Disulfide bonds: #status predicted

Query Match 100.0%; Score 38; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
|||||

Db 56 WASTRES 62

RESULT 35

Ig kappa chain V region (anti-DNA, S5TVK, S41VK, S54VK, S7VK and S204VK) - mouse (fragment)

Ig kappa chain V-J region - human
C/Species: Homo sapiens (man)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C/Accession: S44119
R/Hawkins, R.E.; Zhu, D.; Owecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
A/Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable
A/Reference number: S44105
A/Accession: S44119
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-114 <HAW>
A/Cross-references: UNIPARC:UPI0000116636; EMBL:Z31396; NID:9472973; PIDD:CAA83271.1; PII
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/16-96/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 38; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
Db 56 WASTRES 62

RESULT 36
S44116
Ig kappa chain V-J region - human
C/Species: Homo sapiens (man)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C/Accession: S44116
R/Hawkins, R.E.; Zhu, D.; Owecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
A/Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable
A/Reference number: S44105
A/Accession: S44116
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-114 <HAW>
A/Cross-references: UNIPARC:UPI0000116633; EMBL:Z31391; NID:9472970; PIDD:CAA83266.1; PII
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/16-96/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 38; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
Db 56 WASTRES 62

RESULT 37
PT0356
Ig kappa chain V region (2B11.1) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 21-Jan-2000
C/Accession: PT0356
R/Shelton, R.; Kleiner, G.; Turken, A.; Papazian, L.; Diamond, B.
J. Exp. Med. 173, 287-296, 1991
A/Title: A novel class of anti-DNA antibodies identified in BALB/c mice.
A/Reference number: PT0352; MUID:91108325; PMID:1986536
A/Accession: PT0356
A/Molecule type: mRNA
A/Residues: 1-118 <SHE>
A/Cross-references: UNIPARC:UPI0000176791
A/Experimental source: strain BALB/c
A/Note: The authors translated the codon CTT for residue 32 as Ser
C/Comment: This protein is an anti-double-stranded DNA antibody.
C/Superfamily: immunoglobulin V region; immunoglobulin homology
F/19-99/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 38; DB 2; Length 118;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
Db 59 WASTRES 65

RESULT 38
S51147
antibody light chain V region - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
C/Accession: S51147
R/de Knijf, J.; Boel, E.; Logtenberg, T.
submitted to the EMBL Data Library, January 1995
A/Description: Selection and application of human SCFV antibody fragments from a semi-syn
A/Reference number: S51147
A/Accession: S51147
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-120 <DEK>
A/Cross-references: UNIPARC:UPI0000116210; EMBL:X83714; NID:9633227; PIDD:CAA58689.1; PII
F/16-96/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 38; DB 2; Length 120;
Best Local Similarity 100.0%; Pred. No. 0.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
Db 56 WASTRES 62

RESULT 39
G33932
Ig kappa chain precursor V region (D23) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 21-Jan-2000
C/Accession: G33932
R/Baccala, R.; Vo Quang, T.; Gilbert, M.; Tarnynck, T.; Avrameas, S.
Proc. Natl. Acad. Sci. U.S.A. 86, 4624-4628, 1989
A/Title: Two murine natural polyclonal autoantibodies are encoded by nonmutated germ-li
A/Reference number: A33932; MUID:89282823; PMID:2499887
A/Accession: G33932
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-120 <BAC>
A/Cross-references: UNIPARC:UPI0000176793
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/36-116/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 38; DB 2; Length 120;
Best Local Similarity 100.0%; Pred. No. 0.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
Db 76 WASTRES 82

RESULT 40
K4HV
Ig kappa chain precursor V-IV region - human
C/Species: Homo sapiens (man)
C/Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C/Accession: A01902
R/Klobbeck, H.G.; Bornkamm, G.W.; Combrat, G.; Mochkat, R.; Pohlenz, H.D.; Zachau, H.G.
Nucleic Acids Res. 13, 6515-6529, 1985

A>Title: Subgroup IV of human immunoglobulin K light chains is encoded by a single germ
A:Reference number: A93589; MUID:6041853; PMID:2997712
A:Accession: A01902
A:Molecule type: DNA
A:Residues: 1-121 <KLO>
A:Cross-references: UNIPROT:P06312; UNIPARC:UPI0000113B70
A>Note: the sequence was determined from the germline gene
A>Note: there is only one Ig kappa V-IV gene
C:Genetics:
A:Introns: 17/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-121/Product: Ig kappa chain precursor V-IV region #status predicted <MAT>
F:21-43/Region: framework 1
F:36-116/Domain: immunoglobulin homology <IMM>
F:44-60/Region: complementarity-determining 1
F:61-75/Region: framework 2
F:76-82/Region: complementarity-determining 2
F:83-114/Region: complementarity-determining 3
F:115-121/Region: complementarity-determining 3
F:43-114/Disulfide bonds: #status predicted
Query Match 100.0%; Score 38; DB 1; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.51; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WASTRES 7
DB 76 WASTRES 82
RESULT 41
S40329
Ig kappa chain V-J-C region - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40329
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A>Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40329
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-129 <KLE>
A:Cross-references: UNIPARC:UPI0000176CAF; EMBL:X72439
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:27-107/Domain: immunoglobulin homology <IMM>
Query Match 100.0%; Score 38; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.54; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WASTRES 7
DB 67 WASTRES 73
RESULT 42
S40347
Ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40347
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A>Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40347

A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-129 <KLE>
A:Cross-references: UNIPARC:UPI0000116161; EMBL:X72457; NID:G441382; PIDN:CA51125.1; PII
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:33-113/Domain: immunoglobulin homology <IMM>
Query Match 100.0%; Score 38; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.54; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WASTRES 7
DB 73 WASTRES 79
RESULT 43
K4HUJ1
Ig kappa chain precursor V-IV region (JI) - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C:Accession: A01904
R:Klobeck, H.G.; Bornkamm, G.W.; Combrinato, G.; Moxikat, R.; Pohlens, H.D.; Zachau, H.G.
Nucleic Acids Res. 13, 6515-6529, 1985
A>Title: Subgroup IV of human immunoglobulin K light chains is encoded by a single germ
A:Reference number: A93589; MUID:6041853; PMID:2997712
A:Accession: A01904
A:Molecule type: DNA
A:Residues: 1-133 <KLO>
A:Cross-references: UNIPROT:P06313; UNIPARC:UPI000012E165; GB:Z00022; GB:X51570; NID:G333
A>Note: the sequence was determined from the differentiated gene
C:Genetics:
A:Gene: GDB:IGKV
A:Cross-references: GDB:119341; OMIM:146980
A:Map position: Zp12-2p12
A:Introns: 17/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-133/Product: Ig kappa chain V-IV region (JI) #status predicted <MAT>
F:21-43/Region: framework 1
F:36-116/Domain: immunoglobulin homology <IMM>
F:44-60/Region: complementarity-determining 1
F:61-75/Region: framework 2
F:76-82/Region: complementarity-determining 2
F:83-114/Region: framework 3
F:115-122/Region: complementarity-determining 3
F:123-133/Region: framework 4
F:43-114/Disulfide bonds: #status predicted
Query Match 100.0%; Score 38; DB 1; Length 133;
Best Local Similarity 100.0%; Pred. No. 0.56; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WASTRES 7
DB 76 WASTRES 82
RESULT 44
PS0023
Ig kappa chain precursor V region (6A4) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 21-Jan-2000
C:Accession: PS0023
R:Margot, M.; Eckhardt, A.; Ehret, W.; von Specht, B.U.; Duchene, M.; Domdey, H.
Gene 74, 335-345, 1988
A>Title: Cloning and characterization of cDNAs coding for the heavy and light chains of
A:Reference number: PS0023; MUID:89232725; PMID:3149944
A:Accession: PS0023

A:Molecule type: mRNA
A:Residues: 1-133 <MAR>
A:Cross-references: UNIPARC:UPI0000176787
A:Experimental source: strain BALB/c
A>Note: the amino-terminal four residues of the mature protein were directly sequenced
C:Comment: This chain was obtained from a monoclonal antibody against Pseudomonas aeruginosa
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-133/Product: Ig kappa chain V region 6A4 #status experimental <IGV>
F:36-116/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 38; DB 2; Length 133;
Best Local Similarity 100.0%; Pred. No. 0.56;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
DB 76 WASTRES 82

RESULT 45
S49531
anti-Sm antibody VL chain (V kappa 4/J kappa 3) - human
C:Species: Homo sapiens (man)
C>Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 21-Jan-2000
C:Accession: S49531
R:Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
submitted to the EMBL Data Library, October 1994
A:Description: Molecule characterization of natural human anti-Sm autoantibodies.
A:Reference number: S48797
A:Accession: S49531
A:Molecule type: mRNA
A>Status: preliminary
A:Residues: 1-134 <MAH>
A:Cross-references: UNIPARC:UPI00001166FE; EMBL:Z46347; NID:G560841; PIDN:CAA6466.1; PI
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:36-116/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 38; DB 2; Length 134;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
DB 76 WASTRES 82

RESULT 46
PC1214
Ig kappa chain precursor V region (mab H8) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: PC1214
R:Hong, H.-J.; Kim, A.K.; Ryu, C.-J.; Park, S.-S.; Chung, H.-K.; Kwon, K.-S.; Kim, K.-L.; Kim, Gene 121, 331-335, 1992
A:Title: Cloning and characterization of cDNAs coding for heavy and light chains of a mAb
A:Reference number: PC1213; MUID:93077049; PMID:1446832
A:Accession: PC1214
A:Molecule type: mRNA
A:Residues: 1-134 <HON>
A:Cross-references: UNIPARC:UPI00001153C0; GB:M98042; NID:G196749; PIDN:AAA3877.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-134/Product: Ig light chain V region #status predicted <MAT>
F:36-116/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 38; DB 2; Length 134;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7

DB 76 WASTRES 82

RESULT 47
A53261
Ig kappa chain precursor V-J-C region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 21-Jan-2000
C:Accession: A53261
R:Cogne, M.; Preud'homme, J.-L.; Bauwens, M.; Touchard, G.; Aucouturier, P.
U. Clin. Invest. 87, 2186-2190, 1991
A:Title: Structure of a monoclonal kappa chain of the Vκ-IV subgroup in the kidney and p
A:Reference number: A53261; MUID:91250576; PMID:1904072
A:Accession: A53261
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-138 <COG>
A:Cross-references: UNIPARC:UPI000017678D; GB:M38267
A>Note: authors translated the codon TTG for residue 12 as Phe
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:36-116/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 38; DB 2; Length 138;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
DB 76 WASTRES 82

RESULT 48
S26040
Ig kappa chain precursor - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 21-Jan-2000
C:Accession: S26040; S78098
R:Okamoto, M.; Honjo, T.
Nucleic Acids Res. 18, 1895, 1990
A:Title: Nucleotide sequences of the gene/cDNA coding for anti-murine erythrocyte autoant
A:Reference number: S09216; MUID:90245589; PMID:2336368
A:Accession: S26040
A:Molecule type: DNA
A:Residues: 1-138 <OKA>
A:Cross-references: UNIPARC:UPI00001769D0; EMBL:X51742
A>Note: the authors translated the codon AGC for residue 107 as Thr and AGT for residue 1
R:Okamoto, M.
submitted to the EMBL Data Library, February 1990
A:Reference number: S78098
A:Accession: S78098
A:Molecule type: DNA
A:Residues: 1-87, 'W', 89-138 <OKW>
A:Cross-references: UNIPARC:UPI0000116D53; EMBL:X51742; NID:G52697; PIDN:CAA36032.1; PID
C:Genetics: 22/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-138/Product: Ig kappa chain (fragment) #status predicted <MAT>
F:41-121/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 38; DB 2; Length 138;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
DB 81 WASTRES 87

RESULT 49

PL0014

Ig kappa chain precursor V region (F6-3) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000

C/Accession: PL0014

R/Cheng, H.L.; Sood, A.K.; Ward, R.E.; Kleber-Emmons, T.; Kohler, H. Mol. Immunol. 25, 33-40, 1988

A/Title: Structural basis of stimulatory anti-idiotypic antibodies.

A/Reference number: PL0011; MUID:88142863; PMID:3125424

A/Accession: PL0014

A/Molecule type: mRNA

A/Residues: 1-145 <CHE>

A/Cross-references: UNIPARC:UPI00001767A7

A/Experimental source: cell line F6-3

C/Comment: This protein is an anti-idiotypic antibody that induces an anti-phosphorylch

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/1-20/Domain: signal sequence #status predicted <SIG>

F/21-134/Product: Ig heavy chain V region (4C11) #status predicted <MAT>

F/36-116/Domain: immunoglobulin homology <IMM>

F/4-60/Region: complementarity-determining 1

F/76-82/Region: complementarity-determining 2

F/115-123/Region: complementarity-determining 3

F/135-145/Domain: constant region (fragment) #status predicted <COR>

Query Match

Best Local Similarity 100.0%; Score 38; DB 2; Length 145;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7

Db 76 WASTRES 82

RESULT 50

A31790

Ig kappa chain V region (17/9) - mouse

C/Species: Mus musculus (house mouse)

C/Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000

C/Accession: A31790

R/Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, I.A.

J. Biol. Chem. 263, 17100-17105, 1988

A/Title: Preliminary crystallographic data, primary sequence, and binding data for an an

A/Reference number: A92686; MUID:89034213; PMID:3182835

A/Accession: A31790

A/Molecule type: mRNA

A/Residues: 1-220 <SCH>

A/Cross-references: UNIPARC:UPI000014E12; GB:M23626; GB:U04061; NID:G533234; PIDN:AAA39

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/16-96/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 100.0%; Score 38; DB 2; Length 220;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7

Db 56 WASTRES 62

Search completed: May 4, 2006, 13:08:59
Job time : 26 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OW protein - protein search, using sw model

May 4, 2006, 12:46:39 ; Search time 65.5556 Seconds

(Without alignments)
75.336 Million cell updates/sec

Title: US-10-700-632-5

Perfect score: 38

Sequence: 1 MASTRES 7

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 segs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 1000 summaries

Database : UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	38	100.0	109	1 KV4D_HUMAN	P83593 homo sapien
2	38	100.0	114	1 KV4A_HUMAN	P01625 homo sapien
3	38	100.0	121	1 KV40_HUMAN	P06312 homo sapien
4	38	100.0	133	1 KV4B_HUMAN	P06313 homo sapien
5	38	100.0	134	1 KV4C_HUMAN	P06314 homo sapien
6	38	100.0	130	2 Q52L64_MOUSE	Q52L64 mus musculu
7	35	92.1	130	2 Q9NP29_HUMAN	Q9NP29 homo sapien
8	35	92.1	251	2 Q51SP9_MAGGR	Q51SP9 pseudomonas
9	34	89.5	159	2 Q5H5B2_XANOR	Q5H5B2 xanthomonas
10	34	89.5	934	2 Q6G2K3_BARRIE	Q6G2K3 bartonella
11	34	89.5	980	2 Q8PL66_XANAC	Q8PL66 xanthomonas
12	34	89.5	11999	2 Q4HVM0_GIBBE	Q4HVM0 gibberella
13	33	86.8	266	2 Q6PJU5_HUMAN	Q6PJU5 homo sapien
14	33	86.8	448	2 Q4FWS7_LEIMA	Q4FWS7 leishmania
15	33	86.8	453	2 Q4Q865_LEIMA	Q4Q865 leishmania
16	33	86.8	1298	2 Q4MS81_ASPTU	Q4MS81 aspergillus
17	33	86.8	1317	2 Q8TFZ3_ASPTU	Q8TFZ3 aspergillus
18	33	86.8	1472	2 Q520D0_MAGGR	Q520D0 magnaporthe
19	32	84.2	201	2 Q5VFP0_9HIV1	Q5VFP0 human immun
20	32	84.2	203	2 Q5M874_RAT	Q5M874 rattus norv
21	32	84.2	347	2 Q915J7_PSEAB	Q915J7 pseudomonas
22	32	84.2	458	2 Q7XUI8_ORYSA	Q7XUI8 oryza sativ
23	32	84.2	537	2 Q4SKL4_TETNG	Q4SKL4 tetraodon n
24	32	84.2	685	1 SYM_NEIMA	SYM_NEIMA
25	31	81.6	71	2 Q7QYCI_GIALA	Q7QYCI giardia lam
26	31	81.6	108	2 Q5BG03_EMENI	Q5BG03 caenorhabdi
27	31	81.6	171	2 Q9NSV2_CAEEL	Q9NSV2 caenorhabdi
28	31	81.6	177	2 Q6Z1F0_ORYSA	Q6Z1F0 oryza sativ
29	31	81.6	183	2 Q57000_ZYMMO	Q57000 zymomonas m
30	31	81.6	183	2 Q5NP04_ZYMMO	Q5NP04 zymomonas m
31	31	81.6	226	2 Q88087_ENTRA	Q88087 enterococcu

32	31	81.6	228	2 Q5T8A5_HUMAN	Q5T8A5 homo sapien
33	31	81.6	230	2 Q8NU75_CORGL	Q8NU75 corneibacte
34	31	81.6	237	2 Q4UHH3_TREAN	Q4UHH3 thelaria a
35	31	81.6	248	2 Q4UTJ2_CORJK	Q4UTJ2 corneibacte
36	31	81.6	304	2 Q4SRL7_TETNG	Q4SRL7 tetraodon n
37	31	81.6	338	2 Q7ZQV2_9HIV1	Q7ZQV2 human immun
38	31	81.6	338	2 Q7ZQV3_9HIV1	Q7ZQV3 human immun
39	31	81.6	340	2 Q7ZQV5_9HIV1	Q7ZQV5 human immun
40	31	81.6	344	2 Q5CJF5_SCHJA	Q5CJF5 schistosoma
41	31	81.6	371	2 Q4QIL2_LEIMA	Q4QIL2 leishmania
42	31	81.6	382	1 THRC_STVY3	THRC_STVY3
43	31	81.6	391	2 Q4NPS1_9DELT	Q4NPS1 anaeromyxob
44	31	81.6	404	1 Y2619_TREED	Y2619 streptomyces
45	31	81.6	404	2 Q9AMJ2_STRTAT	Q9AMJ2 streptomyces
46	31	81.6	406	2 Q5DFA7_SCHJA	Q5DFA7 schistosoma
47	31	81.6	460	2 Q5Z6K2_ORYSA	Q5Z6K2 oryza sativ
48	31	81.6	466	2 Q6AVV5_ORYSA	Q6AVV5 oryza sativ
49	31	81.6	478	2 Q56W17_ARATH	Q56W17 arabidopsis
50	31	81.6	504	2 Q5LA43_BACPN	Q5LA43 bacteroides
51	31	81.6	504	2 Q64QF9_BACPN	Q64QF9 bacteroides
52	31	81.6	555	2 Q61ZC8_CAEER	Q61ZC8 caenorhabdi
53	31	81.6	572	2 Q92X10_RHIME	Q92X10 rhizobium m
54	31	81.6	574	2 Q9NA93_CAEEL	Q9NA93 caenorhabdi
55	31	81.6	642	2 Q8RMG0_NOS89	Q8RMG0 nostoc sp.
56	31	81.6	642	2 Q9A8Q5_CAUCR	Q9A8Q5 caulobacter
57	31	81.6	642	2 Q8ZOC9_ANABP	Q8ZOC9 anabaena sp
58	31	81.6	727	2 Q9BNW8_GMYAI	Q9BNW8 scutigerell
59	31	81.6	735	2 Q989J7_RHIL0	Q989J7 rhizobium l
60	31	81.6	733	2 Q52AK1_MAGGR	Q52AK1 magnaporthe
61	31	81.6	783	2 Q8KJN0_RHIL0	Q8KJN0 rhizobium l
62	31	81.6	875	2 Q7RMP2_NEUCR	Q7RMP2 neurospora
63	31	81.6	900	2 Q4TJM9_9SPHN	Q4TJM9 erythroba
64	31	81.6	900	2 Q4TLV9_9SPHN	Q4TLV9 erythroba
65	31	81.6	1336	2 Q6MP53_BDEBA	Q6MP53 bdellovibri
66	31	81.6	1459	2 Q9LH44_ARATH	Q9LH44 arabidopsis
67	31	81.6	1648	2 Q57XF2_9TRYE	Q57XF2 trypanosoma
68	31	81.6	1819	2 Q4IBU1_GIBBE	Q4IBU1 gibberella
69	30	78.9	29	2 Q8C837_MOUSE	Q8C837 mus musculu
70	30	78.9	62	2 Q8B8F5_HPBVO	Q8B8F5 hepaticis b
71	30	78.9	78	2 Q80W72_MOUSE	Q80W72 mus musculu
72	30	78.9	94	2 Q7SEH6_NEUCR	Q7SEH6 neurospora
73	30	78.9	103	2 Q8Z272_PYRDE	Q8Z272 pyrobaculum
74	30	78.9	118	2 Q9BGP0_MACPA	Q9BGP0 macaca fasc
75	30	78.9	119	2 Q8JYX1_HPBVO	Q8JYX1 hepaticis b
76	30	78.9	119	2 Q8JYX2_HPBVO	Q8JYX2 hepaticis b
77	30	78.9	119	2 Q8JYX3_HPBVO	Q8JYX3 hepaticis b
78	30	78.9	130	2 Q96G01_HUMAN	Q96G01 homo sapien
79	30	78.9	137	2 Q88P49_PSEBK	Q88P49 pseudomonas
80	30	78.9	152	2 Q4ZKX5_PSEBK	Q4ZKX5 pseudomonas
81	30	78.9	152	2 Q72P11_LEPFC	Q72P11 leptospira
82	30	78.9	152	2 Q88710_PSEBM	Q88710 pseudomonas
83	30	78.9	192	2 Q5BM95_SCHJA	Q5BM95 schistosoma
84	30	78.9	206	2 Q9CTW1_MOUSE	Q9CTW1 mus musculu
85	30	78.9	207	2 Q9JB47_9HIV1	Q9JB47 human immun
86	30	78.9	209	2 P94650_CHLH1	P94650 chlorobium
87	30	78.9	228	2 Q7MUB3_PORDI	Q7MUB3 porphyromon
88	30	78.9	238	2 Q58EU4_MOUSE	Q58EU4 mus musculu
89	30	78.9	256	2 Q91XW8_PSEAB	Q91XW8 pseudomonas
90	30	78.9	259	2 Q63PW8_BURPS	Q63PW8 burkholderi
91	30	78.9	260	2 Q6ZQR8_HUMAN	Q6ZQR8 homo sapien
92	30	78.9	285	2 Q6ZBR8_RHIL0	Q6ZBR8 rhizobium l
93	30	78.9	301	2 Q8JMAS_9NUCL	Q8JMAS mamestra co
94	30	78.9	310	2 Q9C939_ARATH	Q9C939 arabidopsis
95	30	78.9	326	2 Q5NEV2_ORYSA	Q5NEV2 oryza sativ
96	30	78.9	330	2 Q5NKJ0_CRYBE	Q5NKJ0 crypococcu
97	30	78.9	341	2 Q416U2_GIBBE	Q416U2 gibberella
98	30	78.9	349	2 Q8TCZ4_HUMAN	Q8TCZ4 homo sapien
99	30	78.9	349	2 Q5VWX1_HUMAN	Q5VWX1 homo sapien
100	30	78.9	349	2 Q9WU01_MOUSE	Q9WU01 mus musculu
101	30	78.9	350	2 Q6FEX1_ACTAD	Q6FEX1 acinetobact
102	30	78.9	356	2 Q8RYX9_ORYSA	Q8RYX9 oryza sativ
103	30	78.9	358	2 Q5N8X0_ORYSA	Q5N8X0 oryza sativ
104	30	78.9	408	2 Q8UG04_AGR75	Q8UG04 agrobacteri


```

981 27 71.1 198 2 Q73960.9H1V1 073960 human immun
982 27 71.1 202 1 VA51_VESCR p35781 vespa crabr
983 27 71.1 202 1 VA52_VESCR p35782 vespa crabr
984 27 71.1 202 1 VA5_VESMA p81657 vespa munda
985 27 71.1 202 2 P88444_9H1V1 p88444 human immun
986 27 71.1 203 2 Q8FT28_COREF Q8FT28 corynebacte
987 27 71.1 203 2 Q5VES5_9H1V1 Q5VES5 human immun
988 27 71.1 203 2 Q5VES6_9H1V1 Q5VES6 human immun
989 27 71.1 203 2 Q5VES7_9H1V1 Q5VES7 human immun
990 27 71.1 204 2 Q97UJ1_SULSO Q97UJ1 sulfolobus
991 27 71.1 205 1 VA5_POLFU p35780 polistes fu
992 27 71.1 205 1 VA5_VESQO p35786 vespula squ
993 27 71.1 205 2 Q90037_9H1V1 Q90037 human immun
994 27 71.1 205 2 Q9YV81_9H1V1 Q9YV81 human immun
995 27 71.1 205 2 Q9YV82_9H1V1 Q9YV82 human immun
996 27 71.1 205 2 Q9YV83_9H1V1 Q9YV83 human immun
997 27 71.1 205 2 Q9YV84_9H1V1 Q9YV84 human immun
998 27 71.1 205 2 Q9YV85_9H1V1 Q9YV85 human immun
999 27 71.1 206 1 VA5_VESVI p35787 vespula vid
1000 27 71.1 206 2 Q8ALT5_9H1V1 Q8ALT5 human immun

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ALIGNMENTS

```

RESULT 1
KV4D_HUMAN STANDARD; PRT; 109 AA.
ID KV4D_HUMAN STANDARD; PRT; 109 AA.
AC P83593;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-IV region STM (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OC NCBI_TaxID=9606;
OX [1]
RN PROTEIN SEQUENCE.
RP TISSUE=Abdominal adipose tissue;
RX MEDLINE=98249779; PubMed=9588180; DOI=10.1006/birc.1998.8515;
RA Olsen K.B., Sletten K., Westermarck P.;
RT "Extended analysis of AL-amyloid protein from abdominal wall
RT subcutaneous fat biopsy: kappa IV immunoglobulin light chain.";
RL Biochem. Biophys. Res. Commun. 245:713-716(1998).
CC -!- FUNCTION: May play an important role in fibrillogenesis.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC SMR; P83593; 1-109.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR SMART: SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23 Framework-1.
FT REGION 2 40 Complementarity-determining-1.
FT REGION 3 41 Framework-2.
FT REGION 4 55 Framework-3.
FT REGION 5 62 Complementarity-determining-2.
FT REGION 6 62 Complementarity-determining-3.
FT REGION 7 94 Complementarity-determining-4.
FT REGION 8 95 Complementarity-determining-3.
FT REGION 9 101 Framework-4.
FT REGION 10 102 Framework-4.
FT REGION 11 109 By similarity.
FT DISULFID 23 94
FT UNSURE 23 23
FT UNSURE 94 94
FT NON TER 109 109
SQ SEQUENCE 109 AA; 12060 MW; 0C4F31EAI1E12A0B CRC64;

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Query Match 100.0%; Score 38; DB 1; Length 109;
 Best Local Similarity 100.0%; Pred. No. 3.7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MASTRES 7
 Db 56 MASTRES 62

```

RESULT 2
KV4A_HUMAN STANDARD; PRT; 114 AA.
ID KV4A_HUMAN STANDARD; PRT; 114 AA.
AC P01625;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-IV region Len.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OC NCBI_TaxID=9606;
OX [1]
RN PROTEIN SEQUENCE.
RP MEDLINE=76004342; PubMed=50995;
RX Schneider M., Hilschmann N.;
RA "The primary structure of a monoclonic immunoglobulin-L-chain of
RA subgroup IV of the kappa type (Bence-Jones protein Len).";
RL Hoppe-Seyler's Z. Physiol. Chem. 356:507-557(1975).
RN [2]
RP SEQUENCE REVISION TO 9.
RA Salomon A.;
RL Submitted (AUG-1996) to Swiss-Prot.
CC -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PDB; 1EEQ; X-ray; A/B=1-114.
CC PDB; 1EEU; X-ray; A/B=1-114.
CC PDB; 1ERQ; X-ray; A=1-114.
CC PDB; 1EKJ; X-ray; A/B=1-114.
CC PDB; 1LVE; X-ray; @=1-114.
CC PDB; 2LVE; X-ray; @=1-114.
CC PDB; 3LVE; X-ray; @=1-114.
CC PDB; 4LVE; X-ray; A/B=1-114.
CC PDB; 5LVE; X-ray; A=1-114.
CC GO; GO:0005576; C:extracellular region; NAS.
CC GO; GO:0003623; F:antigen binding; NAS.
CC GO; GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR SMART: SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
KW 3D-structure; Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin domain; Immunoglobulin V region.
FT REGION 1 23 Framework-1.
FT REGION 2 40 Complementarity-determining-1.
FT REGION 3 41 Framework-2.
FT REGION 4 55 Framework-3.
FT REGION 5 62 Complementarity-determining-2.
FT REGION 6 62 Complementarity-determining-3.
FT REGION 7 94 Complementarity-determining-4.
FT REGION 8 95 Complementarity-determining-3.
FT REGION 9 101 Framework-4.
FT REGION 10 102 Framework-4.
FT REGION 11 109 By similarity.
FT DISULFID 23 94
FT NON TER 114 114
FT STRAND 4 7
FT STRAND 10 13
FT TURN 15 16

```

```

FT STRAND 19 25
FT STRAND 30 31
FT TURN 32 35
FT STRAND 36 37
FT STRAND 39 44
FT TURN 46 47
FT STRAND 51 55
FT TURN 56 58
FT STRAND 59 60
FT TURN 62 63
FT STRAND 66 67
FT TURN 68 73
FT STRAND 74 75
FT STRAND 76 81
FT HELIX 86 88
FT STRAND 90 96
FT STRAND 103 104
FT STRAND 108 112
SQ SEQUENCE 114 AA; 12640 MM; 0647FD17F236485 CRC64;

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Query Match Best Local Similarity 100.0%; Score 38; DB 1; Length 114;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
Db 56 WASTRES 62

RESULT 3

ID KV40 HUMAN STANDARD; PRT; 121 AA.

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AC P06312;
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-IV region precursor (Fragment).
GN Name=IGKV4-1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86041853; PubMed=2997712;
RA Klobbeck H.G., Bornkamm G.W., Combratio G., Mociakat R., Pohlenz H.D.,
RA Zechau H.G.;
RT "Subgroup IV of human immunoglobulin K light chains is encoded by a
RT single germline gene."
RL Nucleic Acids Res. 13:6515-6529(1985).
CC -1- MISCELLANEOUS: There is only one Ig kappa V-IV gene.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; Z00023; CAAT7318.1; -; Genomic_DNA.
DR PIR; A01902; KAHU.
DR HSSP; P01625; 1LVE.
DR SMR; P06312; 21-121.
DR Ensembl; ENSG00000153586; Homo sapiens.
DR HGNC; HGNC:5834; IGKV4-1.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.

```

```

FT SIGNAL 1 20
FT CHAIN 21 >121
FT REGION 21 43
FT REGION 44 60
FT REGION 61 75
FT REGION 76 82
FT REGION 83 114
FT REGION 115 121
FT DISULFID 43 114
FT NON TER 121 121
SQ SEQUENCE 121 AA; 13380 MM; 9586AD418BD3974 CRC64;

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Query Match Best Local Similarity 100.0%; Score 38; DB 1; Length 121;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
Db 76 WASTRES 82

RESULT 4

ID KV4B HUMAN STANDARD; PRT; 133 AA.

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AC P06313;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-IV region JI precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86041853; PubMed=2997712;
RA Klobbeck H.G., Bornkamm G.W., Combratio G., Mociakat R., Pohlenz H.D.,
RA Zechau H.G.;
RT "Subgroup IV of human immunoglobulin K light chains is encoded by a
RT single germline gene."
RL Nucleic Acids Res. 13:6515-6529(1985).
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; Z00022; CAAT7317.1; -; Genomic_DNA.
DR PIR; A01904; KAHUJI.
DR HSSP; P01625; 1LVE.
DR SMR; P06313; 21-133.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.

```

```

FT SIGNAL 1 20
FT CHAIN 21 133
FT REGION 21 43
FT REGION 44 60
FT REGION 61 75
FT REGION 76 82
FT REGION 83 114
FT REGION 115 122
FT DISULFID 43 114
FT NON TER 133 133
SQ SEQUENCE 133 AA; 14633 MM; 5FB3953066744AF4 CRC64;

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Query Match 100.0%; Score 38; DB 1; Length 133;
 Best Local Similarity 100.0%; Pred. No. 4.6;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
 DB 76 WASTRES 82

RESULT 5

KV4C_HUMAN STANDARD; PRT; 134 AA.
 ID KV4C_HUMAN

AC P06314;
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Ig kappa chain V-IV region B17 precursor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 OC NCBI_TaxID=9606;
 OX NCBI_TaxID=9606;
 RN NUCLEOTIDE SEQUENCE.
 RP MEDLINE=86041854; PubMed=2997713;
 RX Marsh P., Mills F., Gould H.;
 RA "Detection of a unique human V kappa IV germline gene by a cloned cDNA
 RT probe.";
 RT Nucleic Acids Res. 13:6531-6544(1985).
 RL [2]
 RP SEQUENCE REVISION TO 76.
 RA Marsh P.;
 RL Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.

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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC
 CC EMBL; X02990; CAA26733.1; -; mRNA.
 DR HSSP; P01625; LIVE.
 DR SMR; P06314; 21-134.
 DR GO; GO:0005576; C:extracellular region; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PSS0835; IG_LIKE; 1.
 KM Immunoglobulin domain; Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 1 134
 FT REGION 21 134 Ig kappa chain V-IV region B17.
 FT REGION 21 43 Framework-1.
 FT REGION 44 60 Complementarity-determining-1.
 FT REGION 61 75 Framework-2.
 FT REGION 76 82 Complementarity-determining-2.
 FT REGION 83 114 Framework-3.
 FT REGION 115 121 Complementarity-determining-3.
 FT REGION 122 133 Framework-4.
 FT DISULFID 43 114 By similarity.
 FT NON TER 134 134
 SQ SEQUENCE 134 AA; 14966 MW; 6413A22FPD0738832 CRC64;

Query Match 100.0%; Score 38; DB 1; Length 134;
 Best Local Similarity 100.0%; Pred. No. 4.6;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
 DB 76 WASTRES 82

Query Match 100.0%; Score 38; DB 2; Length 240;
 Best Local Similarity 100.0%; Pred. No. 8.8;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
 DB 76 WASTRES 82

RESULT 6

Q52L64_MOUSE PRELIMINARY; PRT; 240 AA.
 ID Q52L64_MOUSE PRELIMINARY;

AC Q52L64;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 OX NCBI_TaxID=10090;
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=Mix FVB/N;
 RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old.
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Tothiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullen S.J.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalka U., Smilins D.E.,
 RA Smerchek A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RL [2]
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=Mix FVB/N;
 RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
 RG NIH WGC Project;
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC094049; AA94049.1; -; mRNA.
 DR SMR; Q52L64; 21-240.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; IG_C1.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PR07654; C1-set; 1.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGV; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PSS0835; IG_LIKE; 2.
 DR PROSITE; PSS0290; IG_MHC; UNKNOWN_1.
 KM Hypothetical protein.
 SQ SEQUENCE 240 AA; 26609 MW; CF8630CCCT002E52C CRC64;

Query Match 100.0%; Score 38; DB 2; Length 240;
 Best Local Similarity 100.0%; Pred. No. 8.8;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
 DB 76 WASTRES 82

RESULT 7

Q9NP29_HUMAN PRELIMINARY; PRT; 130 AA.
 ID Q9NP29_HUMAN PRELIMINARY;

AC Q9NP29;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 OX NCBI_TaxID=10090;
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=Mix FVB/N;
 RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old.
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Tothiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullen S.J.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalka U., Smilins D.E.,
 RA Smerchek A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RL [2]
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=Mix FVB/N;
 RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
 RG NIH WGC Project;
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC094049; AA94049.1; -; mRNA.
 DR SMR; Q52L64; 21-240.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; IG_C1.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PR07654; C1-set; 1.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGV; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PSS0835; IG_LIKE; 2.
 DR PROSITE; PSS0290; IG_MHC; UNKNOWN_1.
 KM Hypothetical protein.
 SQ SEQUENCE 240 AA; 26609 MW; CF8630CCCT002E52C CRC64;

Query Match 100.0%; Score 38; DB 2; Length 240;
 Best Local Similarity 100.0%; Pred. No. 8.8;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
 DB 76 WASTRES 82

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AC Q9NP29;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE Microtubillar protein 2 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96354815; PubMed=8753791; DOI=10.1006/brc.1996.1202;
RA Ozsvath K.J., Hirose H., Xie S., Hirose H., Tilson M.D.;
RT "Two hypothetical proteins of human aortic adventitia, with Ig kappa,
RT collagenous, and aromatic-rich motifs."
RL Biochem. Biophys. Res. Commun. 225:500-504(1996).
RN
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=9224393; DOI=10.1006/jbre.1997.5030;
RA Ozsvath K.J., Hirose H., Xie S., Chew D., Knoetgen J. III,
RA Tilson M.D.;
RT "Expression of two novel recombinant proteins from aortic adventitia
RT (kappa1b) sharing amino acid sequences with cytomegalovirus."
RL J. Surg. Res. 69:277-282(1997).
RN
RP NUCLEOTIDE SEQUENCE.
RX Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF206020; AAF62402.1; -; mRNA.
DR HSSP; P01625; 11VE.
DR SMK; Q9NP29; 21-84.
DR Ensembl; ENSG0000015386; Homo sapiens.
FT NON_TIR 130 130
SQ SEQUENCE 130 AA; 14128 MW; 51275185AC6FA1E CRC64;

Query Match 92.1%; Score 35; DB 2; Length 130;
Best Local Similarity 85.7%; Pred. No. 20;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
DB 76 WASTRDS 82

RESULT 8
Q51SF9_MAGR PRELIMINARY; PRT; 251 AA.
ID Q51SF9;
AC Q51SF9;
DT 13-SEP-2005 (TREMblrel. 31, Created)
DT 13-SEP-2005 (TREMblrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMblrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=MG10384.4;
OS Magnaporthe grisea 70-15.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes; incertae sedis; Magnaporthaceae; Magnaportha.
OX NCBI_TaxID=242507;
RN
RP NUCLEOTIDE SEQUENCE.
RP STRAIN=70-15;
RC
RA Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,
RA Alt-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,
RA Arachchi H., Armbruster J., Bachantang P., Baldwin J., Barry A.,
RA Bayul T., Blitshteyn B., Bloom T., Blye J., Boguslavsky L.,
RA Brownsky M., Boukhvalter B., Brunache A., Butler J., Calixte N.,
RA Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,
RA Collymore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
RA David R., Dawoe T., Degray S., Dodge S., Doolley K., Dorje P.,
RA Dorjee K., Dorris L., Dufey N., Dupes A., Elkins T., Engels R.,
RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
RA Fitzgerald M., Foley K., Gage D., Galagan J., Geatin G., Gierre S.,
RA Glatke A., Goyette A., Graham J., Grandbois E., Gyaltzen K., Hafez N.,

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RA Hagopian D., Hagos B., Hall J., Hatchev B., Heller A., Higgins H.,
RA Homan T., Horn A., Houde N., Hughes L., Hulme W., Hueby E., Iliev I.,
RA Jaffe D., Jones C., Kamal M., Kamat A., Kamysellis M., Karlsson E.,
RA Kells C., Kieu A., Kienner P., Kodira C., Kulbokas E., Labutti K.,
RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,
RA Lindblad-toh K., Liu X., Lokytang T., Lokytang Y., Lucien O.,
RA Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,
RA Manning J., Marbella R., Maru K., Matthews C., Mauceli E.,
RA McCarthy M., McDonough S., Mcghee T., Meltrin J., Menue L.,
RA Mesirov J., Mihalev A., Mihova T., Mikkelsen T., Mlenga V., Moru K.,
RA Mozes C., Mulrain L., Munson G., Naylor J., Neves C., Nguyen C.,
RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizari M., Norbu C.,
RA Norbu N., O'donnell P., Okoawo O., O'leary S., Onotosho B.,
RA O'Neill K., Osman S., Parker S., Perrin D., Punthang P., Piganti B.,
RA Pucell S., Rachupka T., Ramasamy U., Ramau R., Ray V., Raymond C.,
RA Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,
RA Rutman M., Schnupbach R., Seaman C., Settipilli S., Sharpe T.,
RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougniez C.,
RA Spencer B., Stalker J., Strange-Thomann N., Stavropoulos S.,
RA Stetson K., Stone C., Stone S., Stubbs M., Talamas J., Tchinga P.,
RA Tenzing P., Testafay S., Theodore J., Thoulutang Y., Topham K.,
RA Towey S., Tsamta T., Tsomo N., Vallee D., Vassilev H.,
RA Venkataraman V., Vanson J., Vo A., Wade C., Wang S., Wangchuk T.,
RA Wangdi T., Whitaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,
RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembek L.,
RA Zimmer A., Zody M., Lander E.;
RT "The genome sequence of Magnaporthe grisea."
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
RN
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=70-15;
RC
RA Dean R., Mitchell T., Brown D., Pan H., Thon M.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
RN
RP NUCLEOTIDE SEQUENCE.
RT [3]
SQ SEQUENCE 251 AA; 28860 MW; 0F6C640B4FC826F CRC64;

Query Match 92.1%; Score 35; DB 2; Length 251;
Best Local Similarity 85.7%; Pred. No. 40;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
DB 222 WASTREA 228

RESULT 9
Q5H5B2_XANOR PRELIMINARY; PRT; 159 AA.
ID Q5H5B2;
AC Q5H5B2;
DT 10-MAY-2005 (TREMblrel. 30, Created)
DT 10-MAY-2005 (TREMblrel. 30, Last sequence update)
DT 10-MAY-2005 (TREMblrel. 30, Last annotation update)
DE Putative membrane protein.
GN OrderedLocuNames=XO00604;
OS Xanthomonas oryzae (pv. oryzae).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=64187;

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RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=KACC10331 / KX085;
RX PubMed=15673118; DOI=10.1093/nar/gki206;
RA Lee B.-M., Park Y.-J., Park D.-S., Kang H.-W., Kim J.-G., Song E.-S.,
RA Park I.-C., Yoon U.-H., Hahn J.-H., Koo B.-S., Lee G.-B., Kim H.,
RA Park H.-S., Yoon K.-O., Kim J.-H., Jung C.-H., Koh N.-H., Seo J.-S.,
RA Go S.-J.;
RT "The genome sequence of Xanthomonas oryzae pathovar oryzae KACC10331,
RT the bacterial blight pathogen of rice."
RL Nucleic Acids Res. 33:577-586(2005).
DR EMBL; AB013598; AAM73858.1; -; Genomic_DNA.
KM Complete proteome.
SQ SEQUENCE 159 AA; 17739 MW; D6FB95385E93DEF2 CRC64;

Query Match 89.5%; Score 34; DB 2; Length 159;
Best Local Similarity 85.7%; Pred. No. 40;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WASTRE 7
Db 108 WASTRE 114

RESULT 10
O6G2K3 BARHE PRELIMINARY; PRT; 934 AA.
AC O6G2K3;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=BH11960;
OS Bartonella henselae (Rochalimaea henselae).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bartonellaceae; Bartonella.
OX NCBI_TaxID=38323;
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 49882 / Houston 1;
RX PubMed=15210978; DOI=10.1073/pnas.0305659101;
RA Alsmark U.C.M., Frank A.C., Karlberg E.O., Legault B.-A., Ardell D.H.,
RA Canbaeck B., Eriksson A.-S., Naeslund A.K., Handley S.A., Huvet M.,
RA La Scala B., Holmberg M., Andersson S.G.E.;
RT "The house-borne human pathogen Bartonella quintana is a genomic
RT derivative of the zoonotic agent Bartonella henselae."
RL Proc. Natl. Acad. Sci. U.S.A. 101:9716-9721(2004).
DR EMBL; BX897699; CAF27979.1; -; Genomic_DNA.
DR InterPro; IPR011933; Two anch. 1.
DR TIGRFAMs; TIGR02226; two anch. 1.
KM Complete proteome; Hypothetical protein.
SQ SEQUENCE 934 AA; 104092 MW; 238F0F6DD2D5BF19 CRC64;

Query Match 89.5%; Score 34; DB 2; Length 934;
Best Local Similarity 100.0%; Pred. No. 2,8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WASTRE 6
Db 98 WASTRE 103

RESULT 11
O8P166_XANAC PRELIMINARY; PRT; 960 AA.
AC O8P166;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE GGDEF family protein.
GN OrderedLocustNames=XAC1940;
OS Xanthomonas axonopodis (pv. citri).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;

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OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=92829;
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=306 / ATCC 13902 / XV 101;
RX MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Ouaggo R.B., Monteiro-Vitorello C.B., Van Sluys M.A.,
RA Almeida N.F. Jr., Alves L.M.C., do Amaral A.M., Bercolini M.C.,
RA Canazao L.E.A., Camarotte G., Canavan F., Cardoso J., Chambergo F.,
RA Chaplana L.P., Ciccarelli R.M.B., Coutinho L.L., Cristiano-Santos J.R.,
RA El-Dorri H., Faria J.B., Ferreira A.J.S., Ferreira R.C.C.,
RA Ferro M.I.T., Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishii L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinoia L.A.F., Takita M.A., Tamura R.B., Teixeira E.C., Tezra R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities."
RL Nature 417:459-463(2002).
DR EMBL; AB011829; AAM36802.1; -; Genomic_DNA.
DR InterPro; IPR000160; GGDEF.
DR InterPro; IPR011110; Reg. prop.
DR InterPro; IPR011123; Y_Y_Y.
DR Pfam; PF00990; GGDEF_1.
DR Pfam; PF07494; Reg. prop; 10.
DR Pfam; PF07495; Y_Y_Y; 1.
DR SMART; SM00267; DUF1; 1.
DR TIGRFAMs; TIGR00254; GGDEF; 1.
DR PROSITE; PSS0887; GGDEF; 1.
KM Complete proteome.
SQ SEQUENCE 980 AA; 107940 MW; 47179C81BEDCE442 CRC64;

Query Match 89.5%; Score 34; DB 2; Length 980;
Best Local Similarity 100.0%; Pred. No. 2,9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WASTRE 6
Db 492 WASTRE 497

RESULT 12
Q4HVM0_GIBZE PRELIMINARY; PRT; 11999 AA.
AC Q4HVM0;
DT 13-SEP-2005 (TReMBLrel. 31, Created)
DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=FG10988.1;
OS Gibberella zeae PH-1.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
OX NCBI_TaxID=229353;
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=PH-1;
RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
RA Archchi H.M., Barna N., Bastien V., Blom T., Boguslavsky L.,
RA Boukhalter B., Butler J., Calvo S.E., Camarata U., Chang J.,
RA Choepel Y., Collymore A., Cook A., Cooke P., Corman B., Dearellano K.,
RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA Erickson J., Fayo S., Ferreira P., Fitzgerald M., Gage D., Galagan J.,
RA Gardyna S., Gierke S., Graham L., Grand-Pierre N., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
RA Kelle C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
RA Ma L.-J., Mabbitt R., Maclean C., Macdonald P., Major J., Manning J.,

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RA Matthews C., Mauceli E., McCarthy M., Meldim J., Meneus L.,
 RA Mhova T., Mienga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
 RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,
 RA Oliver J., Peterson K., Phunhphang P., Pierre N., Purcell S.,
 RA Roman J.A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
 RA Roman J., Schauer S., Schupbach R., Seaman S., Severy P., Smitrov S.,
 RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
 RA Talamas J., Testaye S., Theodore J., Topham K., Travers M.,
 RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
 RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
 RA Lander E.,
 RT "Fusarium graminearum genome sequence.";
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL: AACM01000457; EAA75314.1; -; Genomic DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 11999 AA; 1313242 MW; 379296FB8B11F8D8 CRC64;

Query Match 89.5%; Score 34; DB 2; Length 11999;
 Best Local Similarity 100.0%; Pred. No. 4.5e+03;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRE 6
 Db 3477 WASTRE 3482

RESULT 13
 ID 06P05 HUMAN PRELIMINARY; PRT; 266 AA.

AC 06P05;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE AOTS2 protein.

GN Name=AOTS2;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI_TaxID=9606;

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Muscle;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,

RA Datchenko L., Marinsina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares W.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Uudin T.B., Toshlyuk S., Carninci P., Prange C.,

RA Raha S.S., Loguigliano N.A., Peters G.J., Abramson R.D., Mullany S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smallus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

RT "Generation and initial analysis of more than 15,000 full-length human

and mouse cDNA sequences.";

RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RL [2]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Muscle;

RA Director MGC Project;

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

EMBL: BC011643; AAH11643.1; -; mRNA.

SQ SEQUENCE 266 AA; 29322 MW; 5DE33CA2D1AD11A4 CRC64;

Query Match 86.8%; Score 33; DB 2; Length 266;
 Best Local Similarity 85.7%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WASTRES 7
 Db 249 WASTRES 255

RESULT 14
 ID 04FWS7 LEIMA PRELIMINARY; PRT; 448 AA.

AC 04FWS7;

DT 13-SEP-2005 (TrEMBLrel. 31, Created)

DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)

DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)

DE Hypothetical protein.

GN ORFNames=lmj11260;

OS Leishmania major.

OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.

OX NCBI_TaxID=5664;

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=Frledlin;

RX PubMed=16020728; DOI=10.1126/science.1112680;

RA Iyene A.C., Peacock C.S., Worthey E.A., Murphy L., Aggarwal G.,

RA Berriman M., Sisk E., Rajandream M.A., Adlem E., Aert R., Anupama A.,

RA Apostolou Z., Altipoe P., Bason N., Bauser C., Beck A., Beverley S.M.,

RA Blanchettin G., Borzys K., Both G., Brunsch C.V., Collins M.,

RA Cadag E., Charlton L., Clayton C., Coulson R.M., Cronin A., Cruz A.K.,

RA Davies R.M., De Gaudenzi J., Dobson D.B., Duesterhoeft A.,

RA Fazlina G., Foster N., Fraech A.C., Fraser A., Fuchs M., Gabel C.,

RA Goble A., Goffeau A., Harris D., Hertz-Fowler C., Hilbert H., Horn D.,

RA Huang Y., Klages S., Knights A., Kude M., Latke N., Litvin L.,

RA Lord A., Louie T., Matra M., Masuy D., Matthews K., Michael S.,

RA Mottram J.C., Muller-Auer S., Munden H., Nelson S., Norbertczak H.,

RA Oliver K., O'Neill S., Pentony M., Pohl T.M., Price C., Purrelle B.,

RA Quail M.A., Rabinowitsch E., Reinhardt R., Rieger M., Rinta J.,

RA Robben J., Robertson L., Ruiz J.C., Rutter S., Saunders D.,

RA Schaffer M., Schein J., Schwartz D.C., Seeger K., Seyler A., Sharp S.,

RA Shin H., Sivam D., Squares R., Squares S., Tosato V., Vogt C.,

RA Volckaert G., Wambut R., Warren T., Wedler H., Woodward J., Zhou S.,

RA Zimmermann W., Smith D.F., Blackwell J.M., Stuart K.D., Barrett B.,

RA Myler P.J.;

RT "The Genome of the Kinetoplastid Parasite, Leishmania major.";

RL Science 309:436-442(2005).

DR EMBL: CP000081; AA214416.1; -; Genomic DNA.

KW Hypothetical protein.

SQ SEQUENCE 448 AA; 47488 MW; 6B624165311DED90 CRC64;

Query Match 86.8%; Score 33; DB 2; Length 448;
 Best Local Similarity 85.7%; Pred. No. 2e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WASTRES 7
 Db 210 WASTRES 216

RESULT 15
 ID 04Q865 LEIMA PRELIMINARY; PRT; 453 AA.

AC 04Q865;

DT 13-SEP-2005 (TrEMBLrel. 31, Created)

DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)

DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)

DE Hypothetical protein.

GN ORFNames=lmjF17.1260;

OS Leishmania major.

OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.

OX NCBI_TaxID=5664;

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RN [1]
RC NUCLEOTIDE SEQUENCE.
RA Peacock C.S., Murphy L., Ivens A.C., Berriman M., Blackwell J.,
RA Smith D., Collins M., Foster N., Harris D., Oliver K., O'Neill S.,
RA Saunders D., Seeger K., Warren T., Rajandream M.-A., and Barrall B.G.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL: CTO05256; CAJ03987.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ
SEQUENCE 453 AA; 47618 MW; 98B95B1B07CC445 CRC64;

Query Match 86.8%; Score 33; DB 2; Length 453;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 WASTRES 7
Db 153 WASTRES 159

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RESULT 16
Q4WS81_ASPFU PRELIMINARY; PRT; 1298 AA.
ID Q4WS81_ASPFU PRELIMINARY; PRT; 1298 AA.
AC Q4WS81;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE WD repeat protein.
OS ORFNames=Af1ug13690;
OC Aspergillus fumigatus Af293.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=330879;
RN [1]
RC NUCLEOTIDE SEQUENCE.
RA Nierman W., Pain A., Anderson M.J., Wortman J., Kim H., Stanley,
RA Arroyo J., Berriman M., Abe K., Archer D.B., Bernabeo C., Bennett J.,
RA Bowyer P., Chen D., Collins K., Coulson R., Davies R., Dyer P.S.,
RA Farman M., Fedorova N., Fedorova N., Feldblyum T.V., Fischer R.,
RA Foster N., Frazer A., Garcia J.L., Garcia M.J., Goble A.,
RA Goldman G.H., Goni K., Griffith-Jones S., Gwilliam R., Haas B.,
RA Haas H., Harris D., Horluchi H., Huang J., Humphrey S., Jimenez J.,
RA Keller N., Khouri H., Kitamoto K., Kobayashi T., Kulkarni R.,
RA Kumagai T., Latton S., Latge J.-P., Li W., Lord A., Lu C.,
RA Majors W.H., May G.S., Miller B.L., Mohamed Y., Molina M., Monod M.,
RA Mouny I., Mulligan S., Murphy L., O'Neill S., Paulsen I.,
RA Penava M.A., Perlea M., Price C., Pritchard B.L., Quail M.A.,
RA Rabinowitsch E., Rawlins N., Rajandream M.-A., Reichard U.,
RA Renard H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,
RA Rong C.M., Rutter S., Salzberg S.L., Sanchez M.,
RA Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S.,
RA Takeuchi M., Tekala F., Turner G., Vazquez de Aldana C.R., Weidman J.,
RA White O., Woodward J., Yu J.-H., Fraser C., Galagan J.E., Asai K.,
RT "Genomic sequence of the pathogenic and allergenic filamentous fungus
RT Aspergillus fumigatus";
RT Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: AAH0100004; EAL90701.1; -; Genomic_DNA.
DR InterPro: IPR001680; WD40.
DR Pfam: PF00400; WD40; 3.
DR SMART: SM00320; WD40; 3.
DR SMART: SM00320; WD40; 3.
KW Transport.
SQ
SEQUENCE 1298 AA; 146116 MW; F2CE960C731A4D0 CRC64;

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Query Match 86.8%; Score 33; DB 2; Length 1298;
Best Local Similarity 85.7%; Pred. No. 6.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 WASTRES 7

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Db 979 WASARES 985

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RESULT 17
Q8TFZ3_ASPFU PRELIMINARY; PRT; 1317 AA.
ID Q8TFZ3_ASPFU PRELIMINARY; PRT; 1317 AA.
AC Q8TFZ3;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Hypothetical protein.
OS ORFNames=AfA35g10.09C;
OC Aspergillus fumigatus (Sartorya fumigata).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5085;
RN [1]
RC NUCLEOTIDE SEQUENCE.
RX PubMed=1498527; DOI=10.1016/j.fgb.2003.12.003;
RA Pain A., Woodward J., Quail M.A., Anderson M.J., Clark R., Collins M.,
RA Foster N., Frazer A., Harris D., Larke N., Murphy L., Humphrey S.,
RA O'Neill S., Perlea M., Price C., Rabinowitsch E., Rajandream M.-A.,
RA Salzberg S., Saunders D., Seeger K., Sharp S., Warren T.,
RA Denning D.W., Barrall B., Hall N.;
RT "Insight into the genome of Aspergillus fumigatus: analysis of a 922
RT kb region encompassing the nitrate assimilation gene cluster.";
RL Fungal Genet. Biol. 41:443-453(2004).
DR EMBL: BX649606; CAD29602.1; -; Genomic_DNA.
DR InterPro: IPR001680; WD40.
DR Pfam: PF00400; WD40; 3.
DR SMART: SM00320; WD40; 3.
KW Hypothetical protein; Transport.
SQ
SEQUENCE 1317 AA; 148646 MW; 0DC4B0BD149A45DE CRC64;

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Query Match 86.8%; Score 33; DB 2; Length 1317;
Best Local Similarity 85.7%; Pred. No. 6.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 WASTRES 7
Db 979 WASARES 985

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RESULT 18
Q520D0_MAGGR PRELIMINARY; PRT; 1472 AA.
ID Q520D0_MAGGR PRELIMINARY; PRT; 1472 AA.
AC Q520D0;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Hypothetical protein.
OS ORFNames=MG05856.4;
OC Magnaporthe oryzae 70-15.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthae.
OX NCBI_TaxID=242507;
RN [1]
RC NUCLEOTIDE SEQUENCE.
RA Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,
RA Birren B., Allen N., Allen T., An P., Anderson M., Anderson S.,
RA Atchachi H., Amburster J., Bachansang P., Baldwin J., Barry A.,
RA Bayu T., Blitstein B., Bloom T., Blye J., Boguslavsky L.,
RA Borowsky M., Boukhalter B., Brunache A., Butler J., Calixte N.,
RA Calvo S., Camarata J., Campo K., Chang U., Chesatsang Y., Citroen M.,
RA Collymore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,
RA Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,
RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
RA Fitzgerald M., Foley K., Gage D., Galagan J., Geatin G., Gierre S.,
RA Ghitke A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Hatcher A., Higgins H.,

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RA Honan T., Horn A., Houde N., Hughes L., Hulme W., Hubby E., Iliev I.,
 RA Jaffe D., Jones C., Kamal M., Kamat A., Kamyselis M., Karlsson E.,
 RA Kells C., Kieu A., Kiser P., Kodira C., Kulbokas E., Labutti K.,
 RA Liana D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,
 RA Lindblad-toh K., Liu X., Lokitsang T., Lokitsang Y., Lucien O.,
 RA Liu A., Ma L.-J., Mabbitt R., MacDonald J., Maclean C., Major J.,
 RA Manning J., Marbella R., Maru K., Matthews C., Muccelli E.,
 RA McCarthy M., McDonough S., McChae T., Meldrum J., Menus L.,
 RA Mervov J., Mihalev A., Mihova T., Mikkelsen T., Mlenga V., Moru K.,
 RA Mores J., Mulrain L., Munson G., Naylor J., Neves C., Nguyen C.,
 RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizati M., Norbu C.,
 RA Notbu N., O'donnell P., Okoawo O., O'leary S., Omotosho B.,
 RA O'Neill K., Osman S., Parker S., Perrin D., Phunhkhong P., Piquani B.,
 RA Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,
 RA Rector A., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,
 RA Rutman M., Schupbach R., Seaman C., Settipalli S., Sharpe T.,
 RA Sheridan J., Shepa N., Shi J., Smitnov S., Smith C., Sougnuez C.,
 RA Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,
 RA Stetson K., Stone C., Stone S., Stubbs M., Talamas J., Tchinga P.,
 RA Tenzing P., Testaye S., Theodore J., Thoultsang Y., Topham K.,
 RA Towey S., Tsamla T., Tsomo N., Vallee D., Vassiliev H.,
 RA Verkaratman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,
 RA Wangdi T., Whitaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,
 RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,
 RA Zimmer A., Zody M., Lander E.;
 RT "The genome sequence of *Magnaporthe oryzae*.";
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=70-15;
 RA Dean R., Mitchell T., Brown D., Pan H., Thon M.;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=70-15;
 RA Zhu H., Blackmon B.;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 CC -1 CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC EMBL: AACU01000833; EAS52728.1; -; Genomic_DNA.
 DR InterPro: IPR02110; ANK.
 DR Pfam: PF00023; Ank; 9.
 DR PRINTS: PR01415; ANKYRIN.
 DR SMART: SMO0248; ANK_10.
 DR PROSITE: PS50297; ANK_REPEAT; 1.
 DR PROSITE: PS50088; ANK_REPEAT; 6.
 KW ANK repeat; Hypothetical protein; Repeat.
 KW SEQUENCE 1472 AA; 162070 MW; 5007E01F296C1724 CRC64;
 SQ
 Query Match 86.8%; Score 33; DB 2; Length 1472;
 Best Local Similarity 85.7%; Pred. No. 7.5e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=51.6-2;
 RA Bello G., Casado C., Garcia S., Rodriguez C., del Romero J.,
 RA Lopez-Galindez C.;
 RT "Lack of temporal structure for the short term HIV-1 evolution in
 RT naive patients with low viral load.";
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY498207; AAS78060.1; -; Genomic_DNA.
 DR SMR: OSV04; 1-201.
 DR GO: GO:0016021; C: integral to membrane; IEA.
 DR GO: GO:0019031; C: viral envelope; IEA.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 KW AIDS; Envelope protein; Transmembrane.
 FT NON_TER 1
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 201 AA; 22581 MW; 40B49802F4BCDAE CRC64;
 QY 1 WASTRES 7
 Db 115 WASTRES 121
 RESULT 20
 ID OSV04_RAT PRELIMINARY; PRT; 203 AA.
 AC OSV04;
 DT 01-FEB-2005 (TREMBlrel. 29, Created)
 DT 01-FEB-2005 (TREMBlrel. 29, Last sequence update)
 DT 01-FEB-2005 (TREMBlrel. 29, Last annotation update)
 DE Spp-24;
 GN Name=Spp2;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toehiyuki S., Cantucci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.U., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smellins D.E.,
 RA Scherach A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Liver;
 RG NIH MGC Project;
 RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC088193; AA088193.1; -; mRNA.
 DR GO: GO:0005576; C: extracellular region; IEA.
 DR GO: GO:0046849; P: bone remodeling; IEA.

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DR InterPro; IPR010892; Spp-24.
DR Pfam; PF07448; Spp-24; 1.
SQ SEQUENCE 203 AA; 23170 MW; 5B9BCA590DC7F63E CRC64;

Query Match 84.2%; Score 32; DB 2; Length 203;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WASTRES 7
Db 129 WASTRES 135

RESULT 21
Q915J7_PSEAE PRELIMINARY; PRT; 347 AA.
ID Q915J7_PSEAE PRELIMINARY;
AC Q915J7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=PA0732;
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
CX NCBI_TaxId=287;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
RA Hickey M.J., Brinkman F.S.L., Hutnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber L.L., Coulter S.N., Folger K.R., Kas A., Laidis K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Slier M.H. Jr., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
DR EMBL; AE004508; AAC04121.1; -; Genomic_DNA.
DR PIR; D83554; D83554.
DR InterPro; IPR005490; ERFK_YBIS_YHNG.
DR Pfam; PF03734; ERFK_YBIS_YHNG; 1.
KM Complete proteome; Hypothetical protein.
SQ SEQUENCE 347 AA; 37161 MW; 2C4EAD0C64290CC3 CRC64;

Query Match 84.2%; Score 32; DB 2; Length 347;
Best Local Similarity 71.4%; Pred. No. 2.5e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WASTRES 7
Db 318 WASTRES 324

RESULT 22
Q7XU18_ORYSA PRELIMINARY; PRT; 458 AA.
ID Q7XU18_ORYSA PRELIMINARY;
AC Q7XU18;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE OSJNB0103108.17 protein.
GN Name=OSJNB0103108.17;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Gramineae; Oryzaceae; Oryza.
CX NCBI_TaxId=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=2237377; PubMed=12447439; DOI=10.1038/nature01183;
RA Feng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J.,
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RA Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y.,
RA Weng Q., Zhang L., Lu Y., Mu J., Lu Y., Zhang L.S., Yu Z., Fan D.,
RA Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,
RA Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H.,
RA Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y.,
RA Chen J., Ren H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W.,
RA Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W.,
RA Lan L., Lai Y., Cheng Z., Gu M., Jiang Y., Li J., Hong G., Xue Y.,
RA Han B.;
RT "Sequence and analysis of rice chromosome 4.";
RL Nature 420:316-320(2002).
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AL066695; CAD41278.2; -; Genomic_DNA.
DR Gramene; O7XU18; -;
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008220; Ser_Thr_kin_AS.
DR InterPro; IPR002290; Ser_Thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; Tyr_Kc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KM ATP-binding; Kinase; Nucleotide-binding;
KM Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 458 AA; 49421 MW; 754DPA9E237FEE8 CRC64;

Query Match 84.2%; Score 32; DB 2; Length 458;
Best Local Similarity 85.7%; Pred. No. 3.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WASTRES 7
Db 59 WASTRES 65

RESULT 23
Q4SKL4_TETNG PRELIMINARY; PRT; 537 AA.
ID Q4SKL4_TETNG PRELIMINARY;
AC Q4SKL4;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome undetermined SCAF14565, whole genome shotgun sequence.
DE (fragment).
GN ORFNames=GSTENG00016666001;
OS Tetradodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
CX NCBI_TaxId=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jallion O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Muscari E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicard S., Jaffe D., Fisher S., Lutfalla G., Dosat C., Segurens B.,
RA Dastilva C., Salenoudat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Ublin C., Castel V., Katinka M., Vacherie B.,
RA Blemont C., Skalli Z., Catolico L., Boulain J., De Bernardis V.,
RA Crnaud C., Duprat S., Broctier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McBwan P., Bosak S.,
RA Kellis M., Wolff J.V., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Lauder V., Schachter V., Queller F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
```

RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 RT the early vertebrate proto-karyotype.";
 RL Nature 431:946-957(2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RG Genoscope; Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL, CAAB01014565; CAF98818.1; -; Genomic_DNA.
 FT NON_TER 1
 FT MON_TER 537
 SQ SEQUENCE 537 AA; 58267 MW; A2A8F5945C5BC767 CRC64;
 Query Match 84.2%; Score 32; DB 2; Length 537;
 Best Local Similarity 85.7%; Pred. No. 4.1e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 WASTRES 7
 Db 279 WASSRES 285
 RESULT 24
 SYM_NEIMA STANDARD; PRT; 685 AA.
 AC O3JWP0;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Methionyl-tRNA synthetase (EC 6.1.1.10) (Methionine--tRNA ligase)
 DE (MetRS).
 GN Name=metG; OrderedLocuNames=MMA0275;
 OS Neisseria meningitidis (serogroup A).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Neisseria.
 OX NCBI_TaxID=65699;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Z2491 / Serogroup A / Serotype 4A;
 RX MEDLINE=20222556; PubMed=10761919; DOI=10.1038/35006655;
 RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.M.,
 RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
 RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
 RA Jorgels K., Leather S., Moule S., Mungall K.L., Quail M.A.,
 RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
 RA Whitehead S., Spratt B.G., Barrall B.G.;
 RT "Complete DNA sequence of a serogroup A strain of Neisseria
 RT meningitidis Z2491.";
 RL Nature 404:502-506(2000).
 CC -1- FUNCTION: is required not only for elongation of protein synthesis
 CC but also for the initiation of all mRNA translation through
 CC initiator tRNA (fMet) aminoacylation (By similarity).
 CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + tRNA(Met) = AMP +
 CC di-phosphate + L-methionyl-tRNA(Met).
 CC -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: Belongs to the class-I aminoacyl-tRNA synthetase
 CC family. MetG type 1 subfamily.
 CC -1- SIMILARITY: Contains 1 tRNA-binding domain.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC EMBL: AL162752; CAB83583.1; -; Genomic_DNA.
 CC PIR: G82022; G82022.
 CC HSSP: P00959; IMEA.
 DR HAMAP: MF_00098; fused; 1.

DR InterPro; IPR004495; MetG Cterm.
 DR InterPro; IPR008224; MetRS dimerising.
 DR InterPro; IPR012340; OB_NA_bd_sub.
 DR InterPro; IPR002300; tRNA-synt_1a.
 DR InterPro; IPR001412; tRNA-synt_1.
 DR InterPro; IPR002304; tRNA-synt_met.
 DR InterPro; IPR002547; tRNA_bd.
 DR Pfam; PF00133; tRNA-synt_1; 1.
 DR Pfam; PF01588; tRNA_bind_1.
 DR Pfam; PF0001528; MetRS dimerising; 1.
 DR PRINTS; PR01041; TRNASYNTMET.
 DR TIGRFAMs; TIGR00398; metG_C term; 1.
 DR TIGRFAMs; TIGR00399; metG_C term; 1.
 DR PROSITE; PS00178; AA tRNA_LIGASE_1; 1.
 DR PROSITE; PS50866; TRHD; 1.
 KW Aminoacyl-tRNA synthetase; ATP-binding; Complete proteome; Ligase;
 KW Metal-binding; Nucleotide-binding; Protein biosynthesis; RNA-binding;
 KW tRNA-binding; Zinc.
 FT DOMAIN 582 685 tRNA-binding.
 FT MOTIF 12 22 "HIGH" region.
 FT MOTIF 339 343 "KMSKS" region.
 FT METAL 143 143 Zinc (By similarity).
 FT METAL 146 146 Zinc (By similarity).
 FT METAL 156 156 Zinc (By similarity).
 FT METAL 159 159 Zinc (By similarity).
 FT BINDING 342 342 ATP (By similarity).
 SQ SEQUENCE 685 AA; 76984 MW; 07FD45915ED3BER3 CRC64;

Query Match 84.2%; Score 32; DB 1; Length 685;
 Best Local Similarity 71.4%; Pred. No. 5.3e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WASTRES 7
 Db 520 WASTRET 526

RESULT 25
 O7OYCI_GIALA PRELIMINARY; PRT; 71 AA.
 ID O7OYCI_GIALA PRELIMINARY;
 AC O7OYCI;
 DT 01-MAR-2004 (TEMBLrel. 26, Created)
 DT 01-MAR-2004 (TEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
 DE GIP 387 11136 11351.
 OS Giardia_lambia ATCC 50803.
 CC Giardia; Diplomonadida; Hexamitidae; Giardinae; Giardia.
 CC Eukaryota; Diplomonadida; Hexamitidae; Giardinae; Giardia.
 OX NCBI_TaxID=184922;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=WB C6;
 RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
 RA Olsen G.J., Sogin M.L.;
 RT "Draft sequence of the Giardia lamblia genome.";
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AACB0100052; EAA40034.1; -; Genomic_DNA.
 DR SQUENCE 71 AA; 8127 MW; 0374829B52C40EE3 CRC64;

Query Match 81.6%; Score 31; DB 2; Length 71;
 Best Local Similarity 71.4%; Pred. No. 73;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WASTRES 7
 Db 65 WASSROS 71

RESULT 26
 O5BG03_EMENT PRELIMINARY; PRT; 108 AA.
 ID O5BG03_EMENT PRELIMINARY;


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DT 01-MAR-2004 (TrEMBLrel. 26, last annotation update)
DE Secretion activator protein.
GN Name=Z1S;
OS Zymomonas mobilis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
OC Sphingomonadaceae; Zymomonas.
OX NCBI_TaxID=542;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=I1013756;
RA Kondo Y., Toyoda A., Fukushi H., Yanase H., Tomomura K., Kawasaki H., Sakai T.;
RT "Cloning and characterization of a pair of genes that stimulate the production and secretion of Zymomonas mobilis extracellular levansucrase and invertase."
RT levansucrase and invertase."
RT Biosci. Biotechnol. Biochem. 0:0-0(1994).
RL [2]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=I1013756;
RA Kondo Y., Toyoda A., Fukushi H., Yanase H., Tomomura K., Kawasaki H., Sakai T.;
RT "Cloning and characterization of a pair of genes that stimulate the production and secretion of Zymomonas mobilis extracellular levansucrase and invertase."
RT Biosci. Biotechnol. Biochem. 58:526-530(1994).
RL EMBL; D17522; BAA04473.1; -; Genomic_DNA.
DR PIR; JC2104; JC2104.
DR InterPro: IPR008565; DUF847.
DR Pfam; PF05838; DUF847; 1.
SQ SEQUENCE 183 AA; 20629 MW; F8F00828108BD66F CRC64;

Query Match 81.6%; Score 31; DB 2; Length 183;
Best Local Similarity 71.4%; Pred. No. 2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WASTRES 7
Db 145 WAKTREN 151

RESULT 30
Q5NP04_ZYMMO PRELIMINARY; PRT; 183 AA.
ID Q5NP04;
AC Q5NP04;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, last annotation update)
DE Secretion activator protein.
OS Zymomonas mobilis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
OC Sphingomonadaceae; Zymomonas.
OX NCBI_TaxID=542;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 31821 / ZM4 / CP4;
RA PubMed=15592456; DOI=10.1038/nbt1045;
RA Seo J.-S., Chong H., Park H.S., Yoon K.-O., Jung C., Kim J.J., Hong J.H., Kim H., Kim J.-H., Kil J.-I., Park C.J., Oh H.-M., Lee J.-S., Jin S.-O., Um H.-W., Lee K.-J., Oh S.-J., Kim J.Y., Kang H.L., Lee S.Y., Lee K.J., Kang H.S.;
RT "The genome sequence of the ethanologenic bacterium Zymomonas mobilis ZM4."
RT Nat. Biotechnol. 23:63-68(2005).
DR EMBL; AE008692; AA89556.1; -; Genomic_DNA.
DR InterPro: IPR008565; DUF847.
DR Pfam; PF05838; DUF847; 1.
KM Complete Proteome.
SQ SEQUENCE 183 AA; 20562 MW; AB601CA956A9773 CRC64;

Query Match 81.6%; Score 31; DB 2; Length 183;
Best Local Similarity 71.4%; Pred. No. 2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 WASTRES 7
Db 145 WAKTREN 151

RESULT 31
Q58087_ENTFA PRELIMINARY; PRT; 226 AA.
ID Q58087_ENTFA
AC Q58087;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, last annotation update)
DE ABC transporter ATP-binding protein.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=OG1RF;
RA MEDLINE=98380380; PubMed=9712783;
RA Xu Y., Murray B.E., Weinstein G.M.;
RT "A cluster of genes involved in polysaccharide biosynthesis from Enterococcus faecalis OG1RF."
RT Infect. Immun. 66:4313-4323(1998).
RL -1- SUBCELLULAR LOCATION: Membrane-associated (By similarity).
CC -1- SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; AF071085; AAC55826.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016887; F:ATPase activity; IEA.
DR GO; GO:0015087; F:cobalt ion transporter activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0006824; P:cofactor ion transport; IEA.
DR GO; GO:0006811; P:ion transport; IEA.
DR GO; GO:0006811; P:ion transport; IEA.
DR InterPro: IPR003439; AAA_ATPase.
DR InterPro: IPR003439; ABC_transp_like.
DR Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; UNKNOWN 1.
DR PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
KM ATP-binding; Membrane; Nucleotide-binding; Transport.
SQ SEQUENCE 226 AA; 25420 MW; 68C6D5C85CDA2A5 CRC64;

Query Match 81.6%; Score 31; DB 2; Length 226;
Best Local Similarity 71.4%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WASTRES 7
Db 219 WATRES 225

RESULT 32
Q5T8A5_HUMAN PRELIMINARY; PRT; 228 AA.
ID Q5T8A5_HUMAN
AC Q5T8A5;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, last annotation update)
DE Odorant binding protein 2A.
OS Homo sapiens (Human).
OC Mammalia; Chordata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Babbage A.;
RM Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.

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DR EMBL; AL161452; CA114041.1; -; Genomic DNA.
 DR Ensembl; ENSG00000122136; Homo sapiens
 DR GO; GO:0005215; F:transporter activity; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR000566; LipidIn_cyPABP.
 DR InterPro; IPR002450; vonEdner_gland.
 DR Pfam; PF00061; Lipocalin; 1.
 DR PRINTS; PRO1175; VNEBNERGLAND.
 SQ SEQUENCE 228 AA; 25985 MW; 7506B5D23F8C07C2 CRC64;

Query Match 81.6%; Score 31; DB 2; Length 228;
 Best Local Similarity 71.4%; Pred. No. 2.6e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WASTRES 7
 Db 168 WASTRES 174

RESULT 33

08NU75 CORGL PRELIMINARY; PRT; 230 AA.
 ID 08NU75; Q6M8T5; 22, Created)
 AC 08NU75; Q6M8T5; 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 31, Last annotation update)
 DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
 DE Nicotianamide mononucleotide transporter.
 GN OrderedLocustNames=Cg10064, cg0083;
 OS Corynebacterium glutamicum (Brevibacterium flavum).
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
 OX NCBI_TaxID=1718;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
 RA Nakagawa S.;
 RT "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032."
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
 RX PubMed=12948626; DOI=10.1016/S0168-1656(03)00154-8;
 RA Kalinowski J., Bathe B., Bartels D., Bischoff N., Bock M.,
 RA Burkowski A., Dusch N., Eggeling L., Elkmann B.J., Gaigalat L.,
 RA Goessmann A., Hartmann M., Hutmacher K., Kraemer R., Linke B.,
 RA Mohrhardt A.C., Meyer F., Moeckel B., Pfeiffer W., Puchler A.,
 RA Ray D.A., Rueckert C., Rupp O., Sahn H., Wendisch V.F., Wiegand I.,
 RA Tsuch A.;
 RT "The complete Corynebacterium glutamicum ATCC 13032 genome sequence
 RT and its impact on the production of L-aspartate-derived amino acids
 RT and vitamins";
 RL J. Biotechnol. 104:5-25 (2003).
 DR EMBL; BA000046; BAB97457.1; -; Genomic DNA.
 DR EMBL; BX227148; CAF18652.1; -; Genomic DNA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR006419; NMN transp. PnuC.
 DR Pfam; PF04973; NMN transporter; 1.
 DR TIGRPFAMs; TIGR01528; NMN_trans_PnuC; 1.
 KW Complete proteome.
 SQ SEQUENCE 230 AA; 25546 MW; 93429B9438A8E45 CRC64;

Query Match 81.6%; Score 31; DB 2; Length 230;
 Best Local Similarity 83.3%; Pred. No. 2.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WASTRE 6
 Db 113 WASTRE 118

RESULT 34
 Q4UHH3 THEAN

ID Q4UHH3 THEAN PRELIMINARY; PRT; 237 AA.
 AC Q4UHH3;
 DT 13-SEP-2005 (TREMBlrel. 31, Created)
 DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=TA03010;
 OS Theileria annulata.
 OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae;
 OC Theileria.
 OX NCBI_TaxID=5874;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Ankara isolate clone C9;
 RA Pain A., Renaud H., Murphy L., Harris D.A., Quail M.A., Berriman M.,
 RA Hall N., Barrell B.G.;
 RT "The chromosome 1 sequence of Theileria annulata";
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CR940347; CA173466.1; -; Genomic DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 237 AA; 27734 MW; 0BCCB3B567D6456 CRC64;

Query Match 81.6%; Score 31; DB 2; Length 237;
 Best Local Similarity 85.7%; Pred. No. 2.7e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WASTRES 7
 Db 155 WASTRES 161

RESULT 35

Q4UJ32 CORJK PRELIMINARY; PRT; 248 AA.
 ID Q4UJ32 CORJK
 AC Q4UJ32;
 DT 13-SEP-2005 (TREMBlrel. 31, Created)
 DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
 DE PnuC protein.
 GN Name=pnuC; ORFNames=jK1502;
 OS Corynebacterium jeikeium (strain K411).
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
 OX NCBI_TaxID=306537;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=K411;
 RX PubMed=15968079; DOI=10.1128/JB.187.13.4671-4682.2005;
 RA Tsuch A., Kaiser O., Hahn T., Goessmann A., Weissnaar B.,
 RA Albersmeier A., Bekel T., Bischoff N., Brune I., Chakraborty T.,
 RA Kalinowski J., Meyer F., Rupp O., Schneider S., Viehoveer P.,
 RA Puhler A.;
 RT "Complete Genome Sequence and Analysis of the Multiresistant
 RT Nosocomial Pathogen Corynebacterium jeikeium K411, a Lipid-Regulating
 RT Bacterium of the Human Skin Flora";
 RL J. Bacteriol. 187:4671-4682(2005).
 DR EMBL; CR931997; CA137675.1; -; Genomic DNA.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=K411;
 RA Linke B., Tsuch A.;
 RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CR931997; CA137675.1; -; Genomic DNA.
 SQ SEQUENCE 248 AA; 27042 MW; D39A97BBE6BB35A1 CRC64;

Query Match 81.6%; Score 31; DB 2; Length 248;
 Best Local Similarity 83.3%; Pred. No. 2.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WASTRE 6
 Db 134 WASTRE 139

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RESULT 36
ID Q4SRL7_TETNG PRELIMINARY; PRT; 304 AA.
AC Q4SRL7;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DE Chromosome undetermined SCAF14518, whole genome shotgun sequence.
GN ORFNames=GSTENG00013856001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorphi; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_Taxid=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Uallion O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Desilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthoard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Crnaud C., Duprat S., Broctier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Lauder V., Schacherer V., Querier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Genoscope, Whitehead Institute Centre for Genome Research;
RG Submitted (Feb-2004) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -! SIMILARITY: Contains 1 PH domain.
DR EMBL: CA601014518; CAF96715.1; -; Genomic_DNA.
DR InterPro: IPR002197; HTH_Fis.
DR InterPro: IPR001849; PH.
DR Pfam: PF00169; PH; 1.
DR PRINTS: PR01590; HTHFS.
DR SMART: SM00233; PH; 1.
DR PROSITE: PSS0003; PH_DOMAIN; 1.
SQ SEQUENCE 304 AA; 34505 MW; 8219583D8E1D5957 CRC64;

Query Match 81.6%; Score 31; DB 2; Length 304;
Best Local Similarity 83.3%; Pred. No. 3,6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRE 6
Db 225 WASTKE 230

RESULT 37
Q7ZOV2_9HIV1 PRELIMINARY; PRT; 338 AA.
AC Q7ZOV2;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_Taxid=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.

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RX MEDLINE=22472311; PubMed=12584330;
RX DOI=10.1128/JVI.77.5.3050-3057.2003;
RA Verhofstede C., Demehcheer E., De Cabooter N., Gaillard P.,
RA Mwanumba F., Claey s P., Chohan V., Mandaliya K., Temmerman M.,
RA Plum J.;
RT "Diversity of the human immunodeficiency virus type 1 (HIV-1) env
RT sequence after vertical transmission in mother-child pairs infected
RT with HIV-1 subtype A.";
RL J. Virol. 77:3050-3057(2003).
DR EMBL: AY175013; AA020492.1; -; Genomic_DNA.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0019031; C: viral envelope; IEA.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
KM AIDS; Envelope protein; Transmembrane.
FT NON_TER 1
FT NON_TER 338
SQ SEQUENCE 338 AA; 37377 MW; 840D6473E081290F CRC64;

Query Match 81.6%; Score 31; DB 2; Length 338;
Best Local Similarity 71.4%; Pred. No. 4e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
Db 276 WASTOET 282

RESULT 38
Q7ZOV3_9HIV1 PRELIMINARY; PRT; 338 AA.
AC Q7ZOV3;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_Taxid=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22472311; PubMed=12584330;
RX DOI=10.1128/JVI.77.5.3050-3057.2003;
RA Verhofstede C., Demehcheer E., De Cabooter N., Gaillard P.,
RA Mwanumba F., Claey s P., Chohan V., Mandaliya K., Temmerman M.,
RA Plum J.;
RT "Diversity of the human immunodeficiency virus type 1 (HIV-1) env
RT sequence after vertical transmission in mother-child pairs infected
RT with HIV-1 subtype A.";
RL J. Virol. 77:3050-3057(2003).
DR EMBL: AY175012; AA020491.1; -; Genomic_DNA.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0019031; C: viral envelope; IEA.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
KM AIDS; Envelope protein; Transmembrane.
FT NON_TER 1
FT NON_TER 338
SQ SEQUENCE 338 AA; 37442 MW; A578F21F91D249DF CRC64;

Query Match 81.6%; Score 31; DB 2; Length 338;
Best Local Similarity 71.4%; Pred. No. 4e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
Db 276 WASTOET 282

RESULT 39
Q7ZOV5_9HIV1

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ID Q7ZOV5 9HIV1 PRELIMINARY; PRT; 340 AA.
AC Q7ZOV5;
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentiviruses; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22472311; PubMed=12584330;
RX DOI=10.1128/JVI.77.5.3050-3057.2003;
RA Verhoefstede C., Demecheleer E., De Cabooter N., Gailard P.,
RA Manyamba F., Claey's P., Chohan V., Mandaliya K., Temmerman M.,
RA Plum J.;
RT "Diversity of the human immunodeficiency virus type 1 (HIV-1) env
RT sequence after vertical transmission in mother-child pairs infected
RT with HIV-1 subtype A."
RL J. Virol. 77:3050-3057(2003).
DR EMBL; AY175010; AAC20469.1; -; Genomic_DNA.
DR GO; GO:0016031; C:Integral to membrane; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00518; GP120; 1.
DR AIDS; Envelope protein; Transmembrane.
FT NON_TER 1
FT TER 1
FT SEQUENCE 340 AA; 37604 MW; E69656A6B41F7A CRC64;
SQ

Query Match 81.6%; Score 31; DB 2; Length 340;
Best Local Similarity 71.4%; Pred. No. 4e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
Db 278 WASTRES 284

RESULT 40
Q5CF5 SCHUA PRELIMINARY; PRT; 344 AA.
ID Q5CF5 SCHUA PRELIMINARY;
AC Q5CF5;
DT 10-MAY-2005 (Tremblrel. 30, Created)
DT 10-MAY-2005 (Tremblrel. 30, Last sequence update)
DT 10-MAY-2005 (Tremblrel. 30, Last annotation update)
DE Hypothetical protein.
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigoidida;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Han Z.;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
RA EMBL; AY809931; AAX25820.1; -; mRNA.
DR InterPro; IPR011992; EF-Hand_type.
DR InterPro; IPR011025; GProtein_insert.
DR InterPro; IPR002477; G_binding.
KM Hypothetical protein.
SQ SEQUENCE 344 AA; 40306 MW; 789CBF344C057E1F CRC64;

Query Match 81.6%; Score 31; DB 2; Length 344;
Best Local Similarity 71.4%; Pred. No. 4.1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
Db 138 WASTRES 144

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RESULT 41
Q4Q1L2 LEIMA PRELIMINARY; PRT; 371 AA.
ID Q4Q1L2 LEIMA PRELIMINARY;
AC Q4Q1L2;
DT 13-SEP-2005 (Tremblrel. 31, Created)
DT 13-SEP-2005 (Tremblrel. 31, Last sequence update)
DT 13-SEP-2005 (Tremblrel. 31, Last annotation update)
DE Hypothetical protein.
OS ORFNames=LmjF36.2100;
GN Leishmania major.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Fielding.
RA Pascock C.S., Murphy L., Ivens A.C., Berriman M., Blackwell J.,
RA Smith D., Collins M., Foster N., Harris D., Oliver K., O'Neill S.,
RA Saunders D., Seeger K., Warren T., Rajandream M., and Barrell B.G.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; C705272; CAJ09167.1; -; Genomic_DNA.
KM Hypothetical protein.
SQ SEQUENCE 371 AA; 41081 MW; CED104B0210148B2 CRC64;

Query Match 81.6%; Score 31; DB 2; Length 371;
Best Local Similarity 83.3%; Pred. No. 4.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRE 6
Db 32 WASTRE 37

RESULT 42
THRC SYN3 STANDARD; PRT; 388 AA.
ID THRC SYN3 STANDARD;
AC P74193;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Threonine synthase (EC 4.2.3.1).
GN Name=thrc; OrderedLocustNames=s1111172;
OS Synechocystis sp. (strain PCC 6803);
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hirosewa M., Sugita M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naito K., Okumura S.,
RA Shimpo S., Takeuchi C., Wada T., Watanabe A., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions."
RL DNA Res. 3:109-136(1996).
CC -1- CATALYTIC ACTIVITY: O-phospho-L-homoserine + H(2)O = L-threonine +
CC phosphate.
CC -1- COFACTOR: Pyridoxal phosphate (By similarity).
CC -1- PATHWAY: Amino-acid biosynthesis; L-threonine biosynthesis; L-
CC threonine from L-aspartate: step 5 (final step).
CC -1- SIMILARITY: Belongs to the serine/chreonine dehydratase family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; BA000022; BAA18282.1; -; Genomic_DNA.
CC PIR; S75823; S75823.
CC HSP; Q957B5; 1ESX.
CC InterPro; IPR001926; B6_enzyme_beta.

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DR InterPro; IPR000634; S_T dehydrogase_BS.
DR InterPro; IPR004450; Thr_synthase_..
DR Pfam; PF00291; PALP; 1.
DR TIGRFAMs; TIGR00260; thrC; 1.
DR PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
DR Amino-acid biosynthesis; Complete proteome; Lyase;
KW Pyridoxal phosphate; Threonine biosynthesis.
FT BINDING 93 Pyridoxal phosphate (covalent)
SQ SEQUENCE 382 AA; 40414 MW; PFC9A9ECB7F6F35 CRC64;
(Possible).
Query Match 81.6%; Score 31; DB 1; Length 382;
Best Local Similarity 71.4%; Pred. No. 4.6e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 WASTRES 7
Db 285 WAARES 291

RESULT 43
QANPS1_9DELTA PRELIMINARY; PRT; 391 AA.
ID QANPS1;
AC QANPS1;
DT 13-SEP-2005 (TReMBLrel. 31, Created)
DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
DE Histidine kinase, HAMK region precursor.
GN ORFNames=AdelDRAPT_0889;
OS Anaeromyxobacter dehalogenans 2CP-C.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
OC Cytophacterales; Myxococcaceae; Anaeromyxobacter.
OX NCBI_TaxID=290397;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2CP-C;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Terrani S., Pittluck S., Richardson P.;
RT "Sequencing of the draft genome assembly of Anaeromyxobacter
RT dehalogenans 2CP-C.";
RT Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RL [2]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=2CP-C;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Anaeromyxobacter
RT dehalogenans 2CP-C.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAHD0100041; EAL77573.1; -; Genomic_DNA.
KW Kinase; Signal.
FT SIGNAL 1
SQ SEQUENCE 391 AA; 41773 MW; 94E9BAEEF0DAC294 CRC64;
Query Match 81.6%; Score 31; DB 2; Length 391;
Best Local Similarity 83.3%; Pred. No. 4.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 WASTRE 6
Db 211 WAATRE 216

RESULT 44
Y2619 TREDE STANDARD; PRT; 404 AA.
ID Y2619 TREDE
AC Q73JF6;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)

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DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Hypothetical RNA methyltransferase TDE2619 (EC 2.1.1.-).
GN OrderedCusNames=TD2619;
OS Treponema denticola.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=158;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 35405 / DSM 14222;
RX PubMed=15064399; DOI=10.1073/pnas.0307639101;
RA Seshadri R., Myers G.S.A., Tettelin H., Eisen J.A., Heidelberg J.F.,
RA Dodson R.J., Davidson T.M., DeBoy R.T., Fouts D.E., Hatt D.H.,
RA Selengut J., Ren Q., Brinkac L.M., Madupu R., Kolonay J.F.,
RA Durkin S.A., Daugherty S.C., Shetty J., Shvartsbeyn A.,
RA Gebreyes E., Geer K., Tsegaye G., Malik J.A., Ayodeji B.,
RA Shatman S., McLeod M.P., Smajic D., Howell J.K., Pal S., Anin A.,
RA Vashisth P., McNeill T.Z., Xiang Q., Sodergren E., Baca E.,
RA Weinstock G.M., Norris S.J., Fraser C.M., Paulsen I.T.;
RT "Comparison of the genome of the oral pathogen Treponema denticola
RT with other spirochete genomes.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:5646-5651(2004).
CC -!- SIMILARITY: Belongs to the RNA MSU methyltransferase family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AE017254; MAS1336.1; -; Genomic_DNA.
DR TIGR; TDE2619; -.
DR InterPro; IPR002792; TRAM.
DR InterPro; IPR010280; U5_mtfase.
DR Pfam; PR01938; TRAM; 1.
DR Pfam; PF05958; tRNA-US-meth-tr; 1.
DR PROSITE; PS01230; TRNA_1; FALSE_NEG.
DR PROSITE; PS01231; TRNA_2; FALSE_NEG.
KW Complete proteome; Hypothetical protein; Methyltransferase;
KW Transferrase.
FT ACT SITE 361
FT ACT SITE 361 By similarity.
SQ SEQUENCE 404 AA; 46211 MW; 56EA03B2E794C20 CRC64;
Query Match 81.6%; Score 31; DB 1; Length 404;
Best Local Similarity 71.4%; Pred. No. 4.9e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 WASTRES 7
Db 318 WAKTES 324

RESULT 45
Q9AMJ2_STRAT PRELIMINARY; PRT; 404 AA.
ID Q9AMJ2_STRAT
AC Q9AMJ2;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-FEB-2005 (TReMBLrel. 29, Last annotation update)
DE Putative ketosynthase Sim2 (Sim3).
GN Name=Sim2; Synonyms=sim3;
OS Streptomyces antibioticus;
OC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomycetes.
OX NCBI_TaxID=1890;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Tue6040;
RX MEDLINE=21955989; PubMed=11959542;
RX DOI=10.1128/AAC.46.5.1174-1182.2002;
RA Trefer A., Pelzer S., Schimana J., Stockert S., Bihlmaier C.,
RA Fiedler H.P., Welzel K., Vence A., Bechtold A.;
RT "Biosynthetic gene cluster of simocyclinone, a natural multihybrid
antibiotic.";

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RL Antimicrob. Agents Chemother. 46:1174-1182(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Tu 6040;
RA MEDLINE=22109063; PubMed=12115055; DOI=10.1007/s00203-002-0429-z;
RX Galm U., Schimane J., Fiedler H.P., Schmidt J., Li S.M., Heide L.,
RT "Cloning and analysis of the simocyclonone biosynthetic gene cluster
of Streptomyces antibioticus Tu 6040."
RL Arch. Microbiol. 178:102-114(2002).
DR EMBL; AF324838; AAK06785.1; -; Genomic_DNA.
DR EMBL; AF322256; AAL1581.1; -; Genomic_DNA.
DR HSP; P73283; 1ESM.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
DR InterPro; IPR000794; Ketoacyl_synth.
DR Pfam; PF00109; ketoacyl-synt_1.
DR Pfam; PF02801; ketoacyl-synt_C; 1.
DR Transferase.
KW SEQUENCE
SQ
Query Match 81.6%; Score 31; DB 2; Length 404;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WASTRE 6
Db 24 WASTRE 29

RESULT 46
QSDPA7 SCHJA PRELIMINARY; PRT; 406 AA.
AC QSDPA7;
DT 10-MAY-2005 (TREMBlrel. 30, Created)
DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)
DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)
DE Hypothetical protein.
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigoidida;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Han Z.;
RT "The full-length cDNA sequences of Schistosoma japonicum genes.";
RL Submitted (NCU-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY813767; AAW25499.1; -; mRNA.
DR InterPro; IPR001283; Allrgn_V5/TpX1.
DR Pfam; PF00188; SCP; 2.
DR PRINTS; PR00837; V5TPXLIKE.
DR SMART; SM00198; SCP; 2.
DR Hypothetical protein.
KW SEQUENCE
SQ
Query Match 81.6%; Score 31; DB 2; Length 406;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WASTRE 6
Db 111 WASTRE 116

RESULT 47
Q5Z6K2 ORYSA PRELIMINARY; PRT; 460 AA.
AC Q5Z6K2;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 01-FEB-2005 (TREMBlrel. 29, Last annotation update)
DE Putative UDP-glucose glucosyltransferase.
GN Name=OSUNBA0084K06.41; Synonyms=P0662B01.3;
OS Oryza sativa (japonica cultivar-group).
```

```
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Katayose Y.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 6, BAC
clone:OSUNBA0084K06.";
RL Submitted (UTN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 6, PAC
clone:P0662B01.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -1 SIMILARITY: Belongs to the UDP-glucosyltransferase family.
DR EMBL; AP005387; BAD54417.1; -; Genomic_DNA.
DR EMBL; AP003491; BAD68423.1; -; Genomic_DNA.
DR Gramene; Q5Z6K2; -.
DR GO; GO:0016758; F:transferase activity, transferring hexosyl . . .; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002213; UDP_glucos_trans.
DR Pfam; PF00201; UDPGT_1.
DR PROSITE; PS00375; UDPGT_1.
DR Glycoeryltransferase; Transferase.
KW SEQUENCE
SQ
Query Match 81.6%; Score 31; DB 2; Length 460;
Best Local Similarity 85.7%; Pred. No. 5.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WASTRES 7
Db 418 WASTRES 424

RESULT 48
Q6AVV5 ORYSA PRELIMINARY; PRT; 466 AA.
AC Q6AVV5;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Isoamylase N-terminal domain containing protein.
GN Name=OSUNB0024N19.10;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
RA Overton II L.L., Taitlin T., Kim M.M., Bera J.J., Jin S.S.,
RA Padroch D.W., Tallon L.J., Koo H., Zismann V., Hsieh J., Blunt S.,
RA Vanaken S.S., Riedmuller S.B., Utecherack T.T., Feldlym T.V.,
RA Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
RA White O., Salzberg S.L., Fraser C.M.;
RT "Oryza sativa chromosome 3 BAC OSUNB0024N19 genomic sequence.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Buell R.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC092779; AAT85062.1; -; Genomic_DNA.
DR Gramene; Q6AVV5; -.
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR004193; Glyco_hydro_13N.
DR Pfam; PF02922; Isoamylase_N_1.
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SQ
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 DB 170 WASSRET 176

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 DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)
 DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)
 DE Hypothetical protein.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
 OC NCBI_TaxID=3702;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Totsuki Y., Seki M., Ishida J., Nakajima M., Enju A., Kamiya A.,
 RA Narusaka M., Shin-I T., Nakagawa M., Sakamoto N., Oishi K., Kohara Y.,
 RA Kobayashi M., Toyoda A., Sakaki Y., Sakurai T., Iida K., Akiyama K.,
 RA Satou M., Toyoda T., Konagaya A., Carninci P., Kawai J.,
 RA Hayashizaki Y., Shinozaki K.,
 RT "Large-scale analysis of RIKEN Arabidopsis full-length (RAFL) cDNAs";
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK222330; BAD95408.1; -; mRNA.
 KM Hypothetical protein.
 SQ SEQUENCE 478 AA; 54805 MW; 5514B9BDBFA6977 CRC64;

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 DT 01-FEB-2005 (TREMBlrel. 29, Last sequence update)
 DT 01-FEB-2005 (TREMBlrel. 29, Last annotation update)
 DE Putative biotin carboxylase 2 (RC 6.3.4.14).
 GN Name-acc2; Ordered locus names=BR3337;
 OS Bacteroides fragilis (Strain ATCC 25285 / NCTC 9343).
 OC Bacteria; Bacteroidetes; Bacteroidales (class); Bacteroidales;
 OC Bacteroidaceae; Bacteroides.
 OC NCBI_TaxID=272559;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX PubMed=15746427; DOI=10.1126/science.1107008;
 RA Cerdano-Tarraga A.-M., Patrick S., Crossman L.C., Blakely G.,
 RA Abratt V., Lennard N., Poxton I., Duerden B., Harris B., Quail M.A.,
 RA Barron A., Clark L., Corton C., Doggett J., Holden M.T.G., Larke N.,
 RA Line A., Lord A., Norbertczak H., Ormond D., Price C.,
 RA Rabinowitsch E., Woodward J., Barrett B.G., Parkhill J.,
 RT "Extensive DNA inversions in the B. fragilis genome control variable
 gene expression."
 RL Science 307:1463-1465(2005).
 CC -1- FUNCTION: This protein is a component of the acetyl coenzyme A
 carboxylase complex; first, biotin carboxylase catalyzes the
 carboxylation of the carrier protein and then the transcarboxylase
 transfers the carboxyl group to form malonyl-CoA (By similarity).
 CC -1- CATALYTIC ACTIVITY: ATP + biotin-carboxyl-carrier protein + CO(2)

CC = ADP + phosphate + carboxybiotin-carboxyl-carrier protein.
 CC -1- PATHWAY: long-chain fatty acid biosynthesis; first step.
 CC -1- SUBUNIT: Acetyl-CoA carboxylase is a heterohexamer of biotin
 CC carboxyl carrier protein, biotin carboxylase and the two subunits
 CC of carboxyl transferase in a 2:2 complex (By similarity).
 DR EMBL; CR626927; CAH09031.1; -; Genomic_DNA.
 DR InterPro; IPR004549; AccC.
 DR InterPro; IPR011761; ATP_GRASP.
 DR InterPro; IPR005482; Biotin.
 DR InterPro; IPR005481; Cbase_L_N_C.
 DR InterPro; IPR005479; Cbase_D2_ATP_bd.
 DR Pfam; PF02785; Biotin_carb_C; 1.
 DR Pfam; PF02289; CPSase_L_chain; 1.
 DR Pfam; PF02766; CPSase_L_D2; 1.
 DR TIGRFAMs; TIGR00514; accC; 1.
 DR PROSITE; PSS0975; ATP_GRASP; 1.
 DR PROSITE; PSS0979; BC; 1.
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 DR PROSITE; PS00867; CPSASE_2; UNKNOWN_1.
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 KW Lipid synthesis; Nucleotide-binding
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Query Match 81.6%; Score 31; DB 2; Length 504;
 Best Local Similarity 83.3%; Pred. No. 6.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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 DB 392 WATTRE 397

Search completed: May 4, 2006, 13:08:57
 Job time : 113.556 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 4, 2006, 13:09:53 ; Search time 15.7778 Seconds
(without alignments)
36.680 Million cell updates/sec

Title: US-10-700-632-5
Perfect score: 38
Sequence: 1 WASTRES 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :

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4: /cgn2_6/ptodata/1/1aa/PCITUS_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	38	100.0	7	1	US-08-360-125-20 Sequence 20, Appl
2	38	100.0	7	1	US-08-450-578-20 Sequence 20, Appl
3	38	100.0	7	1	US-09-017-628-20 Sequence 20, Appl
4	38	100.0	7	1	US-09-014-880-20 Sequence 20, Appl
5	38	100.0	7	2	US-07-987-264-5 Sequence 20, Appl
6	38	100.0	7	2	US-08-450-363-20 Sequence 20, Appl
7	38	100.0	7	2	US-09-563-222C-15 Sequence 15, Appl
8	38	100.0	7	2	US-09-563-222C-17 Sequence 17, Appl
9	38	100.0	7	2	US-09-467-903-20 Sequence 20, Appl
10	38	100.0	7	2	US-09-830-748B-8 Sequence 8, Appl
11	38	100.0	7	2	US-09-627-896B-18 Sequence 18, Appl
12	38	100.0	7	2	US-09-339-595A-18 Sequence 18, Appl
13	38	100.0	7	2	US-10-146-305-10 Sequence 10, Appl
14	38	100.0	7	4	PCT-US93-08435-24 Sequence 24, Appl
15	38	100.0	7	4	PCT-US93-08435-37 Sequence 37, Appl
16	38	100.0	7	4	PCT-US93-08435-41 Sequence 41, Appl
17	38	100.0	94	2	US-09-905-243-60 Sequence 56, Appl
18	38	100.0	98	2	US-10-330-613A-56 Sequence 56, Appl
19	38	100.0	101	2	US-09-627-896B-28 Sequence 28, Appl
20	38	100.0	101	2	US-10-194-975-89 Sequence 89, Appl
21	38	100.0	101	2	US-10-330-613A-55 Sequence 55, Appl
22	38	100.0	109	1	US-08-308-494A-23 Sequence 23, Appl
23	38	100.0	110	2	US-08-957-001B-5 Sequence 5, Appl
24	38	100.0	110	2	US-08-957-001B-24 Sequence 24, Appl
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26	38	100.0	110	2	US-09-496-301-24 Sequence 24, Appl
27	38	100.0	112	1	US-07-942-245-30 Sequence 30, Appl

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31	38	100.0	113	1	US-08-690-102A-2 Sequence 2, Appl
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33	38	100.0	113	2	US-08-483-749A-16 Sequence 16, Appl
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100	38	100.0	135	2	US-08-812-586-46 Sequence 46, Appl

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103	38	100.0	147	1	US-08-860-174A-8	Sequence 8, Appl	176	33	86.8	113	2	US-10-040-997-14	Sequence 14, Appl
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133	38	100.0	301	1	US-09-188-082-14	Sequence 14, Appl	206	33	86.8	246	2	US-09-791-540-2	Sequence 2, Appl
134	38	100.0	301	2	US-09-364-088-14	Sequence 14, Appl	207	33	86.8	246	1	US-08-323-445A-6	Sequence 6, Appl
135	38	100.0	301	2	US-09-102-716-14	Sequence 14, Appl	208	33	86.8	248	1	US-08-515-903A-6	Sequence 6, Appl
136	38	100.0	342	2	US-08-828-741B-6	Sequence 14, Appl	209	33	86.8	248	4	PCT-US95-12840-6	Sequence 6, Appl
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142	38	100.0	456	2	US-09-495-880A-11	Sequence 11, Appl	215	33	86.8	257	2	US-09-985-442-2	Sequence 2, Appl
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ALIGNMENTS

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Sequence 2, Appl
Sequence 3, Appl
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RESULT 1
US-08-360-125-20
; Sequence 20, Application US/08360125
; Patent No. 5767246
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA
; APPLICANT: Toshiaki TAGAWA
; APPLICANT: Yoko HIRAKAWA
; APPLICANT: No. 5767246hiko ITO
; APPLICANT: Kazuhiro NAGAIKE
; TITLE OF INVENTION: Human Monoclonal Antibody
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESSES:
; ADDRESSES: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20003
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,125
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/905,534
; FILING DATE: June 29, 1992
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
CELL TYPE: Hybridoma producing human antibody G4H
; CELL LINE:
; ORGANELLER:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-08-360-125-20

Query Match 100.0%; Score 38; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 WASTRES 7
RESULT 2
US-08-450-578-20
; Sequence 20, Application US/08450578
; Patent No. 5837845
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA
; APPLICANT: Toshiaki TAGAWA
; APPLICANT: Yoko HIRAKAWA
; APPLICANT: No. 5837845hiko ITO
; APPLICANT: Kazuhiro NAGAIKE
; TITLE OF INVENTION: Human Monoclonal Antibody
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESSES:
; ADDRESSES: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.

COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,578
FILING DATE: May 25, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/360,125
FILING DATE: December 20, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
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TOPOLOGY: linear
MOLECULE TYPE: protein
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ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
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STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Hybridoma producing human antibody GAH
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURES:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
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RESULT 3
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Sequence 20, Application US/09017628
Patent No. 5990287
GENERAL INFORMATION:
APPLICANT: HOSOKAWA, Saiko
APPLICANT: TAGAWA, Toshiaki
APPLICANT: HIRAKAWA, Yoko
APPLICANT: ITO, No. 5990287iniko
APPLICANT: NAGAIKE, Kazuhito
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO
FILE REFERENCE: 177/527361KH
CURRENT APPLICATION NUMBER: US/09/017,628
EARLIER FILING DATE: 1998-02-02
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 20
LENGTH: 7
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Hybridoma producing human antibody GAH
US-09-017-628-20

Query Match 100.0%; Score 38; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WASTRES 7
| | | | |
Db 1 WASTRES 7

RESULT 4
US-09-014-880-20
Sequence 20, Application US/09014880
Patent No. 5990297
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA et al.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY
BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., #800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/014,880
FILING DATE: January 28, 1998
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/450,578
FILING DATE: May 25, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/360,125

;; FILING DATE: December 20, 1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/905,534
;; FILING DATE: June 29, 1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Warren M. Cheek, Jr.
;; REGISTRATION NUMBER: 33,367
;; REFERENCE/DOCKET NUMBER:
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-721-8200
;; TELEFAX: 202-721-8250
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 20:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 7 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; ORIGINAL SOURCE:
;; CELL TYPE: Hybridoma producing human antibody GAH
;; US-09-014-880-20

Query Match 100.0%; Score 38; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WASTRES 7
Db 1 WASTRES 7

RESULT 5
US-07-987-264-5
; Sequence 5, Application US/07987264
; Patent No. 6204366
; GENERAL INFORMATION:
; APPLICANT: VERHOEVEN, MARTINE ELISA
; TITLE OF INVENTION: SPECIFIC BINDING AGENTS
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/987,264
; FILING DATE: 08-MAR-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9019553.8
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB PCT/GB91/01511
; FILING DATE: 05-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 200232/P3095USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids

;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-07-987-264-5

Query Match 100.0%; Score 38; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WASTRES 7
Db 1 WASTRES 7

RESULT 6
US-08-450-363-20
; Sequence 20, Application US/08450363
; Patent No. 6436434
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA
; APPLICANT: Toshiaki TAGAWA
; APPLICANT: Yoko HIRAKAWA
; APPLICANT: No. 6436434/iko ITO
; APPLICANT: Kazuhiro NAGAIKE
; TITLE OF INVENTION: Human Monoclonal Antibody
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
; TITLE OF INVENTION: Cell Membrane
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Penack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,363
; FILING DATE: May 25, 1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/360,125
; FILING DATE: December 20, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/905,534
; FILING DATE: June 29, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:

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DEVELOPMENTAL STAGE:
HAPOTYPE:
TISSUE TYPE:
CELL TYPE: Hybridoma producing human antibody GAH
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-450-363-20
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Query Match          100.0%; Score 38; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 WASTRES 7
    |||||
DB 1 WASTRES 7
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```
RESULT 7
US-09-563-222C-15
; Sequence 15, Application US/09563222C
; Patent No. 6696620
; GENERAL INFORMATION:
; APPLICANT: EPICYTE PHARMACEUTICALS, INC.
; APPLICANT: HIATT, ANDREW C.
; APPLICANT: HEIN, MICH B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
; FILE REFERENCE: 068904-0501
; CURRENT APPLICATION NUMBER: US/09/563,222C
; CURRENT FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: PCT/US01/14349
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/563,222
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-563-222C-15
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Query Match          100.0%; Score 38; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 WASTRES 7
    |||||
DB 1 WASTRES 7
```

```
RESULT 8
US-09-563-222C-27
; Sequence 27, Application US/09563222C
; Patent No. 6696620
; GENERAL INFORMATION:
; APPLICANT: EPICYTE PHARMACEUTICALS, INC.
; APPLICANT: HIATT, ANDREW C.
; APPLICANT: HEIN, MICH B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
; FILE REFERENCE: 068904-0501
; CURRENT APPLICATION NUMBER: US/09/563,222C
; CURRENT FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: PCT/US01/14349
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/563,222
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-563-222C-27
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Query Match          100.0%; Score 38; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY 1 WASTRES 7
    |||||
DB 1 WASTRES 7
```

```
RESULT 9
US-09-467-903-20
; Sequence 20, Application US/09467903
; Patent No. 6787153
; GENERAL INFORMATION:
; APPLICANT: SAIKO HOSOKAWA
; APPLICANT: TOSHIKI TAGAWA
; APPLICANT: YOKO HIRAKAWA
; APPLICANT: NO. 6787153HIKO ITO
; APPLICANT: KAZUHIRO NAGAIKE
; TITLE OF INVENTION: Human Monoclonal Antibody
; Specifically Binding to Surface Antigen of Cancer
; Cell Membrane
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Wenderoth, Lind & Ponack
; STREET: 2033 K Street, N.W., #800
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/467,903
; FILING DATE: 21-Dec-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/450,363
; FILING DATE: May 25, 1995
; APPLICATION NUMBER: 08/360,125
; FILING DATE: December 20, 1994
; APPLICATION NUMBER: 07/905,534
; FILING DATE: June 29, 1992
; APPLICATION NUMBER: JP158859/1991
; FILING DATE: June 28, 1991
```

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; APPLICATION NUMBER: JP158860/1991
; FILING DATE: June 28, 1991
; APPLICATION NUMBER: JP158861/1991
; FILING DATE: June 28, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-721-8200
; TELEFAX: <Unknown>
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: <Unknown>
; ANTI-SENSE: <Unknown>
; ORIGINAL SOURCE:
; ORGANISM: <Unknown>
; STRAIN: <Unknown>
; INDIVIDUAL ISOLATE: <Unknown>
; DEVELOPMENTAL STAGE: <Unknown>
; HAPLOTYPE: <Unknown>
; TISSUE TYPE: <Unknown>
; CELL TYPE: Hybridoma producing human antibody GAH
; CELL LINE: <Unknown>
; ORGANELLE: <Unknown>
; IMMEDIATE SOURCE:
; LIBRARY: <Unknown>
; CLONE: <Unknown>
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: <Unknown>
; MAP POSITION: <Unknown>
; UNITS: <Unknown>
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-467-903-20

Query Match          100.0%; Score 38; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
   |||||
Db 1 WASTRES 7

RESULT 10
US-09-830-748B-8
; Sequence 8, Application US/09830748B
; Patent No. 6818749
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as represented by The
```

```

; APPLICANT: Secretary of the Department of Health and Human Services
; APPLICANT: Kashimiri, Syed V.S.
; APPLICANT: Padian, Eduardo A.
; APPLICANT: Jeffrey, Schlom
; TITLE OF INVENTION: VARIANTS OF HUMANIZED ANTI-CARCINOMA MONOCLONAL ANTIBODY CC49
; FILE REFERENCE: 4239-61725
; CURRENT APPLICATION NUMBER: US/09/830,748B
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: PCT/ US99/25552
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/106,757
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: US 60/106,534
; PRIOR FILING DATE: 1998-10-31
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-830-748B-8

Query Match          100.0%; Score 38; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
   |||||
Db 1 WASTRES 7

RESULT 11
US-09-627-896B-18
; Sequence 18, Application US/09627896B
; Patent No. 6827934
; GENERAL INFORMATION:
; APPLICANT: CO, MAN SUNG
; APPLICANT: VASQUEZ, MAXIMILIANO
; APPLICANT: CARRENO, BEATRIZ
; APPLICANT: CELNIKER, ABBIE CHERYL
; APPLICANT: COLLINS, MARY
; APPLICANT: GOLDMAN, SAMUEL
; APPLICANT: GRAY, GARY S.
; APPLICANT: KNIGHT, ANDREA
; APPLICANT: O'HARA, DENISE
; APPLICANT: RUP, BONITA
; APPLICANT: VELDMAN, GERTRUIDA M.
; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
; FILE REFERENCE: 08702,0081-01000
; CURRENT APPLICATION NUMBER: US/09/627,896B
; CURRENT FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDR2 of humanized
; OTHER INFORMATION: murine anti-human B7-2 light chain
US-09-627-896B-18

Query Match          100.0%; Score 38; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
   |||||
Db 1 WASTRES 7

RESULT 12
```


US-09-339-596A-18
; Sequence 18, Application US/09339596A
; Patent No. 6913747
; GENERAL INFORMATION:
; APPLICANT: CO, Man Sung
; APPLICANT: Vasquez, Maximiliano
; APPLICANT: Carreno, Beatriz
; APPLICANT: Celinkner, Abbie Cheryl
; APPLICANT: Collins, Mary
; APPLICANT: Goldman, Samuel
; APPLICANT: Gray, Gary S.
; APPLICANT: Knight, Andrea
; APPLICANT: O'Hara, Denise
; APPLICANT: Rup, Bonita
; APPLICANT: Veldman, Geertuida M.
; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B72 MOLECULES AND METHODS
; FILE REFERENCE: 08702.0082-00000
; CURRENT APPLICATION NUMBER: US/09/339,596A
; CURRENT FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 09/249,011
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CDR2 of humanized murine anti-human B7-2 light chain
US-09-339-596A-18

Query Match 100.0%; Score 38; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WASTRES 7
Db 1 WASTRES 7

RESULT 13
US-10-146-305-10
; Sequence 10, Application US/10146305
; Patent No. 6939956
; GENERAL INFORMATION:
; APPLICANT: YIHAN CORPORATION
; TITLE OF INVENTION: A VARIABLE REGION OF THE MONOCLONAL ANTIBODY AGAINST THE HBV
; FILE REFERENCE: OVI17440
; CURRENT APPLICATION NUMBER: US/10/146,305
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: KR 10-2001-26634
; PRIOR FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: KopatentIn 1.71
; SEQ ID NO 10
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-146-305-10

Query Match 100.0%; Score 38; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WASTRES 7
Db 1 WASTRES 7

RESULT 14
PCT-US93-08435-24

; Sequence 24, Application PC/TUS9308435
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham, Corporation
; APPLICANT: U. S. Government, Secretary of
; APPLICANT: the Navy
; APPLICANT: U. S. Government, Secretary of
; APPLICANT: the Army
; TITLE OF INVENTION: Novel Antibodies for Confering Passive
; TITLE OF INVENTION: Immunity Against Infection by a Pathogen in Man
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Box 457, 321 Norristown Road
; CITY: Spring House
; STATE: PA
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08435
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/941,654
; FILING DATE: 09-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: SBC P50107
; TELEPHONE: (215) 540-9200
; TELEFAX: (215) 540-5818
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
PCT-US93-08435-24

Query Match 100.0%; Score 38; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WASTRES 7
Db 1 WASTRES 7

RESULT 15
PCT-US93-08435-37
; Sequence 37, Application PC/TUS9308435
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham, Corporation
; APPLICANT: U. S. Government, Secretary of
; APPLICANT: the Navy
; APPLICANT: U. S. Government, Secretary of
; APPLICANT: the Army
; TITLE OF INVENTION: Novel Antibodies for Confering Passive
; TITLE OF INVENTION: Immunity Against Infection by a Pathogen in Man
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Box 457, 321 Norristown Road
; CITY: Spring House
; STATE: PA
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:

RESULT 14
PCT-US93-08435-24

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08435
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,654
FILING DATE: 09-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: SBC P50107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 540-9200
TELEFAX: (215) 540-5818
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
PCT-US93-08435-37

Query Match 100.0%; Score 38; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
Db 1 WASTRES 7

RESULT 16
PCT-US93-08435-41
Sequence 41, Application PC/TUS9308435
GENERAL INFORMATION:
APPLICANT: SmithKline Beecham, Corporation
APPLICANT: U. S. Government, Secretary of
APPLICANT: the Navy
APPLICANT: U. S. Government, Secretary of
APPLICANT: the Army
TITLE OF INVENTION: Novel Antibodies for Confering Passive
TITLE OF INVENTION: Immunity Against Infection by a Pathogen in Man
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Box 457, 321 Norristown Road
CITY: Spring House
STATE: PA
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08435
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,654
FILING DATE: 09-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: SBC P50107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 540-9200
TELEFAX: (215) 540-5818

INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
PCT-US93-08435-41

Query Match 100.0%; Score 38; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
Db 1 WASTRES 7

RESULT 17
US-09-905-243-60
Sequence 60, Application US/09905243
Patent No. 6936698
GENERAL INFORMATION:
APPLICANT: Taylor, Alexander H
TITLE OF INVENTION: Monoclonal Antibodies with Reduced
TITLE OF INVENTION: Immunogenicity
FILE REFERENCE: P50770
CURRENT APPLICATION NUMBER: US/09/905,243
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/300,970
PRIOR FILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 97
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 60
LENGTH: 94
TYPE: PRT
ORGANISM: Macaca cynomolgus
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (24)...(40)
OTHER INFORMATION: CDRI
NAME/KEY: DOMAIN
LOCATION: (56)...(62)
OTHER INFORMATION: CDRII
US-09-905-243-60

Query Match 100.0%; Score 38; DB 2; Length 94;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
Db 56 WASTRES 62

RESULT 18
US-10-330-613A-56
Sequence 56, Application US/10330613A
Patent No. 6924360
GENERAL INFORMATION:
APPLICANT: Guada, Jean
TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
FILE REFERENCE: ABGENIX.022A
CURRENT APPLICATION NUMBER: US/10/330,613A
CURRENT FILING DATE: 2002-12-26
PRIOR APPLICATION NUMBER: 60/346299
PRIOR FILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 90
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 56
LENGTH: 98
TYPE: PRT
ORGANISM: Homo sapiens
US-10-330-613A-56

Query Match 100.0%; Score 38; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WASTRES 7
|||||
Db 55 WASTRES 61

RESULT 19

US-09-627-896B-28
; Sequence 28, Application US/09627896B
; Patent No. 6827934
; GENERAL INFORMATION:
; APPLICANT: CO, MAN SUNG
; APPLICANT: VASQUEZ, MAXIMILIANO
; APPLICANT: CARRERO, BEATRIZ
; APPLICANT: CELINKER, ABIE CHERYL
; APPLICANT: COLLINS, MARY
; APPLICANT: GOLDMAN, SAMUEL
; APPLICANT: GRAY, GARY S.
; APPLICANT: KNIGHT, ANDREA
; APPLICANT: O'HARA, DENISE
; APPLICANT: RUP, BONITA
; APPLICANT: VELDMAN, GERTTRUIDA M.
; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
; FILE REFERENCE: 08702.0081-01000
; CURRENT APPLICATION NUMBER: US/09/627,896B
; CURRENT FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 28
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: H2F light chain variable region
US-09-627-896B-28

Query Match 100.0%; Score 38; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WASTRES 7
|||||
Db 56 WASTRES 62

RESULT 20

US-10-194-975-89
; Sequence 89, Application US/10194975
; Patent No. 6881557
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 89
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-89

Query Match 100.0%; Score 38; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WASTRES 7
|||||
Db 56 WASTRES 62

RESULT 21

US-10-330-613A-55
; Sequence 55, Application US/10330613A
; Patent No. 6924360
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613A
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-330-613A-55

Query Match 100.0%; Score 38; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WASTRES 7
|||||
Db 56 WASTRES 62

RESULT 22

US-08-308-494A-23
; Sequence 23, Application US/08308494A
; Patent No. 5959083
; GENERAL INFORMATION:
; APPLICANT: Bosslet, Klaus
; APPLICANT: Seeman, Gerhard
; TITLE OF INVENTION: Tetravalent Bisppecific Receptors, The
; TITLE OF INVENTION: Preparation and Use Thereof
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSER: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/308,494A
; FILING DATE: 21-SEP-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/891,739
; FILING DATE: 01-JUN-1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P4118120.4
; FILING DATE: 03-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Kulik, David J.
; REGISTRATION NUMBER: 36,576
; REFERENCE/DOCKET NUMBER: 05552-1186-02000

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-308-494A-23

Query Match 100.0%; Score 38; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 3.7; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
|||||
DB 53 WASTRES 59

RESULT 23
US-08-957-001B-5
Sequence 5, Application US/08957001B
Patent No. 6228621
GENERAL INFORMATION:
APPLICANT: Williams, William V.
APPLICANT: Madalo, Michael
APPLICANT: Weiner, David B.
TITLE OF INVENTION: IMPROVED VACCINES
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSER: Woodcock Washburn Kurtz Mackiewicz & No. 6228621iris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: windows
SOFTWARE: wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/957,001B
FILING DATE: 23-OCT-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,592
FILING DATE: 23-OCT-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: UPN-3303
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: amino acid
TOPOLOGY: both
MOLECULE TYPE: peptide
US-08-957-001B-5

Query Match 100.0%; Score 38; DB 2; Length 110;
Best Local Similarity 100.0%; Pred. No. 3.7; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
|||||
DB 56 WASTRES 62

RESULT 24
US-08-957-001B-24
Sequence 24, Application US/08957001B
Patent No. 6228621
GENERAL INFORMATION:
APPLICANT: Williams, William V.
APPLICANT: Madalo, Michael
APPLICANT: Weiner, David B.
TITLE OF INVENTION: IMPROVED VACCINES
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSER: Woodcock Washburn Kurtz Mackiewicz & No. 6228621iris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: windows
SOFTWARE: wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/957,001B
FILING DATE: 23-OCT-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,592
FILING DATE: 23-OCT-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: UPN-3303
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3439
TELEFAX: 215-568-3100
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-957-001B-24

Query Match 100.0%; Score 38; DB 2; Length 110;
Best Local Similarity 100.0%; Pred. No. 3.7; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
|||||
DB 56 WASTRES 62

RESULT 25
US-09-496-301-5
Sequence 5, Application US/09496301
Patent No. 6248565
GENERAL INFORMATION:
APPLICANT: Williams, William V.
APPLICANT: Madalo, Michael
APPLICANT: Weiner, David B.
TITLE OF INVENTION: IMPROVED VACCINES
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSER: Woodcock Washburn Kurtz Mackiewicz & No. 6248565iris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19103

```
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: windows
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/496,301
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/957,001
FILING DATE: 23-OCT-1997
APPLICATION NUMBER: US 60/029,592
FILING DATE: 23-OCT-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: UPN-3303
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: amino acid
TOPOLOGY: both
MOLECULE TYPE: peptide
US-09-496-301-5
```

```
Query Match      100.0%; Score 38; DB 2; Length 110;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

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Qy      1 WASTRES 7
        |||||
Db      56 WASTRES 62
```

```
RESULT 26
US-09-496-301-24
Sequence 24, Application US/09496301
Patent No. 6248565
GENERAL INFORMATION:
APPLICANT: Williams, William V.
APPLICANT: Madato, Michael
APPLICANT: Weiner, David B.
TITLE OF INVENTION: IMPROVED VACCINES
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSER: Woodcock Washburn Kurtz Mackiewicz & No. 6248565rls
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: windows
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/496,301
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/957,001
FILING DATE: 23-OCT-1997
APPLICATION NUMBER: US 60/029,592
FILING DATE: 23-OCT-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
```

```
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: UPN-3303
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-496-301-24
```

```
Query Match      100.0%; Score 38; DB 2; Length 110;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 WASTRES 7
        |||||
Db      56 WASTRES 62
```

```
RESULT 27
US-07-942-245-30
Sequence 30, Application US/07942245
Patent No. 5639641
GENERAL INFORMATION:
APPLICANT: PEDERSEN, Jan T.
APPLICANT: SEARLE, Stephen M.J.
APPLICANT: REES, Anthony R.
APPLICANT: ROGUSKA, Michael A.
APPLICANT: GUILD, Braydon C.
TITLE OF INVENTION: SURFACE RESIDUE VENERING OF RODENT
NUMBER OF SEQUENCES: 522
CORRESPONDENCE ADDRESS:
ADDRESSER: Sughrie, Mion, Zimm, Macpeak & Seas
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: United States
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HP 9000/700 Workstation
OPERATING SYSTEM: UNIX
SOFTWARE: In house
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/942,245
FILING DATE: 09-SEP-1992
CLASSIFICATION: 530
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-942-245-30
```

```
Query Match      100.0%; Score 38; DB 1; Length 112;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 WASTRES 7
        |||||
Db      56 WASTRES 62
```

```
RESULT 28
```

US-07-916-098A-15
; Sequence 15, Application US/07916098A
; Patent No. 5871732
; GENERAL INFORMATION:
; APPLICANT: BURKLY, LINDA C.
; APPLICANT: CHISHOLM, PATRICIA L.
; APPLICANT: THOMAS, DAVID W.
; APPLICANT: ROSA, MARGARET D.
; APPLICANT: ROSA, JOSEPH J.
; TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN
; TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ALLEGRETTI & MITCOFF, LTD.
; STREET: 10 SOUTH WACKER DRIVE
; CITY: CHICAGO
; STATE: ILLINOIS
; COUNTRY: U.S.A.
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/916,098A
; FILING DATE: JULY 24, 1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/08843
; FILING DATE: NO. 5871732ember 27, 1991
; CLASSIFICATION: 424
; APPLICATION NUMBER: 07/618,542
; FILING DATE: NO. 5871732ember 27, 1990
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: JOHN J. MC DONNELL
; REGISTRATION NUMBER: 26,949
; REFERENCE/DOCKET NUMBER: 92,310-G
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 715-1000
; TELEFAX: (312) 715-1234
; TELEX: 910/221-5317
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-916-098A-15

Query Match 100.0%; Score 38; DB 1; Length 112;
Best Local Similarity 100.0%; Pred.No.3.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WASTRES 7
Db 56 WASTRES 62

RESULT 29
US-08-435-516-4
; Sequence 4, Application US/08435516
; Patent No. 6500931
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANIZED ANTIBODIES TO FC RECEPTORS FOR
; TITLE OF INVENTION: IMMUNOBULOBULIN G ON HUMAN MONONUCLEAR PHAGOCYTES
; NUMBER OF SEQUENCES: 28
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,516
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: UK 92 23377.4; PCT/US93/10384
; FILING DATE: 04-NOV-1992; -02-NOV-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MX1-013
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: Internal
; US-08-435-516-4

Query Match 100.0%; Score 38; DB 2; Length 112;
Best Local Similarity 100.0%; Pred.No.3.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WASTRES 7
Db 56 WASTRES 62

RESULT 30
US-08-435-516-28
; Sequence 28, Application US/08435516
; Patent No. 6500931
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANIZED ANTIBODIES TO FC RECEPTORS FOR
; TITLE OF INVENTION: IMMUNOBULOBULIN G ON HUMAN MONONUCLEAR PHAGOCYTES
; NUMBER OF SEQUENCES: 28
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,516
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: UK 92 23377.4; PCT/US93/10384
; FILING DATE: 04-NOV-1992; -02-NOV-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MX1-013
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: Internal
; US-08-435-516-28

Query Match 100.0%; Score 38; DB 2; Length 112;

Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
|||||
Db 56 WASTRES 62

RESULT 31

US-08-690-102A-2

; Sequence 2, Application US/08690102A
; Patent No. 5789554
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR B-CELL LYMPHOMA AND LEUKEMIA CELLS
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/690,102A
; FILING DATE: 01-JUL-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/289,576
; FILING DATE: 12-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 18733/463/IMIN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-690-102A-2

Query Match 100.0%; Score 38; DB 1; Length 113;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
|||||
Db 56 WASTRES 62

RESULT 32

US-08-690-102A-6

; Sequence 6, Application US/08690102A
; Patent No. 5789554
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR B-CELL LYMPHOMA AND LEUKEMIA CELLS
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/690,102A
; FILING DATE: 01-JUL-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/289,576
; FILING DATE: 12-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 18733/463/IMIN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-690-102A-6

Query Match 100.0%; Score 38; DB 1; Length 113;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
|||||
Db 56 WASTRES 62

RESULT 33

US-08-483-749A-16

; Sequence 16, Application US/08483749A
; Patent No. 6054561
; GENERAL INFORMATION:
; APPLICANT: RING, DAVID B.
; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
; TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: INTELLECTUAL PROPERTY - R440, PO BOX 8097
; CITY: EMERYVILLE
; STATE: CA
; COUNTRY: USA
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,749A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: SAVERIDE, PAUL B.
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0508,008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2585
; TELEFAX: (510) 655-3542

;; INFORMATION FOR SEQ ID NO: 16;
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 113 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-483-749A-16

Query Match 100.0%; Score 38; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WASTRES 7
|||||
Db 56 WASTRES 62

RESULT 34
US-09-127-902-2
; Sequence 2, Application US/09127902
; Patent No. 6187287
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR B-CELL LYMPHOMA AND LEUKEMIA CELLS
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/127,902
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/690,102
; FILING DATE: 01-JUL-1996
; APPLICATION NUMBER: US 08/289,576
; FILING DATE: 12-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 18733/463/IMIN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-127-902-2

Query Match 100.0%; Score 38; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WASTRES 7
|||||
Db 56 WASTRES 62

RESULT 35

US-09-127-902-6
; Sequence 6, Application US/09127902
; Patent No. 6187287
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR B-CELL LYMPHOMA AND LEUKEMIA CELLS
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/127,902
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/690,102
; FILING DATE: 01-JUL-1996
; APPLICATION NUMBER: US 08/289,576
; FILING DATE: 12-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 18733/463/IMIN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 6;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-127-902-6

Query Match 100.0%; Score 38; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WASTRES 7
|||||
Db 56 WASTRES 62

RESULT 36
US-09-155-107-2
; Sequence 2, Application US/09155107
; Patent No. 6254868
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; APPLICANT: OU, Zhengxing
; TITLE OF INVENTION: GLYCOSYLATED HUMANIZED B-CELL SPECIFIC ANTIBODIES
; FILE REFERENCE: 018733/0879
; CURRENT APPLICATION NUMBER: US/09/155,107
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: WO PCT/US97/04196
; EARLIER FILING DATE: 1997-03-19
; EARLIER APPLICATION NUMBER: US 60/013,709
; EARLIER FILING DATE: 1996-03-20
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2

LENGTH: 113
TYPE: PRT
ORGANISM: Murine
US-09-155-107-2

Query Match 100.0%; Score 38; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
|||||
Db 56 WASTRES 62

RESULT 37
US-09-155-107-6
Sequence 6, Application US/09155107
Patent No. 6254868
GENERAL INFORMATION:
APPLICANT: LEUNG, Shui-on
APPLICANT: HANSEN, Hans
TITLE OF INVENTION: GLYCOSYLATED HUMANIZED B-CELL SPECIFIC ANTIBODIES
FILE REFERENCE: 018733/0879
CURRENT APPLICATION NUMBER: US/09/155,107
CURRENT FILING DATE: 1998-11-17
EARLIER APPLICATION NUMBER: WO PCT/US97/04196
EARLIER FILING DATE: 1997-03-19
EARLIER APPLICATION NUMBER: US 60/013,709
EARLIER FILING DATE: 1996-03-20
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 113
TYPE: PRT
ORGANISM: Homo sapiens
US-09-155-107-6

Query Match 100.0%; Score 38; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
|||||
Db 56 WASTRES 62

RESULT 38
US-09-155-107-20
Sequence 20, Application US/09155107
Patent No. 6254868
GENERAL INFORMATION:
APPLICANT: LEUNG, Shui-on
APPLICANT: HANSEN, Hans
TITLE OF INVENTION: GLYCOSYLATED HUMANIZED B-CELL SPECIFIC ANTIBODIES
FILE REFERENCE: 018733/0879
CURRENT APPLICATION NUMBER: US/09/155,107
CURRENT FILING DATE: 1998-11-17
EARLIER APPLICATION NUMBER: WO PCT/US97/04196
EARLIER FILING DATE: 1997-03-19
EARLIER APPLICATION NUMBER: US 60/013,709
EARLIER FILING DATE: 1996-03-20
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 20
LENGTH: 113
TYPE: PRT
ORGANISM: Homo sapiens
US-09-155-107-20

Query Match 100.0%; Score 38; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 3.9;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WASTRES 7
|||||
Db 56 WASTRES 62

RESULT 39
US-08-525-539A-80
Sequence 80, Application US/08525539A
Patent No. 6309636
GENERAL INFORMATION:
APPLICANT: DO COUTO, FERNANDO J.R.
APPLICANT: CERIANI, ROBERTO L.
APPLICANT: PETERSON, JERRY A.
TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
TITLE OF INVENTION: MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
METHODS OF HUMANIZING ANTIBODY PEPTIDES
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,539A
FILING DATE: 14-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: DYLAN, TYLER
REGISTRATION NUMBER: 37,612
REFERENCE/DOCKET NUMBER: 27633-20001.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-525-539A-80

Query Match 100.0%; Score 38; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
|||||
Db 56 WASTRES 62

RESULT 40
US-09-301-593-2
Sequence 2, Application US/09301593A
Patent No. 6455677
GENERAL INFORMATION:
APPLICANT: Park, John B.
APPLICANT: Garin-Chesa, Pilar
APPLICANT: Bambergier, Uwe
APPLICANT: Leger, Olivier
APPLICANT: Saldanha, Jose W.
APPLICANT: Retzig, Wolfgang J.
TITLE OF INVENTION: FAP-Specific Antibody with Improved Productibility
FILE REFERENCE: 0652.1890001

```
; CURRENT APPLICATION NUMBER: US/09/301,593A
; EARLIER FILING DATE: 1999-04-29
; EARLIER APPLICATION NUMBER: EP 98107925.4
; EARLIER FILING DATE: 1998-04-30
; EARLIER APPLICATION NUMBER: US 60/086,049
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-301-593-2
```

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Query Match          100.0%; Score 38; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy      1 WASTRES 7
        |||||
Db      56 WASTRES 62
```

```
RESULT 41
US-09-301-593-4
; Sequence 4, Application US/09301593A
; Patent No. 6455677
; GENERAL INFORMATION:
```

```
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saldanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: PAP-specific Antibody with Improved Productibility
; FILE REFERENCE: 0652.1890001
; CURRENT FILING DATE: 1999-04-29
; EARLIER APPLICATION NUMBER: US/09/301,593A
; EARLIER FILING DATE: 1998-04-30
; EARLIER APPLICATION NUMBER: EP 98107925.4
; EARLIER FILING DATE: 1998-05-18
; EARLIER APPLICATION NUMBER: US 60/086,049
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-301-593-4
```

```
Query Match          100.0%; Score 38; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 WASTRES 7
        |||||
Db      56 WASTRES 62
```

```
RESULT 42
US-09-301-593-6
; Sequence 6, Application US/09301593A
; Patent No. 6455677
; GENERAL INFORMATION:
```

```
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saldanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: PAP-specific Antibody with Improved Productibility
; FILE REFERENCE: 0652.1890001
; CURRENT APPLICATION NUMBER: US/09/301,593A
```

```
; CURRENT FILING DATE: 1999-04-29
; EARLIER APPLICATION NUMBER: EP 98107925.4
; EARLIER FILING DATE: 1998-04-30
; EARLIER APPLICATION NUMBER: US 60/086,049
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-301-593-6
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Query Match          100.0%; Score 38; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy      1 WASTRES 7
        |||||
Db      56 WASTRES 62
```

```
RESULT 43
US-09-301-593-32
; Sequence 32, Application US/09301593A
; Patent No. 6455677
; GENERAL INFORMATION:
```

```
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saldanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: PAP-specific Antibody with Improved Productibility
; FILE REFERENCE: 0652.1890001
; CURRENT FILING DATE: 1999-04-29
; EARLIER APPLICATION NUMBER: US/09/301,593A
; EARLIER FILING DATE: 1998-04-30
; EARLIER APPLICATION NUMBER: EP 98107925.4
; EARLIER FILING DATE: 1998-05-18
; EARLIER APPLICATION NUMBER: US 60/086,049
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-301-593-32
```

```
Query Match          100.0%; Score 38; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 WASTRES 7
        |||||
Db      56 WASTRES 62
```

```
RESULT 44
US-09-301-593-33
; Sequence 33, Application US/09301593A
; Patent No. 6455677
; GENERAL INFORMATION:
```

```
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saldanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: PAP-specific Antibody with Improved Productibility
; FILE REFERENCE: 0652.1890001
; CURRENT FILING DATE: 1999-04-29
```

EARLIER APPLICATION NUMBER: EP 98107925.4
EARLIER FILING DATE: 1998-04-30
EARLIER APPLICATION NUMBER: US 60/086,049
EARLIER FILING DATE: 1998-05-18
NUMBER OF SEQ ID NOS: 108
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 33
LENGTH: 113
TYPE: PRT
ORGANISM: Homo sapiens
US-09-301-593-33

Query Match 100.0%; Score 38; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7
|||||
Db 56 WASTRES 62

RESULT 45
US-09-301-593-34
Sequence 34, Application US/09301593A
Patent No. 6455677
GENERAL INFORMATION:
APPLICANT: Park, John E.
APPLICANT: Bamberger, Uwe
APPLICANT: Leger, Olivier
APPLICANT: Saldanha, Jose W.
APPLICANT: Rettig, Wolfgang J.
TITLE OF INVENTION: RAP-specific Antibody with Improved Producibility
FILE REFERENCE: 0652.1890001
CURRENT APPLICATION NUMBER: US/09/301,593A
CURRENT FILING DATE: 1999-04-29
EARLIER APPLICATION NUMBER: EP 98107925.4
EARLIER FILING DATE: 1998-04-30
EARLIER APPLICATION NUMBER: US 60/086,049
EARLIER FILING DATE: 1998-05-18
NUMBER OF SEQ ID NOS: 108
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 34
LENGTH: 113
TYPE: PRT
ORGANISM: Homo sapiens
US-09-301-593-34

Query Match 100.0%; Score 38; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7
|||||
Db 56 WASTRES 62

RESULT 46
US-09-274-163E-16
Sequence 16, Application US/09274163E
Patent No. 6485943
GENERAL INFORMATION:
APPLICANT: STEVENS, Fred J.
APPLICANT: WILKINS STEVENS, Priscilla
APPLICANT: RAFFEN, Rosemarie
APPLICANT: SCHIFFER, Marianne
TITLE OF INVENTION: OPTIMUM RECOMBINANT ANTIBODY PRODUCTION
FILE REFERENCE: 051583/0224
CURRENT APPLICATION NUMBER: US/09/274,163E
CURRENT FILING DATE: 1999-03-22
PRIOR APPLICATION NUMBER: US 08/373,380
PRIOR FILING DATE: 1995-01-17
NUMBER OF SEQ ID NOS: 16

SOFTWARE: PatentIn version 3.1
SEQ ID NO 16
LENGTH: 113
TYPE: PRT
ORGANISM: Escherichia coli
US-09-274-163E-16

Query Match 100.0%; Score 38; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7
|||||
Db 56 WASTRES 62

RESULT 47
US-10-330-613A-22
Sequence 22, Application US/10330613A
Patent No. 6924360
GENERAL INFORMATION:
APPLICANT: Gudas, Jean
TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
FILE REFERENCE: AGENIX, 022A
CURRENT APPLICATION NUMBER: US/10/330,613A
CURRENT FILING DATE: 2002-12-26
PRIOR APPLICATION NUMBER: 60/346299
PRIOR FILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 90
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 22
LENGTH: 113
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-330-613A-22

Query Match 100.0%; Score 38; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7
|||||
Db 56 WASTRES 62

RESULT 48
US-09-823-746-2
Sequence 2, Application US/09823746
Patent No. 6962702
GENERAL INFORMATION:
APPLICANT: HANSEN, HANS J.
APPLICANT: GRIFFITHS, GARY L.
APPLICANT: MCBRIDE, WILLIAM J.
APPLICANT: LEUNG, SHUI-ON
APPLICANT: OU, ZHENGXING
TITLE OF INVENTION: PRODUCTION AND USE OF NOVEL PEPTIDE-BASED AGENTS FOR
TITLE OF INVENTION: USE WITH BI-SPECIFIC ANTIBODIES
FILE REFERENCE: 40923-0074US4
CURRENT APPLICATION NUMBER: US/09/823,746
CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 09/337,756
PRIOR FILING DATE: 1999-06-22
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 2
LENGTH: 113
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic 679 VK
US-09-823-746-2

Query Match 100.0%; Score 38; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 WASTRES 7
|||||
Db 56 WASTRES 62

RESULT 49
PCT-US93-08435-4
; Sequence 4, Application PC/TUS9308435
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham Corporation
; APPLICANT: U.S. Government, Secretary of
; APPLICANT: the Navy
; APPLICANT: U.S. Government, Secretary of
; APPLICANT: the Army
; TITLE OF INVENTION: Novel Antibodies for Confering Passive
; TITLE OF INVENTION: Immunity Against Infection by a Pathogen in Man
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Box 457, 321 Norristown Road
; CITY: Spring House
; STATE: PA
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08435
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/941,654
; FILING DATE: 09-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: SBC P50107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 540-9200
; TELEFAX: (215) 540-5818
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US93-08435-4

Query Match 100.0%; Score 38; DB 4; Length 113;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 WASTRES 7
|||||
Db 56 WASTRES 62

RESULT 50
PCT-US93-08435-6
; Sequence 6, Application PC/TUS9308435
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham Corporation
; APPLICANT: U.S. Government, Secretary of
; APPLICANT: the Navy
; APPLICANT: U.S. Government, Secretary of
; APPLICANT: the Army

; TITLE OF INVENTION: Novel Antibodies for Confering Passive
; TITLE OF INVENTION: Immunity Against Infection by a Pathogen in Man
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Box 457, 321 Norristown Road
; CITY: Spring House
; STATE: PA
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08435
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/941,654
; FILING DATE: 09-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: SBC P50107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 540-9200
; TELEFAX: (215) 540-5818
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US93-08435-6

Query Match 100.0%; Score 38; DB 4; Length 113;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 WASTRES 7
|||||
Db 56 WASTRES 62

Search completed: May 4, 2006, 13:13:03
Job time : 22.7778 secs

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OM protein - protein search, using sw model

Run on: May 4, 2006, 13:43:49 ; Search time 50.7778 Seconds
(without alignments)
57.600 Million cell updates/sec

Title: US-10-700-632-5

Perfect score: 38

Sequence: 1. WASTRES 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published_Applications_AA_Main:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	38	100.0	7	3	US-09-749-831-5
2	38	100.0	7	3	US-09-828-708-43
3	38	100.0	7	3	US-09-828-708-46
4	38	100.0	7	3	US-09-249-011A-18
5	38	100.0	7	3	US-09-563-223-15
6	38	100.0	7	3	US-09-563-222-27
7	38	100.0	7	4	US-10-146-305-10
8	38	100.0	7	4	US-10-071-962-19
9	38	100.0	7	4	US-10-312-316-29
10	38	100.0	7	4	US-10-469-125-5
11	38	100.0	7	4	US-10-783-950-15
12	38	100.0	7	4	US-10-783-950-27
13	38	100.0	7	5	US-10-483-994-5
14	38	100.0	7	5	US-10-483-993-5
15	38	100.0	7	5	US-10-883-020-29
16	38	100.0	7	5	US-10-726-333-156
17	38	100.0	7	5	US-10-726-333-165
18	38	100.0	7	5	US-10-726-333-183
19	38	100.0	7	5	US-10-726-332-186
20	38	100.0	7	5	US-10-726-332-201
21	38	100.0	7	5	US-10-630-009-43
22	38	100.0	7	5	US-10-630-009-46
23	38	100.0	7	5	US-10-700-632-5
24	38	100.0	7	5	US-10-893-576-71
25	38	100.0	7	5	US-10-893-576-76
26	38	100.0	7	5	US-10-497-516-5
27	38	100.0	7	5	US-10-927-433-8

28	38	100.0	7	5	US-10-986-099A-18	Sequence 18, Appl
29	38	100.0	7	6	US-11-015-958-5	Sequence 50, Appl
30	38	100.0	12	5	US-10-700-632-50	Sequence 5, Appl
31	38	100.0	82	4	US-10-078-958-15	Sequence 15, Appl
32	38	100.0	94	3	US-09-905-143-60	Sequence 60, Appl
33	38	100.0	94	6	US-11-099-331-60	Sequence 60, Appl
34	38	100.0	99	5	US-10-700-632-60	Sequence 60, Appl
35	38	100.0	101	4	US-10-194-975-89	Sequence 89, Appl
36	38	100.0	101	4	US-10-125-687-25	Sequence 25, Appl
37	38	100.0	101	4	US-10-308-817-36	Sequence 36, Appl
38	38	100.0	101	4	US-10-453-698-36	Sequence 36, Appl
39	38	100.0	101	4	US-10-379-392-103	Sequence 103, Appl
40	38	100.0	101	5	US-10-996-191-25	Sequence 25, Appl
41	38	100.0	105	4	US-10-010-729-37	Sequence 37, Appl
42	38	100.0	107	4	US-10-325-694-142	Sequence 142, Appl
43	38	100.0	107	4	US-10-325-694-148	Sequence 148, Appl
44	38	100.0	107	4	US-10-325-694-149	Sequence 149, Appl
45	38	100.0	107	4	US-10-325-694-152	Sequence 152, Appl
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50	38	100.0	109	5	US-10-630-009-4	Sequence 4, Appl
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54	38	100.0	112	4	US-10-056-052-18	Sequence 18, Appl
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56	38	100.0	112	4	US-10-229-335-28	Sequence 28, Appl
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58	38	100.0	112	4	US-10-466-242-16	Sequence 16, Appl
59	38	100.0	112	4	US-10-466-242-32	Sequence 32, Appl
60	38	100.0	112	5	US-10-816-938-31	Sequence 31, Appl
61	38	100.0	113	3	US-09-301-593-2	Sequence 2, Appl
62	38	100.0	113	3	US-09-301-593-4	Sequence 4, Appl
63	38	100.0	113	3	US-09-301-593-6	Sequence 6, Appl
64	38	100.0	113	3	US-09-301-593-32	Sequence 32, Appl
65	38	100.0	113	3	US-09-301-593-33	Sequence 33, Appl
66	38	100.0	113	3	US-09-301-593-34	Sequence 34, Appl
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68	38	100.0	113	3	US-09-741-843-6	Sequence 6, Appl
69	38	100.0	113	3	US-09-274-163B-16	Sequence 16, Appl
70	38	100.0	113	3	US-09-956-206A-80	Sequence 80, Appl
71	38	100.0	113	3	US-09-894-839-2	Sequence 2, Appl
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77	38	100.0	113	3	US-09-215-163-42	Sequence 42, Appl
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81	38	100.0	113	4	US-10-121-464-6	Sequence 6, Appl
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87	38	100.0	113	4	US-10-159-006-32	Sequence 32, Appl
88	38	100.0	113	4	US-10-159-006-33	Sequence 33, Appl
89	38	100.0	113	4	US-10-159-006-34	Sequence 34, Appl
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91	38	100.0	113	4	US-10-330-613-22	Sequence 22, Appl
92	38	100.0	113	4	US-10-160-906-71	Sequence 71, Appl
93	38	100.0	113	4	US-10-160-906-91	Sequence 91, Appl
94	38	100.0	113	4	US-10-422-049-2	Sequence 2, Appl
95	38	100.0	113	4	US-10-446-689-2	Sequence 2, Appl
96	38	100.0	113	4	US-10-446-689-6	Sequence 6, Appl
97	38	100.0	113	4	US-10-251-085B-138	Sequence 138, Appl
98	38	100.0	113	4	US-10-660-357-22	Sequence 22, Appl
99	38	100.0	113	4	US-10-449-379-71	Sequence 71, Appl
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101	38	100.0	113	4	US-10-688-015-71	Sequence 71, Appl	174	38	100.0	135	4	US-10-353-708-1	Sequence 1, Appl1
102	38	100.0	113	4	US-10-688-015-91	Sequence 91, Appl	175	38	100.0	135	4	US-10-731-984-35	Sequence 35, Appl
103	38	100.0	113	4	US-10-737-252-118	Sequence 118, App	176	38	100.0	135	5	US-10-723-003-18	Sequence 18, Appl
104	38	100.0	113	4	US-10-160-505-71	Sequence 71, Appl	177	38	100.0	135	6	US-11-004-639-18	Sequence 18, Appl
105	38	100.0	113	4	US-10-160-505-91	Sequence 91, Appl	178	38	100.0	141	4	US-10-390-986-16	Sequence 16, Appl
106	38	100.0	113	5	US-10-787-378-2	Sequence 2, Appl1	179	38	100.0	146	5	US-10-830-889-56	Sequence 56, Appl
107	38	100.0	113	5	US-10-787-378-6	Sequence 6, Appl1	180	38	100.0	146	5	US-10-830-889-63	Sequence 63, Appl
108	38	100.0	113	5	US-10-787-378-20	Sequence 20, Appl1	181	38	100.0	146	5	US-10-861-662-56	Sequence 56, Appl
109	38	100.0	113	5	US-10-722-849-2	Sequence 2, Appl1	182	38	100.0	146	5	US-10-861-662-63	Sequence 63, Appl
110	38	100.0	113	5	US-10-722-849-4	Sequence 4, Appl1	183	38	100.0	149	5	US-10-644-277-108	Sequence 108, App
111	38	100.0	113	5	US-10-974-678-2	Sequence 2, Appl1	184	38	100.0	149	5	US-10-627-556-34	Sequence 34, App
112	38	100.0	113	5	US-10-974-678-6	Sequence 6, Appl1	185	38	100.0	153	3	US-09-187-693-62	Sequence 62, Appl
113	38	100.0	113	5	US-10-700-632-8	Sequence 8, Appl1	186	38	100.0	153	6	US-11-021-795-62	Sequence 62, Appl
114	38	100.0	113	5	US-10-700-632-10	Sequence 10, Appl	187	38	100.0	154	3	US-09-925-299-1226	Sequence 1226, Ap
115	38	100.0	113	5	US-10-700-632-71	Sequence 71, Appl	188	38	100.0	154	3	US-09-925-299-1226	Sequence 1226, Ap
116	38	100.0	113	5	US-10-893-576-173	Sequence 173, App	189	38	100.0	154	5	US-10-644-277-48	Sequence 48, Appl
117	38	100.0	113	5	US-10-893-576-174	Sequence 174, App	190	38	100.0	155	4	US-10-346-618-11	Sequence 11, Appl
118	38	100.0	113	5	US-10-880-028-29	Sequence 29, Appl	191	38	100.0	159	3	US-09-187-693-66	Sequence 66, Appl
119	38	100.0	113	5	US-10-880-320-29	Sequence 29, Appl	192	38	100.0	159	5	US-10-644-277-8	Sequence 8, Appl1
120	38	100.0	113	5	US-10-965-616-80	Sequence 80, Appl	193	38	100.0	159	5	US-10-644-277-88	Sequence 88, Appl
121	38	100.0	113	6	US-11-003-819-14	Sequence 14, Appl	194	38	100.0	159	5	US-10-644-277-116	Sequence 116, App
122	38	100.0	113	6	US-11-013-558-8	Sequence 8, Appl1	195	38	100.0	159	6	US-11-021-795-66	Sequence 66, Appl
123	38	100.0	113	6	US-11-004-659-2	Sequence 2, Appl1	196	38	100.0	161	6	US-11-131-648-23	Sequence 23, Appl
124	38	100.0	113	6	US-11-004-659-4	Sequence 4, Appl1	197	38	100.0	161	6	US-11-131-648-55	Sequence 55, Appl
125	38	100.0	114	3	US-09-810-502-38	Sequence 38, Appl	198	38	100.0	163	5	US-10-644-277-16	Sequence 16, Appl
126	38	100.0	114	3	US-09-749-831-16	Sequence 16, Appl	199	38	100.0	163	5	US-10-644-277-52	Sequence 52, Appl
127	38	100.0	114	3	US-09-749-831-62	Sequence 62, Appl	200	38	100.0	163	5	US-10-644-277-100	Sequence 100, App
128	38	100.0	114	3	US-09-274-163E-2	Sequence 2, Appl1	201	38	100.0	163	5	US-10-644-277-104	Sequence 104, App
129	38	100.0	114	3	US-09-274-163E-4	Sequence 4, Appl1	202	38	100.0	165	4	US-10-364-743-26	Sequence 26, Appl
130	38	100.0	114	3	US-09-274-163E-6	Sequence 6, Appl1	203	38	100.0	165	5	US-10-452-553-26	Sequence 26, Appl
131	38	100.0	114	4	US-10-125-687-11	Sequence 11, Appl	204	38	100.0	173	5	US-10-644-277-116	Sequence 116, App
132	38	100.0	114	4	US-10-422-049-3	Sequence 3, Appl1	205	38	100.0	173	5	US-10-644-277-144	Sequence 144, App
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134	38	100.0	114	5	US-10-483-994-8	Sequence 8, Appl1	207	38	100.0	211	4	US-10-264-049-4266	Sequence 4266, Ap
135	38	100.0	114	5	US-10-483-993-8	Sequence 8, Appl1	208	38	100.0	214	5	US-10-778-915-2	Sequence 2, Appl1
136	38	100.0	114	5	US-10-625-307A-16	Sequence 16, Appl	209	38	100.0	220	3	US-09-301-593-17	Sequence 17, Appl
137	38	100.0	114	5	US-10-938-353-112	Sequence 112, App	210	38	100.0	220	3	US-09-995-693-1	Sequence 1, Appl1
138	38	100.0	114	5	US-10-706-689-15	Sequence 15, Appl	211	38	100.0	220	4	US-10-232-408-1	Sequence 1, Appl1
139	38	100.0	114	5	US-10-700-632-62	Sequence 62, Appl	212	38	100.0	220	4	US-10-159-006-17	Sequence 17, Appl
140	38	100.0	114	5	US-10-700-632-70	Sequence 70, Appl	213	38	100.0	220	5	US-10-644-277-40	Sequence 40, Appl
141	38	100.0	114	5	US-10-497-516-8	Sequence 8, Appl1	214	38	100.0	220	5	US-10-644-277-92	Sequence 92, Appl
142	38	100.0	114	5	US-10-877-467A-3	Sequence 3, Appl1	215	38	100.0	238	6	US-11-013-537-1	Sequence 1, Appl1
143	38	100.0	114	5	US-10-988-360-15	Sequence 15, Appl	216	38	100.0	239	3	US-09-825-012-9	Sequence 9, Appl1
144	38	100.0	114	5	US-10-996-191-11	Sequence 11, Appl	217	38	100.0	239	3	US-09-249-011A-22	Sequence 22, Appl
145	38	100.0	114	6	US-11-031-485-127	Sequence 127, App	218	38	100.0	239	5	US-10-723-003-14	Sequence 14, Appl
146	38	100.0	115	4	US-10-320-231A-29	Sequence 29, Appl	219	38	100.0	239	6	US-11-004-639-14	Sequence 14, Appl
147	38	100.0	115	5	US-10-867-506-29	Sequence 29, Appl	220	38	100.0	240	3	US-09-301-593-28	Sequence 28, Appl
148	38	100.0	115	5	US-10-700-632-63	Sequence 63, Appl	221	38	100.0	240	3	US-09-799-514-8	Sequence 36, Appl
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150	38	100.0	115	5	US-10-700-632-65	Sequence 65, Appl	223	38	100.0	240	4	US-10-159-006-28	Sequence 28, Appl
151	38	100.0	115	5	US-10-700-632-66	Sequence 66, Appl	224	38	100.0	240	4	US-10-159-006-36	Sequence 36, Appl
152	38	100.0	115	5	US-10-700-632-67	Sequence 67, Appl	225	38	100.0	240	5	US-10-938-353-24	Sequence 24, Appl
153	38	100.0	115	5	US-10-734-661A-88	Sequence 88, Appl	226	38	100.0	241	5	US-10-723-003-22	Sequence 22, Appl
154	38	100.0	115	5	US-10-505-313-228	Sequence 228, App	227	38	100.0	241	6	US-11-004-639-22	Sequence 22, Appl
155	38	100.0	116	4	US-10-312-316-53	Sequence 53, Appl	228	38	100.0	242	3	US-09-819-266-26	Sequence 26, Appl
156	38	100.0	119	4	US-10-010-729-13	Sequence 13, Appl	229	38	100.0	255	4	US-10-239-656-69	Sequence 69, Appl
157	38	100.0	122	4	US-10-010-729-51	Sequence 51, Appl	230	38	100.0	258	4	US-10-239-656-71	Sequence 71, Appl
158	38	100.0	126	4	US-10-473-287-51	Sequence 51, Appl	231	38	100.0	258	4	US-10-239-656-71	Sequence 71, Appl
159	38	100.0	130	4	US-10-146-305-7	Sequence 7, Appl1	232	38	100.0	259	4	US-10-239-656-53	Sequence 53, Appl
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161	38	100.0	132	3	US-09-249-011A-8	Sequence 8, Appl1	234	38	100.0	260	4	US-10-270-071-22	Sequence 22, Appl
162	38	100.0	132	5	US-10-986-089A-4	Sequence 4, Appl1	235	38	100.0	267	4	US-10-270-071-26	Sequence 26, Appl
163	38	100.0	132	5	US-10-986-089A-8	Sequence 8, Appl1	236	38	100.0	267	4	US-10-270-071-30	Sequence 30, Appl
164	38	100.0	132	6	US-11-013-537-2	Sequence 2, Appl1	237	38	100.0	267	4	US-10-270-071-36	Sequence 36, Appl
165	38	100.0	133	3	US-09-301-593-24	Sequence 24, Appl	238	38	100.0	268	4	US-10-270-071-10	Sequence 10, Appl
166	38	100.0	133	4	US-10-159-006-24	Sequence 24, Appl	239	38	100.0	268	4	US-10-270-071-12	Sequence 12, Appl
167	38	100.0	133	4	US-10-469-125-41	Sequence 41, Appl	240	38	100.0	268	4	US-10-270-071-16	Sequence 16, Appl
168	38	100.0	133	5	US-10-723-003-10	Sequence 10, Appl	241	38	100.0	268	4	US-10-270-071-15	Sequence 15, Appl
169	38	100.0	133	5	US-10-893-576-26	Sequence 26, Appl	242	38	100.0	268	4	US-10-270-071-32	Sequence 32, Appl
170	38	100.0	133	5	US-10-893-576-36	Sequence 36, Appl	243	38	100.0	268	4	US-10-328-190-2	Sequence 2, Appl1
171	38	100.0	133	6	US-11-004-639-10	Sequence 10, Appl	244	38	100.0	268	4	US-10-328-190-4	Sequence 4, Appl1
172	38	100.0	134	4	US-10-955-478-58	Sequence 58, Appl	245	38	100.0	270	5	US-10-627-556-338	Sequence 338, App
173	38	100.0	135	4	US-10-171-452A-1	Sequence 1, Appl1	246	38	100.0	270	5	US-10-627-556-342	Sequence 342, App

247	38	100.0	272	4	US-10-207-655-14	Sequence 14, Appl	320	33	86.8	113	5	US-10-880-028-30	Sequence 30, Appl
248	38	100.0	272	4	US-10-053-530-14	Sequence 14, Appl	321	33	86.8	113	5	US-10-880-028-31	Sequence 31, Appl
249	38	100.0	272	6	US-11-089-511-14	Sequence 14, Appl	322	33	86.8	113	5	US-10-880-120-28	Sequence 28, Appl
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252	38	100.0	272	6	US-11-088-737-14	Sequence 14, Appl	325	33	86.8	113	5	US-10-927-433-13	Sequence 13, Appl
253	38	100.0	272	6	US-11-088-569-14	Sequence 14, Appl	326	33	86.8	113	5	US-10-501-262-2974	Sequence 2974, Ap
254	38	100.0	272	6	US-11-088-367-14	Sequence 14, Appl	327	33	86.8	220	5	US-10-880-028-19	Sequence 19, Appl
255	38	100.0	272	6	US-11-089-367-14	Sequence 14, Appl	328	33	86.8	220	5	US-10-880-028-27	Sequence 27, Appl
256	38	100.0	272	6	US-11-089-368-14	Sequence 14, Appl	329	33	86.8	220	5	US-10-880-120-19	Sequence 19, Appl
257	38	100.0	274	4	US-10-255-478-66	Sequence 66, Appl	330	33	86.8	220	5	US-10-880-120-27	Sequence 27, Appl
258	38	100.0	284	4	US-10-255-478-70	Sequence 70, Appl	331	33	86.8	241	3	US-09-791-578-6	Sequence 6, Appl
259	38	100.0	342	4	US-10-345-618-6	Sequence 6, Appl	332	33	86.8	241	3	US-09-791-540-6	Sequence 6, Appl
260	38	100.0	352	3	US-09-203-958A-2	Sequence 2, Appl	333	33	86.8	241	5	US-10-915-069-6	Sequence 6, Appl
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ALIGNMENTS

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; GENERAL INFORMATION:
; APPLICANT: VERHOEYEN, MARTINE ELISA
; TITLE OF INVENTION: SPECIFIC BINDING AGENTS
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLBURY WINTHROP LLP
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/749,831
; FILING DATE: 04-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/987,264
; FILING DATE: 08-MAR-1993
; APPLICATION NUMBER: GB PCT/GB91/01511
; FILING DATE: 05-SEP-1991
; APPLICATION NUMBER: GB 9019553.8
; FILING DATE: 07-SEP-1990
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-749-831-5

```

```

Query Match 100.0%; Score 38; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 WASTRES 7
Db 1 WASTRES 7

```

```

RESULT 2
US-09-828-708-43
; Sequence 43, Application US/09828708
; Patent No. US20020146753A1
; GENERAL INFORMATION:
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partici
; FILE REFERENCE: 1361.005U51
; CURRENT APPLICATION NUMBER: US/09/828,708
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-708-43

```

```

Query Match 100.0%; Score 38; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 WASTRES 7
Db 1 WASTRES 7

```

```

RESULT 3
US-09-828-708-46
; Sequence 46, Application US/09828708
; Patent No. US20020146753A1
; GENERAL INFORMATION:
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partici
; FILE REFERENCE: 1361.005U51
; CURRENT APPLICATION NUMBER: US/09/828,708
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-708-46

```

```

Query Match 100.0%; Score 38; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 WASTRES 7
Db 1 WASTRES 7

```

```

RESULT 4
US-09-249-011A-18
; Sequence 18, Application US/09249011A
; Patent No. US20020176855A1
; GENERAL INFORMATION:
; APPLICANT: CO, MAN SUNG
; APPLICANT: VASQUEZ, MAXIMILIANO

```

APPLICANT: CARENNO, BEATRIZ
APPLICANT: CHLINER, ABBIE CHERYL
APPLICANT: COLLINS, MARY
APPLICANT: GOLDMAN, SAMUEL
APPLICANT: GRAY, GARY S.
APPLICANT: KNIGHT, ANDREA
APPLICANT: O'HARA, DENISE
APPLICANT: RUP, BONITA
APPLICANT: VELDMAN, GEERTRUIDA M.
TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
FILE REFERENCE: 08702.0081-00000
CURRENT APPLICATION NUMBER: US/09/249,011A
CURRENT FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 18
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: CDR2 of humanized
OTHER INFORMATION: murine anti-human B7-2 light chain
US-09-249-011A-18

Query Match 100.0%; Score 38; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
Db 1 WASTRES 7

RESULT 5
US-09-563-222-15
Sequence 15, Application US/09563222
Publication No. US2003079253A1
GENERAL INFORMATION:
APPLICANT: Hiate, Andrew
TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
FILE REFERENCE: 310098.406
CURRENT APPLICATION NUMBER: US/09/563,222
CURRENT FILING DATE: 2000-05-02
NUMBER OF SEQ ID NOS: 197
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15
LENGTH: 7
TYPE: PRT
ORGANISM: Homo sapien
US-09-563-222-15

Query Match 100.0%; Score 38; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
Db 1 WASTRES 7

RESULT 6
US-09-563-222-27
Sequence 27, Application US/09563222
Publication No. US2003079253A1
GENERAL INFORMATION:
APPLICANT: Hiate, Andrew
TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
FILE REFERENCE: 310098.406
US-09-563-222-27

CURRENT APPLICATION NUMBER: US/09/563,222
CURRENT FILING DATE: 2000-05-02
NUMBER OF SEQ ID NOS: 197
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 27
LENGTH: 7
TYPE: PRT
ORGANISM: Mus musculus
US-09-563-222-27

Query Match 100.0%; Score 38; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
Db 1 WASTRES 7

RESULT 7
US-10-146-305-10
Sequence 10, Application US/10146305
Publication No. US20020173035A1
GENERAL INFORMATION:
APPLICANT: YUHAN CORPORATION
TITLE OF INVENTION: A VARIABLE REGION OF THE MONOCLONAL ANTIBODY AGAINST THE HBV
FILE REFERENCE: CV17440
CURRENT APPLICATION NUMBER: US/10/146,305
CURRENT FILING DATE: 2002-05-15
PRIOR APPLICATION NUMBER: KR 10-2001-26634
PRIOR FILING DATE: 2001-05-16
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Kopatentin 1.71
SEQ ID NO 10
LENGTH: 7
TYPE: PRT
ORGANISM: Escherichia coli
US-10-146-305-10

Query Match 100.0%; Score 38; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
Db 1 WASTRES 7

RESULT 8
US-10-071-962-19
Sequence 19, Application US/10071962
Publication No. US2003017023A1
GENERAL INFORMATION:
APPLICANT: Baifu Ni
APPLICANT: Billi R.Y. Sun
TITLE OF INVENTION: G-CSF Receptor Agonist Antibodies and
SCREENING METHOD THEREFOR
FILE REFERENCE: 98-3
CURRENT APPLICATION NUMBER: US/10/071,962
CURRENT FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US/09/303,155A
PRIOR FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: 60/083,575
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 19
LENGTH: 7
TYPE: PRT
ORGANISM: mouse
US-10-071-962-19

Query Match 100.0%; Score 38; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WASTRES 7
Db 1 WASTRES 7

RESULT 9
US-10-312-316-29
; Sequence 29, Application US/10312316
; Publication No. US20040137513A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Devaux, Brigitte
; APPLICANT: Hongo, Jo-Anne S.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shelton, David L.
; TITLE OF INVENTION: AGONIST ANTI-TRK-C MONOCLONAL ANTIBODIES
; FILE REFERENCE: GENENT.0400PC
; CURRENT FILING DATE: US/10/312,316
; PRIOR APPLICATION NUMBER: 2002-12-20
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-312-316-29

Query Match 100.0%; Score 38; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WASTRES 7
Db 1 WASTRES 7

RESULT 10
US-10-469-125-5
; Sequence 5, Application US/10469125
; Publication No. US20040143101A1
; GENERAL INFORMATION:
; APPLICANT: Soltis, Daniel A.
; APPLICANT: Burch, Ronald M.
; APPLICANT: Shukla, Rajiv
; TITLE OF INVENTION: IMMUNOGLOBULIN CONSTRUCT CONTAINING ANTI-MUCIN VARIABLE DOMAIN SE
; FILE REFERENCE: 02755/1006273-US1
; CURRENT FILING DATE: US/10/469,125
; PRIOR APPLICATION NUMBER: 2003-08-25
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 60/281,182
; PRIOR FILING DATE: 2002-04-02
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-469-125-5

Query Match 100.0%; Score 38; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WASTRES 7

Db 1 WASTRES 7

RESULT 11
US-10-783-950-15
; Sequence 15, Application US/10783950
; Publication No. US2004019945A1
; GENERAL INFORMATION:
; APPLICANT: EPICYTE PHARMACEUTICALS, INC.
; APPLICANT: HIATT, ANDREW C.
; APPLICANT: HEIN, MICH B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
; FILE REFERENCE: 068904-0501
; CURRENT FILING DATE: US/10/783,950
; PRIOR APPLICATION NUMBER: US/09/563,222
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: PCT/US01/14349
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/563,222
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-783-950-15

Query Match 100.0%; Score 38; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WASTRES 7
Db 1 WASTRES 7

RESULT 12
US-10-783-950-27
; Sequence 27, Application US/10783950
; Publication No. US2004019945A1
; GENERAL INFORMATION:
; APPLICANT: EPICYTE PHARMACEUTICALS, INC.
; APPLICANT: HIATT, ANDREW C.
; APPLICANT: HEIN, MICH B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
; FILE REFERENCE: 068904-0501
; CURRENT FILING DATE: US/10/783,950
; PRIOR APPLICATION NUMBER: 2004-02-19
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: PCT/US01/14349
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/563,222
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-783-950-27

Query Match 100.0%; Score 38; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WASTRES 7
Db 1 WASTRES 7

```
RESULT 13
; Sequence 5, Application US/10483994
; Publication No. US20050032132A1
; GENERAL INFORMATION:
; APPLICANT: MITSUBISHI PHARMA CORPORATION
; TITLE OF INVENTION: CANCER DIAGNOSTICS
; FILE REFERENCE: 02030MO0
; CURRENT APPLICATION NUMBER: US/10/483,994
; PRIOR FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: JP P2001-224054
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 5
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-483-994-5
```

```
Query Match          100.0%; Score 38; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WASTRES 7
        |||||
Db      1 WASTRES 7
```

```
RESULT 14
US-10-483-993-5
; Sequence 5, Application US/10483993
; Publication No. US20050037061A1
; GENERAL INFORMATION:
; APPLICANT: MITSUBISHI PHARMA CORPORATION
; TITLE OF INVENTION: REMEDIES FOR MAMMARY CANCER
; FILE REFERENCE: 02031W00
; CURRENT APPLICATION NUMBER: US/10/483,993
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: JP P2001-224596
; PRIOR FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 5
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-483-993-5
```

```
Query Match          100.0%; Score 38; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WASTRES 7
        |||||
Db      1 WASTRES 7
```

```
RESULT 15
US-10-883-020-29
; Sequence 29, Application US/10883020
; Publication No. US20050048070A1
; GENERAL INFORMATION:
; APPLICANT: Ditzel, Henrik
; APPLICANT: Jensenius, Jens
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: Cancer-Associated Epitope
; FILE REFERENCE: 1361.017U51
; CURRENT APPLICATION NUMBER: US/10/883,020
; CURRENT FILING DATE: 2004-07-01
; PRIOR APPLICATION NUMBER: PCT/US03/00297
; PRIOR FILING DATE: 2003-01-03
; PRIOR APPLICATION NUMBER: US 60/345,208
; PRIOR FILING DATE: 2002-01-03
```

```
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-883-020-29
```

```
Query Match          100.0%; Score 38; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WASTRES 7
        |||||
Db      1 WASTRES 7
```

```
RESULT 16
US-10-726-332-156
; Sequence 156, Application US/10726332
; Publication No. US20050058649A1
; GENERAL INFORMATION:
; APPLICANT: Gregory M. Landes
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Ling Chen
; APPLICANT: Yen-Wah R. Lee
; APPLICANT: Meina Liang
; APPLICANT: Xiao Feng
; APPLICANT: Xiao-Chi Jia
; APPLICANT: Mark R. Nocerini
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2
; FILE REFERENCE: ABGENIX.072A
; CURRENT APPLICATION NUMBER: US/10/726,332
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: n/a
; NUMBER OF SEQ ID NOS: 222
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 156
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-726-332-156
```

```
Query Match          100.0%; Score 38; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WASTRES 7
        |||||
Db      1 WASTRES 7
```

```
RESULT 17
US-10-726-332-165
; Sequence 165, Application US/10726332
; Publication No. US20050058649A1
; GENERAL INFORMATION:
; APPLICANT: Gregory M. Landes
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Ling Chen
; APPLICANT: Yen-Wah R. Lee
; APPLICANT: Meina Liang
; APPLICANT: Xiao Feng
; APPLICANT: Xiao-Chi Jia
; APPLICANT: Mark R. Nocerini
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2
; FILE REFERENCE: ABGENIX.072A
; CURRENT APPLICATION NUMBER: US/10/726,332
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: n/a
```

```
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 222
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 165
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-726-332-165
```

```
Query Match      100.0%; Score 38; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 WASTRES 7
Db      1 WASTRES 7
```

RESULT 18

```
US-10-726-332-183
; Sequence 183, Application US/10726332
; Publication No. US20050058649A1
; GENERAL INFORMATION:
; APPLICANT: Gregory M. Landes
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Ling Chen
; APPLICANT: Yen-Wah R. Lee
; APPLICANT: Meina Liang
; APPLICANT: Xiao Feng
; APPLICANT: Xiao-Chi Jia
; APPLICANT: Mark R. Nocerini
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: ABGENIX.072A
; CURRENT APPLICATION NUMBER: US/10/726,332
; PRIOR FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: n/a
; NUMBER OF SEQ ID NOS: 222
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 183
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-726-332-183
```

```
Query Match      100.0%; Score 38; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 WASTRES 7
Db      1 WASTRES 7
```

RESULT 19

```
US-10-726-332-186
; Sequence 186, Application US/10726332
; Publication No. US20050058649A1
; GENERAL INFORMATION:
; APPLICANT: Gregory M. Landes
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Ling Chen
; APPLICANT: Yen-Wah R. Lee
; APPLICANT: Meina Liang
; APPLICANT: Xiao Feng
; APPLICANT: Xiao-Chi Jia
; APPLICANT: Mark R. Nocerini
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: ABGENIX.072A
; CURRENT APPLICATION NUMBER: US/10/726,332
; PRIOR FILING DATE: 2003-12-02
```

```
; PRIOR APPLICATION NUMBER: n/a
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 222
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 186
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-726-332-186
```

```
Query Match      100.0%; Score 38; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 WASTRES 7
Db      1 WASTRES 7
```

RESULT 20

```
US-10-726-332-201
; Sequence 201, Application US/10726332
; Publication No. US20050058649A1
; GENERAL INFORMATION:
; APPLICANT: Gregory M. Landes
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Ling Chen
; APPLICANT: Yen-Wah R. Lee
; APPLICANT: Meina Liang
; APPLICANT: Xiao Feng
; APPLICANT: Xiao-Chi Jia
; APPLICANT: Mark R. Nocerini
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: ABGENIX.072A
; CURRENT APPLICATION NUMBER: US/10/726,332
; PRIOR FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: n/a
; NUMBER OF SEQ ID NOS: 222
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 201
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-726-332-201
```

```
Query Match      100.0%; Score 38; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 WASTRES 7
Db      1 WASTRES 7
```

RESULT 21

```
US-10-630-009-43
; Sequence 43, Application US/10630009
; Publication No. US20050080239A1
; GENERAL INFORMATION:
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Antibodies to glucose-6-phosphate isomerase and their partici
; FILE REFERENCE: 1361.005052
; CURRENT APPLICATION NUMBER: US/10/630,009
; PRIOR FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: US 09/828,708
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0
```


SEQ ID NO 43
LENGTH: 7
TYPE: PRT
ORGANISM: Homo sapiens
US-10-630-009-43

Query Match 100.0%; Score 38; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
Db 1 WASTRES 7

RESULT 22
US-10-630-009-46
Sequence 46, Application US/10630009
Publication No. US20050080239A1
GENERAL INFORMATION:
APPLICANT: Ditzel, H.
APPLICANT: Burton, D.
APPLICANT: Schaller, M.
TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partici
FILE REFERENCE: 1361, 005US2
CURRENT APPLICATION NUMBER: US/10/630, 009
CURRENT FILING DATE: 2003-07-29
PRIOR APPLICATION NUMBER: US 09/828, 708
PRIOR FILING DATE: 2001-04-06
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 46
LENGTH: 7
TYPE: PRT
ORGANISM: Homo sapiens
US-10-630-009-46

Query Match 100.0%; Score 38; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
Db 1 WASTRES 7

RESULT 23
US-10-700-632-5
Sequence 5, Application US/10700632
Publication No. US20050118183A1
GENERAL INFORMATION:
APPLICANT: Immunogen, Inc.
TITLE OF INVENTION: ANTI-CD33 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID
FILE REFERENCE: A8427
CURRENT APPLICATION NUMBER: US/10/700, 632
CURRENT FILING DATE: 2003-11-05
PRIOR APPLICATION NUMBER: US 60/424, 332
PRIOR FILING DATE: 2002-11-07
NUMBER OF SEQ ID NOS: 94
SOFTWARE: PatentIn version 3.2
SEQ ID NO 5
LENGTH: 7
TYPE: PRT
ORGANISM: Mus musculus
US-10-700-632-5

Query Match 100.0%; Score 38; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7

Db 1 WASTRES 7

RESULT 24
US-10-893-576-71
Sequence 71, Application US/10893576
Publication No. US20050118643A1
GENERAL INFORMATION:
APPLICANT: BURGESS, TERESA L.
APPLICANT: COXON, ANGELA
APPLICANT: GREEN, LARRY L.
APPLICANT: ZHANG, KE
TITLE OF INVENTION: SPECIFIC BINDING AGENTS TO HEPATOCYTE GROWTH FACTOR
FILE REFERENCE: 06843.0051-00000
CURRENT APPLICATION NUMBER: US/10/893, 576
CURRENT FILING DATE: 2004-07-16
PRIOR APPLICATION NUMBER: US 60/488, 681
PRIOR FILING DATE: 2003-07-18
NUMBER OF SEQ ID NOS: 194
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 71
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic light chain
US-10-893-576-71

Query Match 100.0%; Score 38; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
Db 1 WASTRES 7

RESULT 25
US-10-893-576-76
Sequence 76, Application US/10893576
Publication No. US20050118643A1
GENERAL INFORMATION:
APPLICANT: BURGESS, TERESA L.
APPLICANT: COXON, ANGELA
APPLICANT: GREEN, LARRY L.
APPLICANT: ZHANG, KE
TITLE OF INVENTION: SPECIFIC BINDING AGENTS TO HEPATOCYTE GROWTH FACTOR
FILE REFERENCE: 06843.0051-00000
CURRENT APPLICATION NUMBER: US/10/893, 576
CURRENT FILING DATE: 2004-07-16
PRIOR APPLICATION NUMBER: US 60/488, 681
PRIOR FILING DATE: 2003-07-18
NUMBER OF SEQ ID NOS: 194
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 76
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic light chain
US-10-893-576-76

Query Match 100.0%; Score 38; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
Db 1 WASTRES 7

RESULT 26
US-10-497-516-5
; Sequence 5, Application US/10497516
; Publication No. US20050123532A1
; GENERAL INFORMATION:
; APPLICANT: MITSUBISHI PHARMA CORPORATION
; TITLE OF INVENTION: Methods of activating proteins
; FILE REFERENCE: 02046W00
; CURRENT APPLICATION NUMBER: US/10/497,516
; CURRENT FILING DATE: 2004-06-03
; PRIOR APPLICATION NUMBER: JP P2001-370541
; PRIOR FILING DATE: 2001-12-04
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 5
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-497-516-5

Query Match 100.0%; Score 38; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WASTRES 7
Db 1 WASTRES 7

RESULT 27
US-10-927-433-8
; Sequence 8, Application US/10927433
; Publication No. US20050186202A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as represented by The
; APPLICANT: Secretary of the Department of Health and Human Services
; APPLICANT: Kashmiri, Syed V.S.
; APPLICANT: Padlan, Eduardo A.
; APPLICANT: Jeffery, Schlom
; TITLE OF INVENTION: VARIANTS OF HUMANIZED ANTI-CARCINOMA MONOCLONAL ANTIBODY CC49
; FILE REFERENCE: 4239-61725-02
; CURRENT APPLICATION NUMBER: US/10/927,433
; CURRENT FILING DATE: 2004-08-25
; PRIOR APPLICATION NUMBER: US 09/830,748
; PRIOR FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: PCT/ US99/25552
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/106,757
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: US 60/106,534
; PRIOR FILING DATE: 1998-10-31
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-927-433-8

Query Match 100.0%; Score 38; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WASTRES 7
Db 1 WASTRES 7

RESULT 28
US-10-986-089A-18
; Sequence 18, Application US/10986089A
; Publication No. US20050208042A1
; GENERAL INFORMATION:

; APPLICANT: Co, Man Sung
; APPLICANT: Vasquez, Maximiliano
; APPLICANT: Carrero, Beatriz
; APPLICANT: Celinker, Abbie Cheryl
; APPLICANT: Collins, Mary
; APPLICANT: Goldman, Samuel
; APPLICANT: Gray, Gary S.
; APPLICANT: Knight, Andrea
; APPLICANT: O'Hara, Denise
; APPLICANT: Rup, Bonita
; APPLICANT: Veldman, Geerttruida M.
; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7 MOLECULES AND METHODS OF
; FILE REFERENCE: 08702.0082-01000
; CURRENT APPLICATION NUMBER: US/10/986,089A
; CURRENT FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: 09/359,596
; PRIOR FILING DATE: 1999-06-24
; PRIOR APPLICATION NUMBER: 09/249,011
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CDR2 of humanized murine anti-human B7-2 light chain
US-10-986-089A-18

Query Match 100.0%; Score 38; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WASTRES 7
Db 1 WASTRES 7

RESULT 29
US-11-015-558-5
; Sequence 5, Application US/11015558
; Publication No. US20050227324A1
; GENERAL INFORMATION:
; APPLICANT: Arthur Jyh-Yen Huang, Ralph H. Schwall, Daniel G. Yansura
; TITLE OF INVENTION: MONOVALENT ANTIBODY FRAGMENTS USEFUL AS THERAPEUTICS
; FILE REFERENCE: P2081R1
; CURRENT APPLICATION NUMBER: US/11/015,558
; CURRENT FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: US 60/531,409
; PRIOR FILING DATE: 2003-12-19
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO 5
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-015-558-5

Query Match 100.0%; Score 38; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WASTRES 7
Db 1 WASTRES 7

RESULT 30
US-10-700-632-50
; Sequence 50, Application US/10700632
; Publication No. US20050118183A1
; GENERAL INFORMATION:
; APPLICANT: Immunogen, Inc.

; TITLE OF INVENTION: ANTI-CD33 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID
; FILE OF INVENTION: LEUKEMIA USING THE SAME
; FILE REFERENCE: A8427
; CURRENT APPLICATION NUMBER: US/10/700,632
; PRIOR FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: US 60/424,332
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 50
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-700-632-50

Query Match 100.0%; Score 38; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
| | | | |
Db 6 WASTRES 12

RESULT 31
US-10-078-958-15
; Sequence 15, Application US/10078958
; Publication No. US20030070185A1
; GENERAL INFORMATION:
; APPLICANT: JAKOBOVITS, AYA
; APPLICANT: KUCHERLAPATI, RAJU
; APPLICANT: KLAPHOLZ, SUSAN
; APPLICANT: MENDEZ, MICHAEL J.
; APPLICANT: GREEN, LARRY
; TITLE OF INVENTION: TRANSGENIC MAMMALS HAVING HUMAN Ig LOC1 INCLUDING
; TITLE OF INVENTION: PLURAL VH AND VK REGIONS AND ANTIBODIES PRODUCED
; FILE REFERENCE: CELL 4.18 CON
; CURRENT APPLICATION NUMBER: US/10/078,958
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 08/759,620
; PRIOR FILING DATE: 1996-12-03
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-078-958-15

Query Match 100.0%; Score 38; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
| | | | |
Db 37 WASTRES 43

RESULT 32
US-09-905-243-60
; Sequence 60, Application US/09905243
; Patent No. US20020062009A1
; GENERAL INFORMATION:
; APPLICANT: Taylor, Alexander H
; TITLE OF INVENTION: Monoclonal Antibodies with Reduced
; FILE REFERENCE: P50770
; CURRENT APPLICATION NUMBER: US/09/905,243
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/300,970
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 97

; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 60
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Macaca cynomolgus
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (24)...(40)
; OTHER INFORMATION: CDRI
; NAME/KEY: DOMAIN
; LOCATION: (56)...(62)
; OTHER INFORMATION: CDRII
; US-09-905-243-60

Query Match 100.0%; Score 38; DB 3; Length 94;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
| | | | |
Db 56 WASTRES 62

RESULT 33
US-11-099-331-60
; Sequence 60, Application US/11099331
; Publication No. US20050208625A1
; GENERAL INFORMATION:
; APPLICANT: Taylor, Alexander H
; TITLE OF INVENTION: Monoclonal Antibodies with Reduced
; FILE REFERENCE: P50770
; CURRENT APPLICATION NUMBER: US/11/099,331
; CURRENT FILING DATE: 2005-04-05
; PRIOR APPLICATION NUMBER: US/09/905,243
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/300,970
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 60
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Macaca cynomolgus
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (24)...(40)
; OTHER INFORMATION: CDRI
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (56)...(62)
; OTHER INFORMATION: CDRII
; US-11-099-331-60

Query Match 100.0%; Score 38; DB 6; Length 94;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
| | | | |
Db 56 WASTRES 62

RESULT 34
US-10-700-632-60
; Sequence 60, Application US/10700632
; Publication No. US20050118183A1
; GENERAL INFORMATION:
; APPLICANT: Immunogen, Inc.
; TITLE OF INVENTION: ANTI-CD33 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID
; FILE REFERENCE: A8427
; CURRENT APPLICATION NUMBER: US/10/700,632

```
/ CURRENT FILING DATE: 2003-11-05
/ PRIOR APPLICATION NUMBER: US 60/424,332
/ PRIOR FILING DATE: 2002-11-07
/ NUMBER OF SEQ ID NOS: 94
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 60
/ LENGTH: 99
/ TYPE: PRT
/ ORGANISM: Mus musculus
US-10-700-632-60
```

```
Query Match          100.0%; Score 38; DB 5; Length 99;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

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QY      1 WASTRES 7
        |||||
Db      56 WASTRES 62
```

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RESULT 35
US-10-194-975-89
/ Sequence 89; Application US/10194975
/ Publication No. US20030039649A1
/ GENERAL INFORMATION:
/ APPLICANT: Foote, Jefferson
/ TITLE OF INVENTION: Super Humanized Antibodies
/ FILE REFERENCE: 501231.01
/ CURRENT APPLICATION NUMBER: US/10/194,975
/ CURRENT FILING DATE: 2002-10-10
/ PRIOR APPLICATION NUMBER: US 60/305,111
/ PRIOR FILING DATE: 2001-07-12
/ NUMBER OF SEQ ID NOS: 122
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 89
/ LENGTH: 101
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-194-975-89
```

```
Query Match          100.0%; Score 38; DB 4; Length 101;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WASTRES 7
        |||||
Db      56 WASTRES 62
```

```
RESULT 36
US-10-125-687-25
/ Sequence 25; Application US/10125687
/ Publication No. US20030054407A1
/ GENERAL INFORMATION:
/ APPLICANT: Luo, Peter
/ TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
/ FILE REFERENCE: 26050-705
/ CURRENT APPLICATION NUMBER: US/10/125,687
/ CURRENT FILING DATE: 2002-04-17
/ NUMBER OF SEQ ID NOS: 28
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 25
/ LENGTH: 101
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-125-687-25
```

```
Query Match          100.0%; Score 38; DB 4; Length 101;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WASTRES 7
        |||||
```

```
Db      56 WASTRES 62
```

```
RESULT 37
US-10-308-817-36
/ Sequence 36; Application US/10308817
/ Publication No. US20030219861A1
/ GENERAL INFORMATION:
/ APPLICANT: Rocher, Russell
/ APPLICANT: Wu, Dayang
/ TITLE OF INVENTION: HYBRID ANTIBODIES
/ FILE REFERENCE: 1087-37
/ CURRENT APPLICATION NUMBER: US/10/308,817
/ CURRENT FILING DATE: 2002-12-03
/ NUMBER OF SEQ ID NOS: 195
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 36
/ LENGTH: 101
/ TYPE: PRT
/ ORGANISM: human
US-10-308-817-36
```

```
Query Match          100.0%; Score 38; DB 4; Length 101;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WASTRES 7
        |||||
Db      56 WASTRES 62
```

```
RESULT 38
US-10-453-698-36
/ Sequence 36; Application US/10453698
/ Publication No. US20040038308A1
/ GENERAL INFORMATION:
/ APPLICANT: Rocher, Russell
/ TITLE OF INVENTION: HYBRID ANTIBODIES
/ FILE REFERENCE: 82 CIP (1087-37 CIP)
/ CURRENT APPLICATION NUMBER: US/10/453,698
/ CURRENT FILING DATE: 2003-06-03
/ NUMBER OF SEQ ID NOS: 196
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 36
/ LENGTH: 101
/ TYPE: PRT
/ ORGANISM: human
US-10-453-698-36
```

```
Query Match          100.0%; Score 38; DB 4; Length 101;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WASTRES 7
        |||||
Db      56 WASTRES 62
```

```
RESULT 39
US-10-379-392-103
/ Sequence 103; Application US/10379392
/ Publication No. US20040110226A1
/ GENERAL INFORMATION:
/ APPLICANT: Lazar, Gregory Alan
/ APPLICANT: Desjarlais, John Rudolf
/ APPLICANT: Marshall, Shannon Alicia
/ APPLICANT: Dahiyat, Basail I.
/ TITLE OF INVENTION: ANTIBODY OPTIMIZATION
/ FILE REFERENCE: A-71386-3 463077-236
/ CURRENT APPLICATION NUMBER: US/10/379,392
/ CURRENT FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/360,843
/ PRIOR FILING DATE: 2002-03-01
```

PRIOR APPLICATION NUMBER: US 60/384,197
PRIOR FILING DATE: 2002-05-29
NUMBER OF SEQ ID NOS: 184
SOFTWARE: PatentIn version 3.2
SEQ ID NO 103
LENGTH: 101
TYPE: PRT
ORGANISM: Homo sapiens
US-10-379-392-103

Query Match 100.0%; Score 38; DB 4; Length 101;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Indels 0; Gaps 0;

Qy 1 WASTRES 7
Db 56 WASTRES 62

RESULT 40
US-10-996-191-25
Sequence 25, Application US/10996191
Publication No. US20050148001A1
GENERAL INFORMATION:
APPLICANT: Luo, Peizhi
TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
FILE REFERENCE: 26050-705.301
CURRENT APPLICATION NUMBER: US/10/996,191
CURRENT FILING DATE: 2004-11-22
PRIOR APPLICATION NUMBER: US 60/284,407
PRIOR FILING DATE: 2001-04-17
PRIOR APPLICATION NUMBER: US 10/125,687
PRIOR FILING DATE: 2002-04-17
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.1
SEQ ID NO 25
LENGTH: 101
TYPE: PRT
ORGANISM: Homo sapiens
US-10-996-191-25

Query Match 100.0%; Score 38; DB 5; Length 101;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Indels 0; Gaps 0;

Qy 1 WASTRES 7
Db 56 WASTRES 62

RESULT 41
US-10-010-729-37
Sequence 37, Application US/10010729
Publication No. US20030185827A1
GENERAL INFORMATION:
APPLICANT: Rodriguez, Moses
APPLICANT: Miller, David J.
TITLE OF INVENTION: Human IgM Antibodies and Diagnostic and
TITLE OF INVENTION: Therapeutic Uses Thereof Particularly in the Central Nervous
FILE REFERENCE: 1199-1-005CIP2
CURRENT APPLICATION NUMBER: US/10/010,729
CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: 09/730,473
PRIOR FILING DATE: 2000-12-05
PRIOR APPLICATION NUMBER: 09/580,787
PRIOR FILING DATE: 2000-05-30
PRIOR APPLICATION NUMBER: 09/322,862
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 08/779,784
PRIOR FILING DATE: 1997-01-07
PRIOR APPLICATION NUMBER: 08/692,084

PRIOR FILING DATE: 1996-08-08
PRIOR APPLICATION NUMBER: 08/236,520
PRIOR FILING DATE: 1994-04-29
NUMBER OF SEQ ID NOS: 80
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 37
LENGTH: 105
TYPE: PRT
ORGANISM: Homo sapiens
US-10-010-729-37

Query Match 100.0%; Score 38; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Indels 0; Gaps 0;

Qy 1 WASTRES 7
Db 56 WASTRES 62

RESULT 42
US-10-325-694-142
Sequence 142, Application US/10325694
Publication No. US20030148463A1
GENERAL INFORMATION:
APPLICANT: KUPER, PETER
TITLE OF INVENTION: NOVEL METHOD FOR THE PRODUCTION OF ANTI-HUMAN ANTIGEN
FILE REFERENCE: 38164000
CURRENT APPLICATION NUMBER: US/10/325,694
CURRENT FILING DATE: 2002-12-19
PRIOR APPLICATION NUMBER: US/09/403,107
PRIOR FILING DATE: 1999-10-14
NUMBER OF SEQ ID NOS: 152
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 142
LENGTH: 107
TYPE: PRT
ORGANISM: HUMAN
US-10-325-694-142

Query Match 100.0%; Score 38; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Indels 0; Gaps 0;

Qy 1 WASTRES 7
Db 50 WASTRES 56

RESULT 43
US-10-325-694-148
Sequence 148, Application US/10325694
Publication No. US20030148463A1
GENERAL INFORMATION:
APPLICANT: KUPER, PETER
APPLICANT: RAUM, TOBIAS
TITLE OF INVENTION: NOVEL METHOD FOR THE PRODUCTION OF ANTI-HUMAN ANTIGEN
TITLE OF INVENTION: RECEPTORS AND USES THEREOF
FILE REFERENCE: 38164000
CURRENT APPLICATION NUMBER: US/10/325,694
CURRENT FILING DATE: 2002-12-19
PRIOR APPLICATION NUMBER: US/09/403,107
PRIOR FILING DATE: 1999-10-14
NUMBER OF SEQ ID NOS: 152
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 148
LENGTH: 107
TYPE: PRT
ORGANISM: HUMAN
US-10-325-694-148

Query Match 100.0%; Score 38; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
|||||
50 WASTRES 56

RESULT 44
US-10-325-694-149

; Sequence 149, Application US/10325694
; Publication No. US20030148463A1
; GENERAL INFORMATION:

; APPLICANT: KUPER, PETER
; APPLICANT: RAUM, TOBIAS
; TITLE OF INVENTION: NOVEL METHOD FOR THE PRODUCTION OF ANTI-HUMAN ANTIGEN
; FILE REFERENCE: 38164000
; CURRENT APPLICATION NUMBER: US/10/325,694

; PRIOR FILING DATE: 2002-12-19
; PRIOR FILING DATE: 1999-10-14
; NUMBER OF SEQ ID NOS: 152

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 149

; LENGTH: 107
; TYPE: PRT
; ORGANISM: HUMAN
US-10-325-694-149

Query Match 100.0%; Score 38; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
|||||
50 WASTRES 56

RESULT 45
US-10-325-694-152

; Sequence 152, Application US/10325694
; Publication No. US20030148463A1
; GENERAL INFORMATION:

; APPLICANT: KUPER, PETER
; APPLICANT: RAUM, TOBIAS
; TITLE OF INVENTION: NOVEL METHOD FOR THE PRODUCTION OF ANTI-HUMAN ANTIGEN
; FILE REFERENCE: 38164000
; CURRENT APPLICATION NUMBER: US/10/325,694

; PRIOR FILING DATE: 2002-12-19
; PRIOR FILING DATE: 1999-10-14
; NUMBER OF SEQ ID NOS: 152

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 152

; LENGTH: 107
; TYPE: PRT
; ORGANISM: HUMAN
US-10-325-694-152

Query Match 100.0%; Score 38; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
|||||
50 WASTRES 56

RESULT 46
US-10-883-020-35

; Sequence 35, Application US/10883020
; Publication No. US20050048070A1
; GENERAL INFORMATION:

; APPLICANT: Ditzel, Henrik
; APPLICANT: Jensenius, Jens
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: Cancer-Associated Epitope
; FILE REFERENCE: 1361.017US1

; CURRENT APPLICATION NUMBER: US/10/883,020
; CURRENT FILING DATE: 2004-07-01
; PRIOR APPLICATION NUMBER: PCT/US03/00297

; PRIOR FILING DATE: 2003-01-03
; PRIOR APPLICATION NUMBER: US 60/345,208
; PRIOR FILING DATE: 2002-01-03

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US-10-883-020-35

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RESULT 47
US-09-828-708-1

; Sequence 1, Application US/09828708
; Patent No. US20020146753A1
; GENERAL INFORMATION:

; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.

; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partici
; FILE REFERENCE: 1361.005US1
; CURRENT APPLICATION NUMBER: US/09/828,708

; PRIOR FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-708-1

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49 WASTRES 55

RESULT 48
US-09-828-708-4

; Sequence 4, Application US/09828708
; Patent No. US20020146753A1
; GENERAL INFORMATION:

; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.

; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partici
; FILE REFERENCE: 1361.005US1
; CURRENT APPLICATION NUMBER: US/09/828,708

; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 123
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; ORGANISM: Homo sapiens
US-09-828-708-4

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; Sequence 1, Application US/10630009
; Publication No. US20050080239A1
; GENERAL INFORMATION:
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partic
; FILE REFERENCE: 1361.005US2
; CURRENT APPLICATION NUMBER: US/10/630,009
; CURRENT FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: US 09/828,708
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-630-009-1

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QY 1 WASTRES 7
Db 49 WASTRES 55

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; Sequence 4, Application US/10630009
; Publication No. US20050080239A1
; GENERAL INFORMATION:
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partic
; FILE REFERENCE: 1361.005US2
; CURRENT APPLICATION NUMBER: US/10/630,009
; CURRENT FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: US 09/828,708
; PRIOR FILING DATE: 2001-04-06
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; ORGANISM: Homo sapiens
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QY 1 WASTRES 7
Db 49 WASTRES 55

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OM protein - protein search, using sw model

Run on: May 4, 2006, 13:46:13 / Search time 8.1111 Seconds
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Maximum Match 100%
Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	38	100.0	101	US-11-054-669-89	Sequence 89, Appl1
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210	27	71.1	3570	9	US-10-453-372-178	Sequence 178, App
211	27	71.1	3570	9	US-10-453-372-196	Sequence 196, App
212	27	71.1	3570	9	US-10-453-372-198	Sequence 198, App
213	27	71.1	3570	9	US-10-453-372-200	Sequence 200, App
214	27	71.1	3570	9	US-10-453-372-202	Sequence 202, App
215	27	71.1	3570	9	US-10-453-372-204	Sequence 204, App
216	27	71.1	3570	9	US-10-453-372-206	Sequence 206, App
217	27	71.1	15	10	US-11-176-182-45	Sequence 45, Appl1
218	26	68.4	18	10	US-11-176-182-95	Sequence 95, Appl1
219	26	68.4	61	11	US-11-096-568A-25322	Sequence 25322, A
220	26	68.4	101	11	US-11-096-568A-25321	Sequence 25321, A
221	26	68.4	102	9	US-10-218-84-54	Sequence 54, Appl1
222	26	68.4	102	9	US-10-219-061-54	Sequence 54, Appl1
223	26	68.4	102	9	US-10-219-062-54	Sequence 54, Appl1
224	26	68.4	102	9	US-10-219-064-54	Sequence 54, Appl1
225	26	68.4	102	9	US-10-233-134-54	Sequence 54, Appl1
226	26	68.4	111	11	US-11-072-512-2767	Sequence 2767, Ap
227	26	68.4	123	11	US-11-087-099-4923	Sequence 4923, Ap
228	26	68.4	141	11	US-11-087-099-2009	Sequence 2009, Ap
229	26	68.4	141	11	US-11-087-099-9475	Sequence 9475, Ap
230	26	68.4	141	11	US-11-096-568A-4518	Sequence 4518, Ap
231	26	68.4	142	11	US-11-072-512-3143	Sequence 3143, Ap
232	26	68.4	142	11	US-11-087-099-10961	Sequence 10961, A
233	26	68.4	152	9	US-10-927-641-64	Sequence 64, Appl1
234	26	68.4	152	9	US-10-957-569-38	Sequence 38, Appl1
235	26	68.4	152	9	US-10-523-503-3	Sequence 3, Appl1
236	26	68.4	152	11	US-11-097-589-37	Sequence 37, Appl1
237	26	68.4	156	11	US-11-096-568A-25315	Sequence 25315, A
238	26	68.4	157	11	US-11-087-099-642	Sequence 642, App
239	26	68.4	157	11	US-11-087-099-1738	Sequence 1738, Ap
240	26	68.4	157	11	US-11-087-099-1888	Sequence 1888, Ap

241	26	68.4	157	11	US-11-087-099-2936	Sequence 2936, Ap	314	26	68.4	484	9	US-10-784-004-930	Sequence 930, App
242	26	68.4	157	11	US-11-087-099-6590	Sequence 6590, Ap	315	26	68.4	484	11	US-11-096-568A-20334	Sequence 20334, A
243	26	68.4	157	11	US-11-087-099-9844	Sequence 9844, Ap	316	26	68.4	508	11	US-11-096-568A-24531	Sequence 24531, A
244	26	68.4	157	11	US-11-087-099-10071	Sequence 10071, A	317	26	68.4	513	11	US-11-087-099-8601	Sequence 8601, Ap
245	26	68.4	157	11	US-11-087-099-10671	Sequence 10647, A	318	26	68.4	513	11	US-11-188-298-17267	Sequence 17267, A
246	26	68.4	158	11	US-11-087-099-3790	Sequence 3790, Ap	319	26	68.4	520	11	US-11-087-099-2137	Sequence 2137, Ap
247	26	68.4	159	11	US-11-087-099-4510	Sequence 4510, Ap	320	26	68.4	520	11	US-11-087-099-5442	Sequence 5442, Ap
248	26	68.4	159	11	US-11-087-099-5313	Sequence 5313, Ap	321	26	68.4	520	11	US-11-188-298-1233	Sequence 1233, Ap
249	26	68.4	159	11	US-11-087-099-6950	Sequence 6950, Ap	322	26	68.4	520	11	US-11-188-298-9248	Sequence 9248, Ap
250	26	68.4	159	11	US-11-087-099-7724	Sequence 7724, Ap	323	26	68.4	520	11	US-11-127-897-42	Sequence 42, Appl
251	26	68.4	166	11	US-11-264-096-696	Sequence 696, App	324	26	68.4	534	11	US-11-096-568A-32022	Sequence 32022, A
252	26	68.4	164	11	US-11-264-096-697	Sequence 697, App	325	26	68.4	544	11	US-11-096-568A-19501	Sequence 19501, A
253	26	68.4	184	11	US-11-079-463-7546	Sequence 7546, Ap	326	26	68.4	553	11	US-11-096-568A-32021	Sequence 32021, A
254	26	68.4	184	11	US-11-188-298-21398	Sequence 21398, A	327	26	68.4	565	11	US-11-096-568A-1994	Sequence 1994, Ap
255	26	68.4	187	7	US-09-978-360A-758	Sequence 758, App	328	26	68.4	565	11	US-11-096-568A-27236	Sequence 27236, A
256	26	68.4	220	9	US-10-952-251-2	Sequence 2, Appl	329	26	68.4	575	11	US-11-072-512-2815	Sequence 2815, Ap
257	26	68.4	224	11	US-11-096-568A-1294	Sequence 1294, Ap	330	26	68.4	579	11	US-11-043-004-115	Sequence 115, App
258	26	68.4	246	11	US-11-087-099-6025	Sequence 6025, Ap	331	26	68.4	587	11	US-11-188-298-10199	Sequence 10199, A
259	26	68.4	248	11	US-11-087-099-5977	Sequence 5977, Ap	332	26	68.4	590	11	US-11-188-298-8744	Sequence 8744, Ap
260	26	68.4	250	11	US-11-096-568A-30392	Sequence 30392, A	333	26	68.4	611	9	US-10-330-773-852	Sequence 852, App
261	26	68.4	251	11	US-11-087-099-2057	Sequence 2057, Ap	334	26	68.4	624	11	US-11-096-568A-1993	Sequence 1993, Ap
262	26	68.4	251	11	US-11-096-568A-6029	Sequence 6029, Ap	335	26	68.4	624	11	US-11-096-568A-27235	Sequence 27235, A
263	26	68.4	259	11	US-11-072-512-3858	Sequence 3858, Ap	336	26	68.4	625	11	US-11-096-568A-1992	Sequence 1992, Ap
264	26	68.4	274	11	US-11-096-568A-10768	Sequence 10768, A	337	26	68.4	625	11	US-11-096-568A-27234	Sequence 27234, A
265	26	68.4	276	11	US-11-096-568A-16388	Sequence 16388, A	338	26	68.4	648	11	US-11-188-298-9716	Sequence 9716, Ap
266	26	68.4	282	11	US-11-077-619-54	Sequence 54, Appl	339	26	68.4	650	11	US-11-096-568A-30432	Sequence 30432, A
267	26	68.4	283	11	US-11-072-512-2687	Sequence 2687, Ap	340	26	68.4	670	11	US-11-188-298-7985	Sequence 7985, Ap
268	26	68.4	289	9	US-10-793-626-234	Sequence 234, App	341	26	68.4	713	11	US-11-096-568A-30499	Sequence 3020, A
269	26	68.4	291	9	US-10-793-626-1458	Sequence 1458, App	342	26	68.4	750	11	US-11-096-568A-30499	Sequence 30499, A
270	26	68.4	314	11	US-11-087-099-874	Sequence 874, App	343	26	68.4	754	11	US-11-188-298-503	Sequence 503, App
271	26	68.4	320	11	US-11-188-298-4669	Sequence 4669, Ap	344	26	68.4	755	11	US-11-242-650-16	Sequence 16, Appl
272	26	68.4	330	11	US-11-087-099-2708	Sequence 2708, Ap	345	26	68.4	775	11	US-11-087-099-6419	Sequence 6419, Ap
273	26	68.4	333	11	US-11-096-568A-14947	Sequence 14947, A	346	26	68.4	781	9	US-10-242-586-98	Sequence 98, Appl
274	26	68.4	335	11	US-11-087-099-3628	Sequence 3628, Ap	347	26	68.4	781	9	US-10-242-586-98	Sequence 98, Appl
275	26	68.4	335	11	US-11-188-298-13088	Sequence 13088, A	348	26	68.4	781	9	US-10-243-116-98	Sequence 98, Appl
276	26	68.4	335	11	US-11-188-298-19819	Sequence 19819, A	349	26	68.4	781	9	US-10-243-136-98	Sequence 98, Appl
277	26	68.4	335	11	US-11-087-099-9299	Sequence 9299, Ap	350	26	68.4	781	9	US-10-243-189-98	Sequence 98, Appl
278	26	68.4	341	11	US-11-188-298-11084	Sequence 11084, A	351	26	68.4	781	9	US-10-243-215-98	Sequence 98, Appl
279	26	68.4	351	11	US-11-188-298-5018	Sequence 5018, Ap	352	26	68.4	781	9	US-10-243-316-98	Sequence 98, Appl
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281	26	68.4	351	11	US-11-188-298-9568	Sequence 9568, Ap	354	26	68.4	781	9	US-10-243-304-98	Sequence 98, Appl
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284	26	68.4	355	11	US-11-188-298-5061	Sequence 5061, Ap	357	26	68.4	781	9	US-10-243-357-98	Sequence 98, Appl
285	26	68.4	355	11	US-11-188-298-8938	Sequence 8938, Ap	358	26	68.4	781	9	US-10-245-083-98	Sequence 98, Appl
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288	26	68.4	377	11	US-11-188-298-20562	Sequence 20562, A	361	26	68.4	794	11	US-11-188-298-19197	Sequence 19197, A
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290	26	68.4	407	11	US-11-188-298-21310	Sequence 21310, A	363	26	68.4	837	11	US-11-188-298-5137	Sequence 5137, Ap
291	26	68.4	427	11	US-11-096-568A-18822	Sequence 18822, A	364	26	68.4	839	11	US-11-096-568A-24462	Sequence 24462, A
292	26	68.4	428	11	US-11-096-568A-19503	Sequence 19503, A	365	26	68.4	844	11	US-11-096-568A-27752	Sequence 27752, A
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294	26	68.4	437	11	US-11-087-099-5390	Sequence 5390, App	367	26	68.4	856	11	US-11-188-298-9689	Sequence 9689, Ap
295	26	68.4	438	11	US-11-096-568A-30764	Sequence 30764, A	368	26	68.4	859	11	US-11-087-099-2292	Sequence 2292, Ap
296	26	68.4	449	11	US-11-096-568A-20336	Sequence 20336, A	369	26	68.4	859	11	US-11-087-099-4580	Sequence 4580, Ap
297	26	68.4	453	11	US-11-087-099-7865	Sequence 7865, App	370	26	68.4	859	11	US-11-188-298-4225	Sequence 4225, Ap
298	26	68.4	453	11	US-11-188-298-7254	Sequence 7254, Ap	371	26	68.4	869	11	US-11-188-298-13250	Sequence 13250, A
299	26	68.4	456	11	US-11-096-568A-30763	Sequence 30763, A	372	26	68.4	876	11	US-11-087-099-7291	Sequence 7291, Ap
300	26	68.4	461	11	US-11-087-099-1753	Sequence 1753, App	373	26	68.4	876	11	US-11-087-099-11074	Sequence 11074, A
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303	26	68.4	463	11	US-11-096-568A-22044	Sequence 22044, A	376	26	68.4	876	11	US-11-096-568A-24461	Sequence 24461, A
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306	26	68.4	469	11	US-11-188-298-15873	Sequence 15973, A	379	26	68.4	885	11	US-11-096-568A-30498	Sequence 30498, A
307	26	68.4	470	11	US-11-188-298-22302	Sequence 22302, A	380	26	68.4	909	11	US-11-096-568A-24460	Sequence 24460, A
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312	26	68.4	484	9	US-10-784-004-372	Sequence 372, App	385	26	68.4	1275	11	US-10-724-598-49	Sequence 49, Appl
313	26	68.4	484	9	US-10-784-004-906	Sequence 906, App	386	26	68.4	1386	9	US-10-517-939-284	Sequence 284, App

387	26	68.4	2215	8	US-10-505-928-310	Sequence 310, App	460	25	65.8	2664	11	US-11-096-568A-18841	Sequence 18841, A
388	26	68.4	8746	11	US-11-098-686-10232	Sequence 10232, A	461	25	65.8	2674	11	US-11-096-568A-1634	Sequence 4634, Ap
389	25	65.8	12	10	US-11-041-893-98	Sequence 98, App1	462	25	65.8	2684	11	US-11-096-568A-18840	Sequence 18840, A
390	25	65.8	15	10	US-11-176-182-43	Sequence 43, App1	463	25	65.8	2704	11	US-11-096-568A-1633	Sequence 4633, Ap
391	25	65.8	17	11	US-11-264-096-776	Sequence 776, App	464	25	65.8	2784	9	US-10-506-454-934	Sequence 934, App
392	25	65.8	21	9	US-10-966-371-22	Sequence 22, App1	465	25	65.8	2819	9	US-10-980-556-102	Sequence 10, App1
393	25	65.8	29	9	US-10-467-657-8294	Sequence 4294, Ap	466	25	65.8	2819	9	US-10-980-556-102	Sequence 10, App1
394	25	65.8	40	11	US-11-109-161-8	Sequence 8, App1	467	25	65.8	2819	11	US-11-166-004A-47	Sequence 47, App1
395	25	65.8	53	9	US-10-815-320-8	Sequence 8, App1	468	25	65.8	2884	11	US-11-096-568A-18839	Sequence 18839, A
396	25	65.8	72	9	US-10-815-320-6	Sequence 6, App1	469	25	65.8	3014	11	US-11-166-004A-44	Sequence 44, App1
397	25	65.8	72	11	US-11-096-568A-780	Sequence 780, App	470	25	65.8	3024	11	US-11-098-686-10927	Sequence 10927, A
398	25	65.8	84	11	US-11-096-568A-8644	Sequence 8644, Ap	471	25	65.8	3024	11	US-11-096-568A-11249	Sequence 11249, A
399	25	65.8	87	11	US-11-166-609-16	Sequence 16, App1	472	25	65.8	3094	11	US-11-166-004A-24	Sequence 24, App1
400	25	65.8	130	11	US-11-031-206-88	Sequence 88, App1	473	25	65.8	3094	11	US-11-166-004A-25	Sequence 25, App1
401	25	65.8	112	11	US-11-096-568A-203	Sequence 203, App	474	25	65.8	3094	11	US-11-166-004A-26	Sequence 26, App1
402	25	65.8	130	11	US-11-096-568A-32836	Sequence 32836, A	475	25	65.8	3094	11	US-11-166-004A-41	Sequence 41, App1
403	25	65.8	136	11	US-11-096-568A-202	Sequence 202, App	476	25	65.8	3114	11	US-11-096-568A-28762	Sequence 28762, A
404	25	65.8	136	11	US-11-096-568A-32835	Sequence 32835, A	477	25	65.8	3154	11	US-11-087-099-5128	Sequence 59, App1
405	25	65.8	137	11	US-11-087-099-9406	Sequence 9406, Ap	478	25	65.8	3154	11	US-11-087-099-5128	Sequence 59, App1
406	25	65.8	146	11	US-11-154-227-38	Sequence 38, App1	479	25	65.8	3224	11	US-11-096-568A-6222	Sequence 6222, Ap
407	25	65.8	154	11	US-11-096-568A-11251	Sequence 11251, A	480	25	65.8	3244	11	US-11-098-686-10889	Sequence 10889, A
408	25	65.8	156	11	US-11-172-740-2081	Sequence 2081, Ap	481	25	65.8	3254	11	US-11-166-004A-40	Sequence 40, App1
409	25	65.8	157	11	US-11-096-568A-6050	Sequence 6050, Ap	482	25	65.8	3264	11	US-11-096-568A-19445	Sequence 19445, A
410	25	65.8	160	11	US-11-087-099-3357	Sequence 3357, Ap	483	25	65.8	3274	11	US-11-079-463-10347	Sequence 10347, A
411	25	65.8	160	11	US-11-166-004A-39	Sequence 39, App1	484	25	65.8	3284	11	US-11-096-568A-7355	Sequence 7355, A
412	25	65.8	160	11	US-11-166-004A-53	Sequence 53, App1	485	25	65.8	3314	9	US-10-454-437-392	Sequence 392, App
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414	25	65.8	161	11	US-11-166-004A-38	Sequence 38, App1	487	25	65.8	3344	11	US-11-188-298-10242	Sequence 10242, A
415	25	65.8	163	11	US-11-096-568A-7283	Sequence 7283, A	488	25	65.8	3354	9	US-10-815-320-2	Sequence 2, App1
416	25	65.8	163	11	US-11-096-568A-32834	Sequence 32834, Ap	489	25	65.8	3354	11	US-11-188-298-55222	Sequence 5222, App
417	25	65.8	164	11	US-11-087-099-6508	Sequence 6508, Ap	490	25	65.8	3394	11	US-11-096-568A-18003	Sequence 18003, A
418	25	65.8	164	11	US-11-087-099-12087	Sequence 12087, A	491	25	65.8	3414	11	US-11-188-298-5060	Sequence 5060, Ap
419	25	65.8	165	11	US-11-087-099-9748	Sequence 9748, Ap	492	25	65.8	3434	9	US-10-330-773-803	Sequence 803, App
420	25	65.8	165	11	US-11-096-568A-201	Sequence 201, App	493	25	65.8	3434	9	US-10-330-773-805	Sequence 805, App
421	25	65.8	165	11	US-11-096-568A-204	Sequence 204, App	494	25	65.8	3434	9	US-10-330-773-807	Sequence 807, App
422	25	65.8	165	11	US-11-166-004A-50	Sequence 50, App1	495	25	65.8	3484	11	US-11-188-298-6592	Sequence 10301, A
423	25	65.8	171	11	US-11-172-740-2082	Sequence 2082, Ap	496	25	65.8	3484	11	US-11-188-298-6592	Sequence 6592, Ap
424	25	65.8	175	9	US-10-821-234-1615	Sequence 1615, Ap	497	25	65.8	3524	11	US-11-096-568A-19444	Sequence 19444, A
425	25	65.8	179	7	US-09-985-493-134	Sequence 134, App	498	25	65.8	3544	11	US-11-087-099-1112	Sequence 1112, Ap
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427	25	65.8	183	11	US-11-087-099-7870	Sequence 7870, Ap	500	25	65.8	3574	11	US-11-087-099-1857	Sequence 1857, A
428	25	65.8	183	11	US-11-087-099-10648	Sequence 10648, A	501	25	65.8	3574	11	US-11-188-298-14525	Sequence 14525, A
429	25	65.8	183	11	US-11-096-568A-6049	Sequence 6049, Ap	502	25	65.8	3594	11	US-11-188-298-14525	Sequence 14525, A
430	25	65.8	185	11	US-11-096-568A-25833	Sequence 25833, A	503	25	65.8	3594	11	US-11-188-298-15537	Sequence 15537, A
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432	25	65.8	189	11	US-11-096-568A-17657	Sequence 17657, A	505	25	65.8	3614	11	US-11-096-568A-27449	Sequence 27449, A
433	25	65.8	193	11	US-11-096-568A-9456	Sequence 9456, Ap	506	25	65.8	3624	11	US-11-096-568A-31044	Sequence 31044, A
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435	25	65.8	197	11	US-11-166-004A-37	Sequence 37, App1	508	25	65.8	3654	11	US-11-264-096-736	Sequence 736, App
436	25	65.8	200	11	US-11-238-549-2	Sequence 2, App1	509	25	65.8	3654	11	US-11-264-096-736	Sequence 737, App
437	25	65.8	200	11	US-11-238-549-6	Sequence 6, App1	510	25	65.8	3664	11	US-11-096-568A-17143	Sequence 17143, A
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439	25	65.8	204	11	US-11-096-568A-17656	Sequence 17656, A	512	25	65.8	3714	11	US-11-096-568A-8795	Sequence 8795, Ap
440	25	65.8	211	11	US-11-124-368A-11706	Sequence 11706, A	513	25	65.8	3764	11	US-11-055-822-152	Sequence 152, App
441	25	65.8	215	9	US-10-467-657-36	Sequence 36, App1	514	25	65.8	3774	11	US-11-096-568A-21150	Sequence 21150, A
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443	25	65.8	218	11	US-11-072-512-2205	Sequence 2205, Ap	516	25	65.8	3854	11	US-11-096-568A-27447	Sequence 27447, A
444	25	65.8	220	9	US-10-506-454-1635	Sequence 1635, Ap	517	25	65.8	3914	11	US-11-096-568A-8794	Sequence 8794, Ap
445	25	65.8	220	11	US-11-148-012-3	Sequence 3, App1	518	25	65.8	3964	11	US-11-087-099-12242	Sequence 12242, A
446	25	65.8	226	11	US-11-148-012-2	Sequence 2, App1	519	25	65.8	4004	9	US-10-194-487-530	Sequence 530, App
447	25	65.8	226	11	US-11-148-012-2	Sequence 2, App1	520	25	65.8	4004	9	US-10-195-888-530	Sequence 530, App
448	25	65.8	226	11	US-11-166-004A-23	Sequence 23, App1	521	25	65.8	4004	9	US-10-195-888-530	Sequence 530, App
449	25	65.8	226	11	US-11-096-568A-11250	Sequence 11250, A	522	25	65.8	4004	9	US-10-195-888-530	Sequence 530, App
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454	25	65.8	257	11	US-11-096-568A-6223	Sequence 6223, Ap	527	25	65.8	4084	11	US-11-096-568A-16345	Sequence 16345, A
455	25	65.8	259	11	US-11-096-568A-4635	Sequence 4635, Ap	528	25	65.8	4084	11	US-11-096-568A-19443	Sequence 19443, A
456	25	65.8	261	9	US-10-055-877-164	Sequence 164, App	529	25	65.8	4114	9	US-10-621-234-946	Sequence 8799, Ap
457	25	65.8	261	9	US-10-055-877-165	Sequence 165, App	530	25	65.8	4164	11	US-11-096-568A-31573	Sequence 31573, A
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535	25	65.8	423	11	US-11-096-568A-28754	Sequence 28754, A	608	25	65.8	532	11	US-11-096-568A-22026	Sequence 22026, A
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538	25	65.8	428	11	US-11-188-298-8024	Sequence 8024, Ap	611	25	65.8	542	11	US-11-225-768-323	Sequence 323, Appl
539	25	65.8	429	11	US-11-096-568A-28002	Sequence 28002, A	612	25	65.8	572	11	US-11-188-298-13457	Sequence 13457, A
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548	25	65.8	447	11	US-11-096-568A-28752	Sequence 28752, A	621	25	65.8	647	11	US-11-096-568A-27741	Sequence 27741, A
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554	25	65.8	458	11	US-11-096-568A-11092	Sequence 11092, A	627	25	65.8	676	10	US-11-181-115-29	Sequence 29, Appl
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559	25	65.8	461	11	US-11-188-298-13414	Sequence 13414, A	632	25	65.8	756	9	US-10-973-115B-392	Sequence 392, App
560	25	65.8	461	11	US-11-188-298-13888	Sequence 13888, A	633	25	65.8	756	9	US-10-137-873A-392	Sequence 392, App
561	25	65.8	462	11	US-11-188-298-4122	Sequence 4122, Ap	634	25	65.8	756	9	US-10-152-370-392	Sequence 392, App
562	25	65.8	463	11	US-11-096-568A-28796	Sequence 28796, A	635	25	65.8	756	11	US-11-290-153-392	Sequence 392, App
563	25	65.8	463	11	US-11-188-298-776	Sequence 776, App	636	25	65.8	762	11	US-11-087-099-3342	Sequence 3342, Ap
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571	25	65.8	466	11	US-11-188-298-3965	Sequence 3965, Ap	644	25	65.8	802	11	US-11-188-298-13638	Sequence 13638, A
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573	25	65.8	469	11	US-11-188-298-19521	Sequence 19521, A	646	25	65.8	809	11	US-11-188-298-3837	Sequence 3837, Ap
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579	25	65.8	478	11	US-11-087-099-2340	Sequence 2340, Ap	652	25	65.8	858	11	US-11-087-099-9930	Sequence 9930, Ap
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581	25	65.8	480	11	US-11-096-568A-28760	Sequence 28760, A	654	25	65.8	879	9	US-10-204-639-58	Sequence 58, Appl
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586	25	65.8	488	11	US-11-188-298-807	Sequence 807, App	659	25	65.8	931	11	US-11-096-568A-14779	Sequence 14779, A
587	25	65.8	488	11	US-11-188-298-3581	Sequence 3581, Ap	660	25	65.8	1128	11	US-11-037-243-97	Sequence 97, Appl
588	25	65.8	488	11	US-11-188-298-17472	Sequence 17472, A	661	25	65.8	1476	9	US-10-647-956A-4	Sequence 4, Appl1
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591	25	65.8	490	9	US-10-131-826A-310	Sequence 310, App	664	25	65.8	2144	11	US-11-043-889-2	Sequence 2, Appl1
592	25	65.8	490	9	US-10-973-115B-310	Sequence 310, App	665	25	65.8	3389	9	US-10-204-252-10	Sequence 10, Appl1
593	25	65.8	490	9	US-10-137-873A-310	Sequence 310, App	666	25	65.8	3391	9	US-10-204-252-6	Sequence 6, Appl1
594	25	65.8	490	11	US-10-152-370-310	Sequence 310, App	667	25	65.8	3391	9	US-10-204-252-8	Sequence 8, Appl1
595	25	65.8	490	11	US-11-290-153-310	Sequence 310, App	668	25	65.8	3391	9	US-10-204-252-12	Sequence 12, Appl1
596	25	65.8	491	11	US-11-096-568A-20377	Sequence 20377, A	669	25	65.8	3391	9	US-10-204-252-14	Sequence 14, Appl1
597	25	65.8	493	9	US-10-508-263-30	Sequence 30, Appl	670	25	65.8	3391	9	US-10-204-252-16	Sequence 16, Appl1
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601	25	65.8	525	9	US-10-973-115B-56	Sequence 56, Appl	674	25	65.8	3433	11	US-11-223-729-2	Sequence 2, Appl1
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604	25	65.8	525	11	US-11-290-153-56	Sequence 56, Appl	677	25	65.8	4544	11	US-11-076-426A-52	Sequence 32, Appl1
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680	24	63.2	13	10	US-11-176-182-17	Sequence 17, App1	753	24	63.2	252	11	US-11-096-568A-18219	Sequence 18219, A
681	24	63.2	45	11	US-11-004-399-1835	Sequence 1835, Ap	754	24	63.2	253	11	US-11-054-115-860	Sequence 860, App
682	24	63.2	50	11	US-11-233-798-60	Sequence 60, App1	755	24	63.2	253	11	US-11-266-444-860	Sequence 860, App
683	24	63.2	50	11	US-11-233-798-60	Sequence 61, App1	756	24	63.2	254	11	US-11-096-568A-3889	Sequence 3889, App
684	24	63.2	59	11	US-11-233-798-36	Sequence 36, App1	757	24	63.2	256	11	US-11-128-059-68	Sequence 68, App1
685	24	63.2	60	11	US-11-233-798-34	Sequence 34, App1	758	24	63.2	256	11	US-11-096-568A-30349	Sequence 30349, Ap
686	24	63.2	60	11	US-11-233-798-35	Sequence 35, App1	759	24	63.2	256	11	US-11-096-568A-30349	Sequence 30349, A
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693	24	63.2	110	9	US-10-467-657-738	Sequence 738, Ap	766	24	63.2	269	11	US-11-188-298-22015	Sequence 22015, A
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696	24	63.2	122	9	US-10-644-807-357	Sequence 357, App	769	24	63.2	273	11	US-11-188-298-11871	Sequence 11871, A
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704	24	63.2	145	11	US-11-087-099-7837	Sequence 7837, Ap	777	24	63.2	296	11	US-11-096-568A-23305	Sequence 23305, A
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708	24	63.2	153	11	US-11-096-568A-24489	Sequence 24489, A	781	24	63.2	306	9	US-10-644-807-252	Sequence 352, App
709	24	63.2	157	11	US-11-096-568A-2798	Sequence 2798, Ap	782	24	63.2	306	9	US-10-644-807-347	Sequence 347, App
710	24	63.2	157	11	US-11-096-568A-2801	Sequence 2801, Ap	783	24	63.2	307	11	US-11-096-568A-20339	Sequence 20339, A
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712	24	63.2	158	9	US-10-995-561-586	Sequence 586, App	785	24	63.2	312	11	US-11-082-389-346	Sequence 346, App
713	24	63.2	158	9	US-10-530-253-76	Sequence 26, App1	786	24	63.2	313	9	US-10-723-207-3	Sequence 3, App1
714	24	63.2	165	11	US-11-128-059-26	Sequence 26, App1	787	24	63.2	314	11	US-11-188-298-6213	Sequence 6213, Ap
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ALIGNMENTS

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; Publication No. US20060015952A1
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; APPLICANT: FILVAROFF, ELLEN H.
; TITLE OF INVENTION: SCREENING ASSAYS AND METHODS OF TUMOR TREATMENT
; FILE REFERENCE: P2068R1
; CURRENT APPLICATION NUMBER: US/10/981,356A
; CURRENT FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: US 60/520,398
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/557,951
; PRIOR FILING DATE: 2004-03-31
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; OTHER INFORMATION: Sequence is synthesized
US-10-981-356A-19

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; APPLICANT: NIKI, Hisae
; APPLICANT: OIKE, Shinsuke
; APPLICANT: TAGAWA, Toshiki
; APPLICANT: HOSOKAWA, Saiko
; APPLICANT: YOSHIYAMA, Yoshiko
; TITLE OF INVENTION: Antibody recognizing antigen
; FILE REFERENCE: 235054
; CURRENT APPLICATION NUMBER: US/10/530,171
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/JP2003/012732
; PRIOR FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: JP 2002-291953
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 22
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; APPLICANT: ADAMS, CAMELIA W.
; APPLICANT: FERRARA, NAPOLEONE
; APPLICANT: FILVAROFF, ELLEN H.
; APPLICANT: MAO, WEIGUANG
; APPLICANT: PRESTA, LEONARD G.
; APPLICANT: TELADA, MAX L.
; TITLE OF INVENTION: Humanized Anti-TGF-Beta Antibodies
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; SEQ ID NO 19
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-096-046-19

Query Match      100.0%; Score 38; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

RESULT 4
US-11-136-559-28
; Sequence 28, Application US/11136559
; Publication No. US20050287164A1
; GENERAL INFORMATION:
; APPLICANT: PARTI, Joseph M
; APPLICANT: HUTCHINS, Jeff T
; APPLICANT: DOMANSKI, Paul
US-11-136-559-28

Query Match      100.0%; Score 38; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```



```
; APPLICANT: PATEL, Pratiksha
; APPLICANT: HALL, Andrea
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLEA PROTEIN . . .
; FILE REFERENCE: P07069US04/BAS
; CURRENT APPLICATION NUMBER: US/11/136,559
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US/10/056,052
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: 60/308,116
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/298,413
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/274,611
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/264,072
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-11-136-559-28
```

```
Query Match          100.0%; Score 38; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WASTRES 7
        |||||
Db      1 WASTRES 7
```

```
RESULT 5
US-11-221-902-63
; Sequence 63, Application US/11221902
; Publication No. US20060088522A1
; GENERAL INFORMATION:
; APPLICANT: Mycelth
; TITLE OF INVENTION: HUMANIZED ANTI-5T4 ANTIBODIES AND ANTI-5T4/CALICHEAMICIN CONJUGAT
; FILE REFERENCE: 040000-0317285
; CURRENT APPLICATION NUMBER: US/11/221,902
; CURRENT FILING DATE: 2005-09-09
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 63
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-221-902-63
```

```
Query Match          100.0%; Score 38; DB 10; Length 101;
Best Local Similarity 100.0%; Pred. No. 0.89;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WASTRES 7
        |||||
Db      56 WASTRES 62
```

```
RESULT 6
US-11-239-308-57
; Sequence 57, Application US/11239308
; Publication No. US2006008883A1
; GENERAL INFORMATION:
; APPLICANT: Smider, Vaughn
; APPLICANT: Latrick, James W.
; TITLE OF INVENTION: Recombinant Catalytic Polypeptides and Their Uses
; FILE REFERENCE: 021216-000310US
; CURRENT APPLICATION NUMBER: US/11/239,308
; CURRENT FILING DATE: 2005-09-28
; PRIOR APPLICATION NUMBER: US/10/683,733
```

```
; PRIOR FILING DATE: 2003-10-09
; PRIOR APPLICATION NUMBER: US 60/417,979
; PRIOR FILING DATE: 2002-10-09
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 57
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-239-308-57
```

```
Query Match          100.0%; Score 38; DB 10; Length 101;
Best Local Similarity 100.0%; Pred. No. 0.89;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WASTRES 7
        |||||
Db      56 WASTRES 62
```

```
RESULT 7
US-11-054-669-89
; Sequence 89, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
; FILE REFERENCE: 30219/US/3
; CURRENT APPLICATION NUMBER: US/11/054,669
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 10/194,975
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 89
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-054-669-89
```

```
Query Match          100.0%; Score 38; DB 11; Length 101;
Best Local Similarity 100.0%; Pred. No. 0.89;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WASTRES 7
        |||||
Db      56 WASTRES 62
```

```
RESULT 8
US-11-084-554-120
; Sequence 120, Application US/11084554
; Publication No. US20050260679A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Sird-Ai
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
; FILE REFERENCE: ABGENIX.100A
; CURRENT APPLICATION NUMBER: US/11/084,554
; CURRENT FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: 60/554,372
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/574,661
; PRIOR FILING DATE: 2004-05-24
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 120
; LENGTH: 101
; TYPE: PRT
```

ORGANISM: Homo sapiens
US-11-084-554-120.

Query Match 100.0%; Score 38; DB 11; Length 101;
Best Local Similarity 100.0%; Pred. No. 0.89;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
|||||
DB 56 WASTRES 62

RESULT 9

US-11-004-590-94
; Sequence 94, Application US/11004590
; Publication No. US2006008883A1
; GENERAL INFORMATION:
; APPLICANT: Lazari, Gregory Alan
; APPLICANT: Desjarlais, John R.
; APPLICANT: Hammond, Phillip W.
; TITLE OF INVENTION: METHODS OF GENERATING VARIANT PROTEINS WITH INCREASED HOST STRING
; FILE REFERENCE: 185832/US/5
; CURRENT APPLICATION NUMBER: US/11/004,590
; CURRENT FILING DATE: 2004-12-03
; PRIOR APPLICATION NUMBER: US 60/527,167
; PRIOR FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: US 60/581,613
; PRIOR FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US 60/601,665
; PRIOR FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: US 60/619,483
; PRIOR FILING DATE: 2004-10-14
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 94
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-004-590-94

Query Match 100.0%; Score 38; DB 11; Length 101;
Best Local Similarity 100.0%; Pred. No. 0.89;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
|||||
DB 56 WASTRES 62

RESULT 10
US-11-136-250-120
; Sequence 120, Application US/11136250
; Publication No. US20060021074A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Sirid-Ai
; APPLICANT: Green, Larry L.
; APPLICANT: Kotter, Moutier
; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
; TITLE OF INVENTION: ANTIBODIES THROUGH V GENE MANIPULATION
; FILE REFERENCE: ABGENIX.100A2
; CURRENT APPLICATION NUMBER: US/11/136,250
; CURRENT FILING DATE: 2005-05-23
; PRIOR APPLICATION NUMBER: 11/084,554
; PRIOR FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: PCT/US2005/009306
; PRIOR FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: 60/574,661
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: 60/554,372
; PRIOR FILING DATE: 2004-03-19
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 120
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-136-250-120

Query Match 100.0%; Score 38; DB 11; Length 101;
Best Local Similarity 100.0%; Pred. No. 0.89;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
|||||
DB 56 WASTRES 62

RESULT 11
US-10-771-257-101
; Sequence 101, Application US/10771257
; Publication No. US20050288864A1
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; APPLICANT: Sissa - Scuola Superiore Internazionale di Studi Avanzati
; APPLICANT: Cattaneo, Antonino
; APPLICANT: Maritan, Amos
; APPLICANT: Vassilini, Michela
; APPLICANT: Rabbits, Terence H
; APPLICANT: Settanni, Giovanni
; TITLE OF INVENTION: Intracellular antibodies
; FILE REFERENCE: 18396/2272
; CURRENT APPLICATION NUMBER: US/10/771,257
; CURRENT FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: PCT/GB02/03512
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: GB 0119004.0
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: GB 0121577.1
; PRIOR FILING DATE: 2001-09-06
; PRIOR APPLICATION NUMBER: GB 0200928.0
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: GB 0203569.9
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: IT RM2001A000633
; PRIOR FILING DATE: 2001-10-25
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 101
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-771-257-101

Query Match 100.0%; Score 38; DB 9; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.96;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
|||||
DB 56 WASTRES 62

RESULT 12
US-10-771-257-105
; Sequence 105, Application US/10771257
; Publication No. US20050288864A1
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; APPLICANT: Sissa - Scuola Superiore Internazionale di Studi Avanzati
; APPLICANT: Cattaneo, Antonino
; APPLICANT: Maritan, Amos
; APPLICANT: Vassilini, Michela
; APPLICANT: Rabbits, Terence H
; APPLICANT: Settanni, Giovanni
; TITLE OF INVENTION: Intracellular antibodies

FILE REFERENCE: 18396/2272
CURRENT APPLICATION NUMBER: US/10/771,257
CURRENT FILING DATE: 2004-02-03
PRIORITY APPLICATION NUMBER: PCT/GB02/03512
PRIORITY FILING DATE: 2002-08-01
PRIORITY APPLICATION NUMBER: GB 0119004.0
PRIORITY FILING DATE: 2001-08-03
PRIORITY APPLICATION NUMBER: GB 0121577.1
PRIORITY FILING DATE: 2001-09-06
PRIORITY APPLICATION NUMBER: GB 0200928.0
PRIORITY FILING DATE: 2002-01-16
PRIORITY APPLICATION NUMBER: GB 0203569.9
PRIORITY FILING DATE: 2002-02-14
PRIORITY APPLICATION NUMBER: IT RM2001A000633
PRIORITY FILING DATE: 2001-10-25
NUMBER OF SEQ ID NOS: 124
SOFTWARE: PatentIn version 3.1
SEQ ID NO 105
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
US-10-771-257-105

Query Match 100.0%; Score 38; DB 9; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.96;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7
Db 56 WASTRES 62

RESULT 13
US-10-771-257-107
Sequence 107, Application US/10771257
Publication No. US20050288864A1
GENERAL INFORMATION:
APPLICANT: Medical Research Council
APPLICANT: SISSA - Scuola Superiore Internazionale di Studi Avanzati
APPLICANT: Cattaneo, Antonino
APPLICANT: Maritan, Amos
APPLICANT: Viancin, Michela
APPLICANT: Rabbits, Terrence H
APPLICANT: Setlami, Giovanni
TITLE OF INVENTION: Intracellular antibodies
FILE REFERENCE: 18396/2272
CURRENT APPLICATION NUMBER: US/10/771,257
CURRENT FILING DATE: 2004-02-03
PRIORITY APPLICATION NUMBER: PCT/GB02/03512
PRIORITY FILING DATE: 2002-08-01
PRIORITY APPLICATION NUMBER: GB 0119004.0
PRIORITY FILING DATE: 2001-08-03
PRIORITY APPLICATION NUMBER: GB 0121577.1
PRIORITY FILING DATE: 2001-09-06
PRIORITY APPLICATION NUMBER: GB 0200928.0
PRIORITY FILING DATE: 2002-01-16
PRIORITY APPLICATION NUMBER: GB 0203569.9
PRIORITY FILING DATE: 2002-02-14
PRIORITY APPLICATION NUMBER: IT RM2001A000633
PRIORITY FILING DATE: 2001-10-25
NUMBER OF SEQ ID NOS: 124
SOFTWARE: PatentIn version 3.1
SEQ ID NO 107
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
US-10-771-257-107

Query Match 100.0%; Score 38; DB 9; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.96;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7

Db 56 WASTRES 62

RESULT 14
US-10-771-257-112
Sequence 112, Application US/10771257
Publication No. US20050288864A1
GENERAL INFORMATION:
APPLICANT: Medical Research Council
APPLICANT: SISSA - Scuola Superiore Internazionale di Studi Avanzati
APPLICANT: Cattaneo, Antonino
APPLICANT: Maritan, Amos
APPLICANT: Viancin, Michela
APPLICANT: Rabbits, Terrence H
APPLICANT: Setlami, Giovanni
TITLE OF INVENTION: Intracellular antibodies
FILE REFERENCE: 18396/2272
CURRENT APPLICATION NUMBER: US/10/771,257
CURRENT FILING DATE: 2004-02-03
PRIORITY APPLICATION NUMBER: PCT/GB02/03512
PRIORITY FILING DATE: 2002-08-01
PRIORITY APPLICATION NUMBER: GB 0119004.0
PRIORITY FILING DATE: 2001-08-03
PRIORITY APPLICATION NUMBER: GB 0121577.1
PRIORITY FILING DATE: 2001-09-06
PRIORITY APPLICATION NUMBER: GB 0200928.0
PRIORITY FILING DATE: 2002-01-16
PRIORITY APPLICATION NUMBER: GB 0203569.9
PRIORITY FILING DATE: 2002-02-14
PRIORITY APPLICATION NUMBER: IT RM2001A000633
PRIORITY FILING DATE: 2001-10-25
NUMBER OF SEQ ID NOS: 124
SOFTWARE: PatentIn version 3.1
SEQ ID NO 112
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
US-10-771-257-112

Query Match 100.0%; Score 38; DB 9; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.96;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7
Db 56 WASTRES 62

RESULT 15
US-11-136-559-6
Sequence 6, Application US/11136559
Publication No. US20050287164A1
GENERAL INFORMATION:
APPLICANT: PATTI, Joseph M
APPLICANT: HUTCHINS, Jeff T
APPLICANT: DOMANSKI, Paul
APPLICANT: PATEL, Pratiksha
APPLICANT: HALL, Andrea
TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN . . .
FILE REFERENCE: P07069US04/BAS
CURRENT APPLICATION NUMBER: US/11/136,559
CURRENT FILING DATE: 2005-05-25
PRIORITY APPLICATION NUMBER: US/10/056,052
PRIORITY FILING DATE: 2002-01-18
PRIORITY APPLICATION NUMBER: 60/308,116
PRIORITY FILING DATE: 2001-07-30
PRIORITY APPLICATION NUMBER: 60/298,413
PRIORITY FILING DATE: 2001-06-18
PRIORITY APPLICATION NUMBER: 60/274,611
PRIORITY FILING DATE: 2001-03-12
PRIORITY APPLICATION NUMBER: 60/264,072
PRIORITY FILING DATE: 2001-01-26

NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-11-136-559-6

Query Match 100.0%; Score 38; DB 11; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.99;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
|||||
Db 56 WASTRES 62

RESULT 16
US-11-136-559-10
; Sequence 10, Application US/11136559
; Publication No. US20050287164A1
; GENERAL INFORMATION:
; APPLICANT: PATTI, Joseph M
; APPLICANT: HUTCHINS, Jeff T
; APPLICANT: DOMANSKI, Paul
; APPLICANT: PATEL, Pratiksha
; APPLICANT: HALL, Andrea
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLPA PROTEIN . . .
; FILE REFERENCE: P07069US04/BAS
; CURRENT APPLICATION NUMBER: US/11/136,559
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US/10/056,052
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: 60/308,116
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/298,413
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/274,611
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/264,072
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-11-136-559-10

Query Match 100.0%; Score 38; DB 11; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.99;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
|||||
Db 56 WASTRES 62

RESULT 17
US-11-136-559-14
; Sequence 14, Application US/11136559
; Publication No. US20050287164A1
; GENERAL INFORMATION:
; APPLICANT: PATTI, Joseph M
; APPLICANT: HUTCHINS, Jeff T
; APPLICANT: DOMANSKI, Paul
; APPLICANT: PATEL, Pratiksha
; APPLICANT: HALL, Andrea
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLPA PROTEIN . . .
; FILE REFERENCE: P07069US04/BAS
; CURRENT APPLICATION NUMBER: US/11/136,559
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US/10/056,052

; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: 60/308,116
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/298,413
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/274,611
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/264,072
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-11-136-559-14

Query Match 100.0%; Score 38; DB 11; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.99;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
|||||
Db 56 WASTRES 62

RESULT 18
US-11-136-559-18
; Sequence 18, Application US/11136559
; Publication No. US20050287164A1
; GENERAL INFORMATION:
; APPLICANT: PATTI, Joseph M
; APPLICANT: HUTCHINS, Jeff T
; APPLICANT: DOMANSKI, Paul
; APPLICANT: PATEL, Pratiksha
; APPLICANT: HALL, Andrea
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLPA PROTEIN . . .
; FILE REFERENCE: P07069US04/BAS
; CURRENT APPLICATION NUMBER: US/11/136,559
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US/10/056,052
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: 60/308,116
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/298,413
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/274,611
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/264,072
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-11-136-559-18

Query Match 100.0%; Score 38; DB 11; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.99;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
|||||
Db 56 WASTRES 62

RESULT 19
US-11-136-559-22
; Sequence 22, Application US/11136559
; Publication No. US20050287164A1
; GENERAL INFORMATION:
; APPLICANT: PATTI, Joseph M

APPLICANT: HUTCHINS, Jeff T
APPLICANT: DOMANSKI, Paul
APPLICANT: PATEL, Pratiksha
APPLICANT: HALL, Andrea
TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN . . .
FILE REFERENCE: P07069US04/BAS
CURRENT APPLICATION NUMBER: US/11/136,559
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US/10/056,052
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: 60/308,116
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/298,413
PRIOR FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: 60/274,611
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: 60/264,072
PRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn version 3.1
SEQ ID NO 22
LENGTH: 112
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-11-136-559-22

Query Match 100.0%; Score 38; DB 11; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.99;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
Db 56 WASTRES 62

RESULT 20
US-11-219-563-71
Sequence 71, Application US/11219563
Publication No. US20060088539A1
GENERAL INFORMATION:
APPLICANT: Bander, Neil
TITLE OF INVENTION: MODIFIED ANTIBODIES TO PROSTATE-SPECIFIC
FILE REFERENCE: 13651.001 (BZL-001)
CURRENT APPLICATION NUMBER: US/11/219,563
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: PCT/US04/06586
PRIOR FILING DATE: 2004-03-03
PRIOR APPLICATION NUMBER: US 10/379,838
PRIOR FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: 10/449,379
PRIOR FILING DATE: 2003-05-30
NUMBER OF SEQ ID NOS: 144
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 71
LENGTH: 113
TYPE: PRT
ORGANISM: Mus musculus
US-11-219-563-71

Query Match 100.0%; Score 38; DB 10; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.99;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
Db 56 WASTRES 62

RESULT 21
US-11-219-563-91
Sequence 91, Application US/11219563
Publication No. US20060088539A1

GENERAL INFORMATION:
APPLICANT: Bander, Neil
TITLE OF INVENTION: MODIFIED ANTIBODIES TO PROSTATE-SPECIFIC
FILE REFERENCE: 13651.001 (BZL-001)
CURRENT APPLICATION NUMBER: US/11/219,563
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: PCT/US04/06586
PRIOR FILING DATE: 2004-03-03
PRIOR APPLICATION NUMBER: US 10/379,838
PRIOR FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: 10/449,379
PRIOR FILING DATE: 2003-05-30
NUMBER OF SEQ ID NOS: 144
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 91
LENGTH: 113
TYPE: PRT
ORGANISM: Mus musculus
US-11-219-563-91

Query Match 100.0%; Score 38; DB 10; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.99;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
Db 56 WASTRES 62

RESULT 22
US-11-218-813-71
Sequence 71, Application US/11218813
Publication No. US20060062793A1
GENERAL INFORMATION:
APPLICANT: Webb, Iain J.
APPLICANT: Horvath, Christopher J.
TITLE OF INVENTION: MODIFIED ANTIBODIES TO PROSTATE-SPECIFIC
FILE REFERENCE: 10448-163005
CURRENT APPLICATION NUMBER: US/11/218,813
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: PCT/US2004/006543
PRIOR FILING DATE: 2004-03-03
NUMBER OF SEQ ID NOS: 144
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 71
LENGTH: 113
TYPE: PRT
ORGANISM: Mus musculus
US-11-218-813-71

Query Match 100.0%; Score 38; DB 11; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.99;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
Db 56 WASTRES 62

RESULT 23
US-11-218-813-91
Sequence 91, Application US/11218813
Publication No. US20060062793A1
GENERAL INFORMATION:
APPLICANT: Webb, Iain J.
APPLICANT: Horvath, Christopher J.
TITLE OF INVENTION: MODIFIED ANTIBODIES TO PROSTATE-SPECIFIC
FILE REFERENCE: 10448-163005
CURRENT APPLICATION NUMBER: US/11/218,813
CURRENT FILING DATE: 2005-09-02

;; PRIOR APPLICATION NUMBER: PCT/US2004/006543
;; PRIOR FILING DATE: 2004-03-03
;; NUMBER OF SEQ ID NOS: 144
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 91
;; LENGTH: 113
;; TYPE: PRT
;; ORGANISM: Mus musculus
US-11-218-813-91

Query Match 100.0%; Score 38; DB 11; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.99;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
|||||
DB 56 WASTRES 62

RESULT 24
US-10-771-257-68
;; Sequence 68; Application US/10771257
;; Publication No. US20050288864A1
;; GENERAL INFORMATION:
;; APPLICANT: Medical Research Council
;; APPLICANT: SISSA - Scuola Superiore Internazionale di Studi Avanzati
;; APPLICANT: Cattaneo, Antonino
;; APPLICANT: Maritan, Amos
;; APPLICANT: Visintin, Michela
;; APPLICANT: Rabbits, Terrence H
;; APPLICANT: Settanni, Giovanni
;; TITLE OF INVENTION: Intracellular antibodies
;; FILE REFERENCE: 18396/2272
;; CURRENT APPLICATION NUMBER: US/10/771,257
;; PRIOR FILING DATE: 2004-02-03
;; PRIOR APPLICATION NUMBER: PCT/GB02/03512
;; PRIOR FILING DATE: 2002-08-01
;; PRIOR APPLICATION NUMBER: GB 0119004.0
;; PRIOR FILING DATE: 2001-08-03
;; PRIOR APPLICATION NUMBER: GB 0121577.1
;; PRIOR FILING DATE: 2001-09-06
;; PRIOR APPLICATION NUMBER: GB 0200928.0
;; PRIOR FILING DATE: 2002-01-16
;; PRIOR APPLICATION NUMBER: GB 0203569.9
;; PRIOR FILING DATE: 2002-02-14
;; PRIOR APPLICATION NUMBER: IT RM2001A000633
;; PRIOR FILING DATE: 2001-10-25
;; NUMBER OF SEQ ID NOS: 124
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 68
;; LENGTH: 114
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-771-257-68

Query Match 100.0%; Score 38; DB 9; Length 114;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
|||||
DB 56 WASTRES 62

RESULT 25
US-10-771-257-72
;; Sequence 72; Application US/10771257
;; Publication No. US20050288864A1
;; GENERAL INFORMATION:
;; APPLICANT: Medical Research Council
;; APPLICANT: SISSA - Scuola Superiore Internazionale di Studi Avanzati
;; APPLICANT: Cattaneo, Antonino
;; APPLICANT: Maritan, Amos

;; APPLICANT: Visintin, Michela
;; APPLICANT: Rabbits, Terrence H
;; APPLICANT: Settanni, Giovanni
;; TITLE OF INVENTION: Intracellular antibodies
;; FILE REFERENCE: 18396/2272
;; CURRENT APPLICATION NUMBER: US/10/771,257
;; PRIOR FILING DATE: 2004-02-03
;; PRIOR APPLICATION NUMBER: PCT/GB02/03512
;; PRIOR FILING DATE: 2002-08-01
;; PRIOR APPLICATION NUMBER: GB 0119004.0
;; PRIOR FILING DATE: 2001-08-03
;; PRIOR APPLICATION NUMBER: GB 0121577.1
;; PRIOR FILING DATE: 2001-09-06
;; PRIOR APPLICATION NUMBER: GB 0200928.0
;; PRIOR FILING DATE: 2002-01-16
;; PRIOR APPLICATION NUMBER: GB 0203569.9
;; PRIOR FILING DATE: 2002-02-14
;; PRIOR APPLICATION NUMBER: IT RM2001A000633
;; PRIOR FILING DATE: 2001-10-25
;; NUMBER OF SEQ ID NOS: 124
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 72
;; LENGTH: 114
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-771-257-72

Query Match 100.0%; Score 38; DB 9; Length 114;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
|||||
DB 56 WASTRES 62

RESULT 26
US-10-771-257-74
;; Sequence 74; Application US/10771257
;; Publication No. US20050288864A1
;; GENERAL INFORMATION:
;; APPLICANT: Medical Research Council
;; APPLICANT: SISSA - Scuola Superiore Internazionale di Studi Avanzati
;; APPLICANT: Cattaneo, Antonino
;; APPLICANT: Maritan, Amos
;; APPLICANT: Visintin, Michela
;; APPLICANT: Rabbits, Terrence H
;; APPLICANT: Settanni, Giovanni
;; TITLE OF INVENTION: Intracellular antibodies
;; FILE REFERENCE: 18396/2272
;; CURRENT APPLICATION NUMBER: US/10/771,257
;; PRIOR FILING DATE: 2004-02-03
;; PRIOR APPLICATION NUMBER: PCT/GB02/03512
;; PRIOR FILING DATE: 2002-08-01
;; PRIOR APPLICATION NUMBER: GB 0119004.0
;; PRIOR FILING DATE: 2001-08-03
;; PRIOR APPLICATION NUMBER: GB 0121577.1
;; PRIOR FILING DATE: 2001-09-06
;; PRIOR APPLICATION NUMBER: GB 0200928.0
;; PRIOR FILING DATE: 2002-01-16
;; PRIOR APPLICATION NUMBER: GB 0203569.9
;; PRIOR FILING DATE: 2002-02-14
;; PRIOR APPLICATION NUMBER: IT RM2001A000633
;; PRIOR FILING DATE: 2001-10-25
;; NUMBER OF SEQ ID NOS: 124
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 74
;; LENGTH: 114
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-771-257-74

Query Match 100.0%; Score 38; DB 9; Length 114;

Best Local Similarity 100.0%; Pred. No. 1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
|||||
56 WASTRES 62

RESULT 27

US-10-834-397-17
; Sequence 17, Application US/10834397
; Publication No. US2006003334A1
; GENERAL INFORMATION:

APPLICANT: Knappik, Achim
Pack, Peter
Ilag, VIC

Ge, Liming
Moroney, Simon
Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30 (BPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/834,397

FILING DATE: 29-Apr-2004

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/490,324

FILING DATE: 24-Jan-2000

APPLICATION NUMBER: US/09/025,769

FILING DATE: 18-FEB-1998

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)596-9000

TELEFAX: (212)596-9090

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 114 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 17:

US-10-834-397-17

Query Match

Best Local Similarity 100.0%; Score 38; DB 9; Length 114;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
|||||
56 WASTRES 62

Db

US-10-530-171-8

; Sequence 8, Application US/10530171

; Publication No. US20060057147A1

GENERAL INFORMATION:

APPLICANT: HIRAKAWA, Youko

APPLICANT: NIKI, Hisae

APPLICANT: OIKE, Shinsuke

APPLICANT: TAGAWA, Toshitaki

APPLICANT: HOSOKAWA, Saiko

APPLICANT: YOSHIYAMA, Yoshiko

TITLE OF INVENTION: Antibody recognizing antigen

FILE REFERENCE: 235054

CURRENT APPLICATION NUMBER: US/10/530,171

CURRENT FILING DATE: 2005-04-04

PRIOR APPLICATION NUMBER: PCT/JP2003/012732

PRIOR FILING DATE: 2003-10-03

PRIOR APPLICATION NUMBER: JP 2002-291953

PRIOR FILING DATE: 2002-10-04

NUMBER OF SEQ ID NOS: 22

SOFTWARE: Patentin version 3.1

SEQ ID NO 8

LENGTH: 114

TYPE: PRT

ORGANISM: Homo sapiens

US-10-530-171-8

Query Match

Best Local Similarity 100.0%; Score 38; DB 9; Length 114;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
|||||
56 WASTRES 62

Db

US-11-127-677-27

; Sequence 27, Application US/11127677

; Publication No. US20050272107A1

GENERAL INFORMATION:

APPLICANT: Medical Research Council

APPLICANT: Rabbits, Terence H

APPLICANT: Tanaka, Tomoyuki

TITLE OF INVENTION: Intracellular antibodies

FILE REFERENCE: 18396/2462

CURRENT APPLICATION NUMBER: US/11/127,677

CURRENT FILING DATE: 2005-05-12

PRIOR APPLICATION NUMBER: PCT/GB03/04942

PRIOR FILING DATE: 2003-11-14

PRIOR APPLICATION NUMBER: GB 0226729.2

PRIOR FILING DATE: 2002-11-15

NUMBER OF SEQ ID NOS: 150

SOFTWARE: Patentin version 3.1

SEQ ID NO 27

LENGTH: 114

TYPE: PRT

ORGANISM: Artificial sequence

FEATURE:

OTHER INFORMATION: Derived protein sequence of scFv

US-11-127-677-27

Query Match

Best Local Similarity 100.0%; Score 38; DB 11; Length 114;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
|||||
56 WASTRES 62

Db

US-11-127-677-66

; Sequence 66, Application US/11127677

; Publication No. US20050272107A1

GENERAL INFORMATION:

APPLICANT: Medical Research Council

; APPLICANT: Rabbits, Terence H
; TITLE OF INVENTION: Intracellular antibodies
; FILE REFERENCE: 18396/2462
; CURRENT APPLICATION NUMBER: US/11/127,677
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: PCT/GB03/04942
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: GB 0226729.2
; PRIOR FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Derived protein sequence of scFv
US-11-127-677-66

Query Match 100.0%; Score 38; DB 11; Length 114;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WASTRES 7
|||||
Db 56 WASTRES 62

RESULT 31
US-11-127-677-70
; Sequence 70, Application US/11127677
; Publication No. US20050272107A1
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; APPLICANT: Rabbits, Terence H
; APPLICANT: Tanaka, Tomoyuki
; TITLE OF INVENTION: Intracellular antibodies
; FILE REFERENCE: 18396/2462
; CURRENT APPLICATION NUMBER: US/11/127,677
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: PCT/GB03/04942
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: GB 0226729.2
; PRIOR FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 70
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Derived protein sequence of scFv
US-11-127-677-70

Query Match 100.0%; Score 38; DB 11; Length 114;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WASTRES 7
|||||
Db 56 WASTRES 62

RESULT 32
US-11-127-677-72
; Sequence 72, Application US/11127677
; Publication No. US20050272107A1
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; APPLICANT: Rabbits, Terence H
; APPLICANT: Tanaka, Tomoyuki
; TITLE OF INVENTION: Intracellular antibodies

; FILE REFERENCE: 18396/2462
; CURRENT APPLICATION NUMBER: US/11/127,677
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: PCT/GB03/04942
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: GB 0226729.2
; PRIOR FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 72
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Derived protein sequence of scFv
US-11-127-677-72

Query Match 100.0%; Score 38; DB 11; Length 114;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WASTRES 7
|||||
Db 56 WASTRES 62

RESULT 33
US-10-771-257-27
; Sequence 27, Application US/10771257
; Publication No. US2005028864A1
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; APPLICANT: Sissa - Scuola Superiore Internazionale di Studi Avanzati
; APPLICANT: Cattaneo, Antonino
; APPLICANT: Maritan, Amos
; APPLICANT: Vassilini, Michela
; APPLICANT: Rabbits, Terence H
; APPLICANT: Settanni, Giovanni
; TITLE OF INVENTION: Intracellular antibodies
; FILE REFERENCE: 18396/2272
; CURRENT APPLICATION NUMBER: US/10/771,257
; CURRENT FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: PCT/GB02/03512
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: GB 0119004.0
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: GB 0121577.1
; PRIOR FILING DATE: 2001-09-06
; PRIOR APPLICATION NUMBER: GB 0200928.0
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: GB 0203569.9
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: IT RM2001A000633
; PRIOR FILING DATE: 2001-10-25
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-771-257-27

Query Match 100.0%; Score 38; DB 9; Length 115;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WASTRES 7
|||||
Db 57 WASTRES 63

RESULT 34
US-10-834-397-31

; Sequence 31, Application US/10834397
; Publication No. US2006003334A1
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, VIC
; Ge, Liming
; Moroney, Simon
; Plueckhuhn, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/834,397
; FILING DATE: 29-Apr-2004
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,324
; FILING DATE: 24-Jan-2000
; APPLICATION NUMBER: US/09/025,769
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 115 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-10-834-397-31.
Query Match 100.0%; Score 38; DB 9; Length 115;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WASTRES 7
Db 56 WASTRES 62
RESULT 35
US-10-834-397-49
; Sequence 49, Application US/10834397
; Publication No. US2006003334A1
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, VIC
; Ge, Liming
; Moroney, Simon
; Plueckhuhn, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/834,397
; FILING DATE: 29-Apr-2004
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,324
; FILING DATE: 24-Jan-2000
; APPLICATION NUMBER: US/09/025,769
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 115 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 49:
US-10-834-397-49
Query Match 100.0%; Score 38; DB 9; Length 115;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WASTRES 7
Db 56 WASTRES 62
RESULT 36
US-10-981-356A-1
; Sequence 1, Application US/10981356A
; Publication No. US2006015952A1
; GENERAL INFORMATION:
; APPLICANT: FIVAROPF, ELLEN H.
; TITLE OF INVENTION: SCREENING ASSAYS AND METHODS OF TUMOR TREATMENT
; FILE REFERENCE: P2068R1
; CURRENT APPLICATION NUMBER: US/10/981,356A
; CURRENT FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: US 60/520,398
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/557,951
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 45
; SEQ ID NO 1
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-981-356A-1
Query Match 100.0%; Score 38; DB 9; Length 116;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WASTRES 7

Db 56 WASTRES 62

```
RESULT 37
US-10-981-356A-3
; Sequence 3, Application US/10981356A
; Publication No. US2006015952A1
; GENERAL INFORMATION:
; APPLICANT: FLIVAROFF, ELLEN H.
; TITLE OF INVENTION: SCREENING ASSAYS AND METHODS OF TUMOR TREATMENT
; FILE REFERENCE: P2068R1
; CURRENT APPLICATION NUMBER: US/10/981,356A
; CURRENT FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: US 60/520,398
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/557,951
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 45
; SEQ ID NO 3
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-10-981-356A-3
```

Query Match 100.0%; Score 38; DB 9; Length 116;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WASTRES 7
Db 56 WASTRES 62

```
RESULT 38
US-11-096-046-1
; Sequence 1, Application US/11096046
; Publication No. US20050276802A1
; GENERAL INFORMATION:
; APPLICANT: ADAMS, CAMELLIA W.
; APPLICANT: FERRARA, NAPOLEONE
; APPLICANT: FLIVAROFF, ELLEN H.
; APPLICANT: MAO, WEIGUANG
; APPLICANT: PRESTA, LEONARD G.
; APPLICANT: TEJADA, MAX L.
; TITLE OF INVENTION: Humanized Anti-TGF-Beta Antibodies
; FILE REFERENCE: P1954R1US
; CURRENT APPLICATION NUMBER: US/11/096,046
; CURRENT FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: US 60/556,290
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 1
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-096-046-1
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Query Match 100.0%; Score 38; DB 11; Length 116;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WASTRES 7
Db 56 WASTRES 62

```
RESULT 39
US-11-096-046-3
; Sequence 3, Application US/11096046
; Publication No. US20050276802A1
; GENERAL INFORMATION:
```

```
; APPLICANT: ADAMS, CAMELLIA W.
; APPLICANT: FERRARA, NAPOLEONE
; APPLICANT: FLIVAROFF, ELLEN H.
; APPLICANT: MAO, WEIGUANG
; APPLICANT: PRESTA, LEONARD G.
; APPLICANT: TEJADA, MAX L.
; TITLE OF INVENTION: Humanized Anti-TGF-Beta Antibodies
; FILE REFERENCE: P1954R1US
; CURRENT APPLICATION NUMBER: US/11/096,046
; CURRENT FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: US 60/558,290
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 3
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-096-046-3
```

Query Match 100.0%; Score 38; DB 11; Length 116;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WASTRES 7
Db 56 WASTRES 62

```
RESULT 40
US-10-511-937-2965
; Sequence 2965, Application US/10511937
; Publication No. US2006008836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2965
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2965
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Query Match 100.0%; Score 38; DB 8; Length 133;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WASTRES 7
Db 76 WASTRES 82

```
RESULT 41
US-11-158-505-35
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; Sequence 35, Application US/11158505
; Publication No. US2006002921A1
; GENERAL INFORMATION:
; APPLICANT: WINSOR-HINES, DAWN
; APPLICANT: RAO, PATRICIA
; APPLICANT: RINGLER, DOUGLAS J
; APPLICANT: POMATH, PAUL
; TITLE OF INVENTION: OPTIMIZED DOSING OF ANTI-CD4 ANTIBODIES FOR TOLERANCE
; TITLE OF INVENTION: INDUCTION IN PRIMATES
; FILE REFERENCE: TLN-031
; CURRENT APPLICATION NUMBER: US/11/158,505
; CURRENT FILING DATE: 2005-06-21
; PRIOR APPLICATION NUMBER: 60/582,181
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 35
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-158-505-35

```

```

Query Match          100.0%; Score 38; DB 11; Length 135;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 WASTRES 7
        |||||
        76 WASTRES 82

```

```

RESULT 42
; Sequence 31, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur Förderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: scFv VDCw with
; OTHER INFORMATION: specificity against Verticillium dahliae;
; OTHER INFORMATION: originates from Mus musculus.
US-10-512-184-31

```

```

Query Match          100.0%; Score 38; DB 9; Length 259;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 WASTRES 7
        |||||
        193 WASTRES 199

```

```

RESULT 43
; Sequence 33, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur Förderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi

```

```

; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: scFv PL2 with
; OTHER INFORMATION: specificity against Phoma lingam; originates from
; OTHER INFORMATION: Mus musculus.
US-10-512-184-33

```

```

Query Match          100.0%; Score 38; DB 9; Length 259;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 WASTRES 7
        |||||
        193 WASTRES 199

```

```

RESULT 44
; Sequence 68, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur Förderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 68
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: precursor
; OTHER INFORMATION: fusion protein comprising RS - linker scFv VD2.
US-10-512-184-68

```

```

Query Match          100.0%; Score 38; DB 9; Length 329;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 WASTRES 7
        |||||
        263 WASTRES 269

```

```

RESULT 45
; Sequence 70, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur Förderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 70
; LENGTH: 329
; TYPE: PRT

```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: precursor
; OTHER INFORMATION: fusion protein comprising RS - linker - scFv VDM2.
US-10-512-184-70
```

```
Query Match          100.0%; Score 38; DB 9; Length 329;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 WASTRES 7
        |||||
Db       263 WASTRES 269
```

```
RESULT 46
US-10-981-356A-25
; Sequence 25, Application US/10981356A
; Publication No. US20060015952A1
; GENERAL INFORMATION:
; APPLICANT: FILVAROFF, ELLEN H.
; TITLE OF INVENTION: SCREENING ASSAYS AND METHODS OF TUMOR TREATMENT
; FILE REFERENCE: P2068R1
; CURRENT APPLICATION NUMBER: US/10/981,356A
; CURRENT FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: US 60/520,398
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/557,951
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 45
; SEQ ID NO 25
; LENGTH: 666
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-10-981-356A-25
```

```
Query Match          100.0%; Score 38; DB 9; Length 666;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 WASTRES 7
        |||||
Db       56 WASTRES 62
```

```
RESULT 47
US-10-981-356A-27
; Sequence 27, Application US/10981356A
; Publication No. US20060015952A1
; GENERAL INFORMATION:
; APPLICANT: FILVAROFF, ELLEN H.
; TITLE OF INVENTION: SCREENING ASSAYS AND METHODS OF TUMOR TREATMENT
; FILE REFERENCE: P2068R1
; CURRENT APPLICATION NUMBER: US/10/981,356A
; CURRENT FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: US 60/520,398
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/557,951
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 45
; SEQ ID NO 27
; LENGTH: 666
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-10-981-356A-27
```

```
Query Match          100.0%; Score 38; DB 9; Length 666;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 WASTRES 7
        |||||
Db       56 WASTRES 62
```

```
RESULT 48
US-10-981-356A-28
; Sequence 28, Application US/10981356A
; Publication No. US20060015952A1
; GENERAL INFORMATION:
; APPLICANT: FILVAROFF, ELLEN H.
; TITLE OF INVENTION: SCREENING ASSAYS AND METHODS OF TUMOR TREATMENT
; FILE REFERENCE: P2068R1
; CURRENT APPLICATION NUMBER: US/10/981,356A
; CURRENT FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: US 60/520,398
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/557,951
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 45
; SEQ ID NO 28
; LENGTH: 666
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-10-981-356A-28
```

```
Query Match          100.0%; Score 38; DB 9; Length 666;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 WASTRES 7
        |||||
Db       56 WASTRES 62
```

```
RESULT 49
US-10-981-356A-29
; Sequence 29, Application US/10981356A
; Publication No. US20060015952A1
; GENERAL INFORMATION:
; APPLICANT: FILVAROFF, ELLEN H.
; TITLE OF INVENTION: SCREENING ASSAYS AND METHODS OF TUMOR TREATMENT
; FILE REFERENCE: P2068R1
; CURRENT APPLICATION NUMBER: US/10/981,356A
; CURRENT FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: US 60/520,398
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/557,951
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 45
; SEQ ID NO 29
; LENGTH: 666
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-10-981-356A-29
```

```
Query Match          100.0%; Score 38; DB 9; Length 666;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 WASTRES 7
        |||||
Db       56 WASTRES 62
```

```
RESULT 50
US-11-096-046-27
; Sequence 27, Application US/11096046
```

; Publication No. US20050276802A1
; GENERAL INFORMATION:
; APPLICANT: ADAMS, CAMELLIA W.
; APPLICANT: FERRARA, NAPOLÉONE
; APPLICANT: FILVAROFF, ELLEN H.
; APPLICANT: MAO, WEIGUANG
; APPLICANT: PRESTA, LEONARD G.
; APPLICANT: TEJADA, MAX L.
; TITLE OF INVENTION: Humanized Anti-TGF-Beta Antibodies
; FILE REFERENCE: P1954P1US
; CURRENT APPLICATION NUMBER: US/11/096,046
; CURRENT FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: US 60/558,290
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 27
; LENGTH: 666
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-096-046-27

Query Match 100.0%; Score 38; DB 11; Length 666;
Best local Similarity 100.0%; Pred. No. 5.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
|||
Db 56 WASTRES 62

Search completed: May 4, 2006, 13:54:17
Job time : 15.1111 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 4, 2006, 12:46:10 ; Search time 71.111 Seconds
(without alignments)
49.430 Million cell updates/sec

Title: US-10-700-632-6
Perfect score: 42
Sequence: 1 HQYLSRT 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :

- 1: A.Geneseq_21:*
- 2: geneseqp1980s:*
- 3: geneseqp1980s:*
- 4: geneseqp2000s:*
- 5: geneseqp2000s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	42	100.0	8	AD032090	Ad032090 Mouse ant
2	42	100.0	113	AD032094	Ad032094 Humanised
3	42	100.0	113	AD032092	Ad032092 Mouse ant
4	42	100.0	114	AD032146	Ad032146 Mouse ant
5	37	88.1	25	AD085813	Ad085813 Human int
6	37	88.1	112	AAE29264	AAE29264 S. aureus
7	37	88.1	131	ADSI9023	ADSI9023 Mature hu
8	37	88.1	131	ADW43670	ADW43670 Human int
9	37	88.1	131	ADW43678	ADW43678 Human int
10	37	88.1	131	ADW43674	ADW43674 Human int
11	37	88.1	131	ADW43676	ADW43676 Human int
12	37	88.1	131	ADW43684	ADW43684 Predicted
13	37	88.1	131	ADW43672	ADW43672 Human int
14	37	88.1	133	ADW43687	ADW43687 Mature hu
15	37	88.1	133	ADW43682	ADW43682 Human int
16	37	88.1	133	ADW43680	ADW43680 Human int
17	37	88.1	134	ADP70485	ADP70485 Codon opt
18	37	88.1	160	AEAS2828	AEAS2828 Human int
19	37	88.1	162	AAAB18623	AAAB18623 A human z
20	37	88.1	162	AAAB13729	AAAB13729 Human sol
21	37	88.1	162	AAU11965	AAU11965 Human int
22	37	88.1	162	ABR61407	ABR61407 Human IL-
23	37	88.1	162	AAE14934	AAE14934 Human int
24	37	88.1	162	AAE14932	AAE14932 Human int

25	37	88.1	162	ABU62893	ABU62893 Human int
26	37	88.1	162	AD085808	AD085808 Human int
27	37	88.1	162	ADP17046	ADP17046 Human alb
28	37	88.1	162	ADH44572	ADH44572 Human zal
29	37	88.1	162	ADT00908	ADT00908 Immunity-
30	37	88.1	162	ADH10501	ADH10501 Human int
31	37	88.1	162	ADJ25621	ADJ25621 Human int
32	37	88.1	162	ADMA1017	ADMA1017 Human IL-
33	37	88.1	162	ADP12563	ADP12563 Protein e
34	37	88.1	162	ADP19731	ADP19731 Human zal
35	37	88.1	162	ADP70459	ADP70459 Human int
36	37	88.1	162	ADSI19031	ADSI19031 Full leng
37	37	88.1	162	ADV96355	ADV96355 Human zal
38	37	88.1	162	ADY20419	ADY20419 PRO polyp
39	37	88.1	162	ADY17792	ADY17792 PRO polyp
40	37	88.1	162	ADZ20501	ADZ20501 Human int
41	37	88.1	162	AEBS26428	AEBS26428 Human int
42	37	88.1	162	AAAB18627	AAAB18627 Human int
43	37	88.1	519	AAU11971	AAU11971 MBP-human
44	37	88.1	519	ADH44655	ADH44655 Human zal
45	37	88.1	519	ADP100991	ADP100991 MBP (malic
46	37	88.1	519	ADP19814	ADP19814 Human zal
47	37	88.1	519	ADV96438	ADV96438 Human zal
48	37	88.1	742	ADP17042	ADP17042 Human alb
49	35	83.3	8	AAE29276	AAE29276 Anti-ClfA
50	35	83.3	8	ADL23028	ADL23028 Myelin as
51	35	83.3	8	AD088788	AD088788 Light cha
52	35	83.3	8	AEAS8791	AEAS8791 Humanized
53	35	83.3	8	AEAS8760	AEAS8760 Humanized
54	35	83.3	8	AEBO8049	AEBO8049 Chimeric
55	35	83.3	112	AAE29270	AAE29270 S. aureus
56	35	83.3	112	AAE29268	AAE29268 S. aureus
57	35	83.3	112	AAE29266	AAE29266 S. aureus
58	35	83.3	112	ADU39970	ADU39970 Antibody
59	35	83.3	113	ADB97820	ADB97820 HEV relac
60	35	83.3	115	ADL23043	ADL23043 Humanised
61	35	83.3	115	ADL23040	ADL23040 Humanised
62	35	83.3	115	ADL23041	ADL23041 Humanised
63	35	83.3	115	ADL23042	ADL23042 Humanised
64	35	83.3	115	AD088801	AD088801 Amino aci
65	35	83.3	115	AD088800	AD088800 Amino aci
66	35	83.3	115	AD088802	AD088802 Amino aci
67	35	83.3	115	AD088799	AD088799 Amino aci
68	35	83.3	116	AEAS8741	AEAS8741 Murine an
69	35	83.3	116	AEAS8743	AEAS8743 Humanized
70	35	83.3	132	AEBO8042	AEBO8042 HLA-DR sp
71	35	83.3	162	ADY27249	ADY27249 Human int
72	35	83.3	238	ADL23052	ADL23052 Mouse/hum
73	35	83.3	238	ADL23055	ADL23055 Humanised
74	35	83.3	238	AD088793	AD088793 A mouse/h
75	35	83.3	238	AD088804	AD088804 Humanised
76	35	83.3	238	AEBO8041	AEBO8041 Murine/hu
77	35	83.3	238	AEAS8766	AEAS8766 Humanized
78	35	83.3	667	AEAS8767	AEAS8767 Humanized
79	35	83.3	667	AEAS8769	AEAS8769 Humanized
80	35	83.3	667	AEAS8768	AEAS8768 Humanized
81	35	83.3	667	AEAS8765	AEAS8765 Humanized
82	35	83.3	695	AEAS8774	AEAS8774 Humanized
83	35	83.3	8	AD097704	AD097704 Mouse mon
84	35	83.3	8	ADW47146	ADW47146 Anti-CD20
85	35	83.3	112	AAAS4932	AAAS4932 FC recept
86	35	83.3	112	AAAS4933	AAAS4933 MAb 022 V
87	35	83.3	112	ADT02527	ADT02527 Anti-CD22
88	35	83.3	113	AA92215	AA92215 L12 MAb V
89	35	83.3	113	AA92217	AA92217 Humanised
90	35	83.3	113	AAW27695	AAW27695 Variable
91	35	83.3	113	AD097685	AD097685 Mouse mon
92	35	83.3	113	AD097689	AD097689 Human mon
93	35	83.3	115	AAW27697	AAW27697 Variable
94	35	83.3	144	ADW47080	ADW47080 Light cha
95	35	83.3	238	AD064203	AD064203 LL2IC pro
96	35	83.3	244	ADG17461	ADG17461 Anti-CD22
97	35	83.3	244	ADG17477	ADG17477 Anti-CD22

98	34	81.0	244	8	ADG17487	Adg17487	Anti-CD22	171	31	73.8	446	6	ABJ26346	Abj26346	Aspergill1
99	34	81.0	244	8	ADG17479	Adg17479	Anti-CD22	172	31	73.8	661	9	ADV92484	Adv92484	PL/Fc/hus
100	34	81.0	244	8	ADG17482	Adg17482	Anti-CD22	173	31	73.8	661	9	ADV92490	Adv92490	PL/Fc/chs
101	34	81.0	244	8	ADG17483	Adg17483	Anti-CD22	174	31	73.8	661	9	ADV98553	Adv98553	Novel chl
102	34	81.0	244	8	ADG17485	Adg17485	Anti-CD22	175	31	73.8	661	9	ADV98547	Adv98547	Novel chl
103	34	81.0	244	8	ADG17476	Adg17476	Anti-CD22	176	31	73.8	720	5	ABBO7690	Abb07690	R. gramin
104	34	81.0	244	8	ADG17480	Adg17480	Anti-CD22	177	31	73.8	720	5	AAE27938	Aae27938	Rhodocoru
105	34	81.0	244	8	ADG17486	Adg17486	Anti-CD22	178	31	73.8	744	7	AAE270235	Aae270235	C. neofor
106	34	81.0	244	8	ADG17478	Adg17478	Anti-CD22	179	31	73.8	934	7	AAP20016	Aap20016	Sequence
107	34	81.0	244	8	ADG17484	Adg17484	Anti-CD22	180	31	73.8	952	7	ADP95008	Adp95008	A. thalia
108	34	81.0	260	8	ADT02521	Adt02521	Anti-CD22	181	31	73.8	954	8	ADT06581	Adt06581	Plant ful
109	34	81.0	263	8	AAW90226	AAw90226	Anti-B7.2	182	31	73.8	1147	5	ABBT7674	Abb76724	Foot and
110	34	81.0	268	2	AAW90222	AAw90222	Anti-B7.1	183	31	73.8	1620	5	AAAB71471	AAb71471	Cobra pro
111	34	81.0	268	2	AAW90228	AAw90228	Anti-B7.1	184	31	73.8	1620	8	ADOC41966	Adoc41966	Monocled
112	34	81.0	273	2	AAW90224	AAw90224	Anti-B7.1	185	31	73.8	1621	5	AAAB71472	AAb71472	Cobra pro
113	34	81.0	301	2	AAW11507	AAw11507	Single ch	186	31	73.8	1628	5	AAAB71475	AAb71475	Cobra pro
114	34	81.0	301	2	AAW73217	AAw73217	MultiSpec	187	31	73.8	1628	5	AAAB71476	AAb71476	Cobra pro
115	34	81.0	301	4	AAAB61959	AAb61959	Single ch	188	31	73.8	1629	5	AAAB71478	AAb71478	Cobra pro
116	34	81.0	301	4	AAAB85454	AAb85454	Single ch	189	31	73.8	1629	5	AAAB71477	AAb71477	Cobra pro
117	34	81.0	352	2	AAW06272	AAw06272	Anti-Fc g	190	31	73.8	1638	9	ADM20503	Adm20503	Human com
118	34	81.0	553	2	AAW11508	AAw11508	Single ch	191	31	73.8	1638	9	ADM20507	Adm20507	Human com
119	34	81.0	553	2	AAW73223	AAw73223	H22-anti-	192	31	73.8	1642	2	AAAB63223	AAb63223	Cobra CVF
120	34	81.0	553	4	AAAB61960	AAb61960	Bispectifi	193	31	73.8	1642	2	AAAT3729	AAt3729	Cobra ven
121	34	81.0	553	4	AAAB85455	AAb85455	Bispectifi	194	31	73.8	1642	5	AAAE21961	AAe21961	Pre-pro c
122	34	81.0	556	2	AAW90218	AAw90218	Bispectifi	195	31	73.8	1642	5	AAAB71433	AAb71433	Cobra pro
123	34	81.0	580	2	AAW90217	AAw90217	Bispectifi	196	31	73.8	1642	9	ADM20499	Adw20499	Naja naja
124	34	81.0	984	9	AEAS4975	AEa54975	Monovalen	197	31	73.8	1648	2	AAAT3731	AAt3731	Antno aci
125	34	81.0	984	9	AEAS4976	AEa54976	Bivalent	198	31	73.8	1648	5	AAAE21971	AAe21971	Pre-pro c
126	33	78.6	128	8	ADP30073	Adp30073	Human sec	199	31	73.8	1648	5	AAAB71466	AAb71466	Cobra pre
127	33	78.6	188	8	ADU02323	Adu02323	Novel hum	200	31	73.8	1650	5	AAAB71470	AAb71470	Cobra pro
128	33	78.6	603	8	ADX73942	Adx73942	Plant ful	201	31	73.8	1650	5	AAAB71469	AAb71469	Cobra pro
129	32	76.2	136	3	AAAG46988	AAg46988	ArabiDops	202	31	73.8	1651	5	AAAB71474	AAb71474	Cobra pro
130	32	76.2	136	3	AAAG24361	AAg24361	ArabiDops	203	31	73.8	1658	9	AAAB71473	AAb71473	Cobra pro
131	32	76.2	180	8	ADX74893	Adx74893	Plant ful	204	31	73.8	1663	9	ADM20501	Adw20501	Human com
132	32	76.2	205	8	ADX95922	Adx95922	Plant ful	205	31	73.8	1663	9	ADM20505	Adm20505	Human com
133	32	76.2	209	8	ADX72156	Adx72156	Plant ful	206	31	73.8	1666	5	AAAB71480	AAb71480	Cobra pro
134	32	76.2	290	8	ABG14857	Abg14857	Novel hum	207	31	73.8	1666	5	AAAB71479	AAb71479	Cobra pro
135	32	76.2	575	8	ADSA42772	Adsa42772	Bacterial	208	31	73.8	2164	1	AAAP81045	AAp81045	Sequence
136	31	73.8	14	4	AAW97432	AAw97432	Human pep	209	31	73.8	2164	1	AAAP80131	AAp80131	Peptides
137	31	73.8	42	4	ABG21114	Abg21114	Novel hum	210	30	71.4	16	2	AAW19392	AAw19392	Macaque c
138	31	73.8	46	4	ABG21117	Abg21117	Novel hum	211	30	71.4	38	2	AAW18297	AAw18297	Human tes
139	31	73.8	63	5	ABP38698	Abp38698	Staphyloc	212	30	71.4	56	4	AAU22227	AAu22227	Human car
140	31	73.8	88	3	AAAG19601	AAg19601	ArabiDops	213	30	71.4	56	7	ADDE46195	Adde46195	Human car
141	31	73.8	88	3	AAAG60920	AAg60920	ArabiDops	214	30	71.4	56	8	ADJ07613	Adj07613	Human car
142	31	73.8	105	1	AAAP20018	AAp20018	Sequence	215	30	71.4	63	6	ABME5503	Abme5503	Procionib
143	31	73.8	105	4	AAU47521	AAu47521	Procionib	216	30	71.4	97	4	AAU54279	AAu54279	Procionib
144	31	73.8	105	6	ABM44040	ABm44040	Propionib	217	30	71.4	97	6	ABMS0798	ABms0798	Propionib
145	31	73.8	108	3	AAAG60919	AAg60919	ArabiDops	218	30	71.4	100	4	AAU67296	AAu67296	Propionib
146	31	73.8	108	3	AAAG19600	AAg19600	ArabiDops	219	30	71.4	100	6	ABM63815	ABm63815	Propionib
147	31	73.8	112	3	AAAG60918	AAg60918	ArabiDops	220	30	71.4	103	8	ABO55524	ABos5524	Human gen
148	31	73.8	112	3	AAAG19599	AAg19599	ArabiDops	221	30	71.4	119	5	ABP11389	ABp11389	Human ORF
149	31	73.8	113	9	ADX37184	Adx37184	ArabiDops	222	30	71.4	135	4	AAU62730	AAu62730	Procionib
150	31	73.8	113	9	ADX37182	Adx37182	SMs-1 hum	223	30	71.4	135	6	ABMS9249	ABms9249	Procionib
151	31	73.8	113	9	AEAB8699	AEa8699	Humanized	224	30	71.4	191	9	ADX40531	Adx40531	HIV Vi f P
152	31	73.8	113	9	AEAB8701	AEa8701	Mouse ant	225	30	71.4	192	3	AAAB59298	AAb59298	HIV-1 non
153	31	73.8	133	9	ADV92466	Adv92466	Mouse SMS	226	30	71.4	216	2	AAAB35209	AAb35209	Chlamydia
154	31	73.8	133	9	ADV98529	Adv98529	Novel chl	227	30	71.4	237	5	ABBT77460	Abb77460	Fungi str
155	31	73.8	135	9	ADV92474	Adv92474	SMs-1 hum	228	30	71.4	272	5	ABG31024	ABg31024	Synthetic
156	31	73.8	135	9	ADV98537	Adv98537	Novel chl	229	30	71.4	272	7	ADD25453	AdD25453	Binding d
157	31	73.8	239	9	ADV92470	Adv92470	SMs-1 chi	230	30	71.4	272	7	ADDM42728	Adm42728	Synthetic
158	31	73.8	239	9	ADV98533	Adv98533	Novel chl	231	30	71.4	272	9	AEBS9396	AEb94430	Mouse G28
159	31	73.8	241	9	ADV92478	Adv92478	SMs-1 hum	232	30	71.4	287	9	AEBA94430	AEb94430	Mouse ant
160	31	73.8	241	9	ADV98541	Adv98541	Novel chl	233	30	71.4	288	9	ADX40459	Adx40459	HIV Vi f P
161	31	73.8	269	1	AAAP1054	AAp1054	Sequence	234	30	71.4	288	9	ADX40444	Adx40444	HIV Vi f P
162	31	73.8	309	8	ADL04341	Adl04341	M. catarr	235	30	71.4	290	6	ABM67596	ABm67596	Photobab
163	31	73.8	318	6	ABRS5341	ABr5341	Protein s	236	30	71.4	313	6	ADA35723	Ada35723	Acinetoba
164	31	73.8	318	7	ADK63428	Adk63428	Disease t	237	30	71.4	328	6	ABM69000	ABm69000	Photobab
165	31	73.8	377	8	ADN24357	Adn24357	Bacterial	238	30	71.4	391	6	ABU16731	ABu16731	Protein e
166	31	73.8	379	3	AAAB01290	AAb01290	Mature co	239	30	71.4	415	8	AAV06910	AAv06910	Plant ful
167	31	73.8	379	3	ABO1294	ABo1294	Altered c	240	30	71.4	462	3	AAAY92344	AAy92344	Human can
168	31	73.8	391	6	ABU25746	ABu25746	Aspergill1	241	30	71.4	472	7	ABO74094	ABo74094	Pseudom
169	31	73.8	398	6	ABM68272	ABm68272	Photobab	242	30	71.4	477	4	ABB947726	ABb947726	Human pro
170	31	73.8	403	2	AAAR71933	AAr71933	Cobra ven	243	30	71.4	481	5	ABP27319	ABp27319	Streptoco

244	30	71.4	481	5	ABP29790	Abp29790	Streptococ	317	30	71.4	2733	8	ADH71246	Adh71246	Human pro
245	30	71.4	481	8	ADV88022	Adv88022	Streptococ	318	30	71.4	2733	8	ADH71258	Adh71258	Human pro
246	30	71.4	481	8	ADV79275	Adv79275	Streptococ	319	30	71.4	2759	5	ADH16608	Adh16608	Human NOV
247	30	71.4	481	8	ADV81460	Adv81460	Streptococ	320	30	71.4	2759	8	ADH71272	Adh71272	Human pro
248	30	71.4	591	5	ABP91527	Abp91527	Herpeticida	321	30	71.4	2754	5	ADH16951	Adh16951	Murine NO
249	30	71.4	630	5	ABP73858	Abp73858	Candida a	322	30	71.4	2764	5	ADH76262	Adh76262	Walker ge
250	30	71.4	635	2	AAW75855	Aaw75855	Human sec	323	30	71.4	2765	5	ADH16952	Adh16952	Rat NOV
251	30	71.4	635	2	AAW45160	Aaw45160	Human sec	324	30	71.4	2765	5	ADH71220	Adh71220	Human pro
252	30	71.4	635	3	AAW71060	Aaw71060	Human mem	325	30	71.4	2769	8	ADH42262	Adh42262	Human nov
253	30	71.4	635	6	ABP97203	Abp97203	Tumour-as	326	29	69.0	9	9	ADU70700	Adu70700	Human hep
254	30	71.4	635	7	ADH54790	Adh54790	Human pro	327	29	69.0	9	9	ADU70639	Adu70639	Human hep
255	30	71.4	635	7	ADH54794	Adh54794	Human pro	328	29	69.0	14	7	ADO70291	Ado70291	Human mit
256	30	71.4	635	8	ABM80279	Abm80279	Tumour-as	329	29	69.0	14	8	ADR88216	Adr88216	Human hep
257	30	71.4	635	8	ADU06664	Adu06664	Novel bro	330	29	69.0	14	8	ADT78183	Adt78183	Functiona
258	30	71.4	670	5	AAU82972	Aau82972	C. albica	331	29	69.0	14	9	AEA42432	Aea42432	Human hep
259	30	71.4	673	7	ABO80071	Abm95278	Pseudomon	332	29	69.0	15	9	ADU70841	Adu70841	Human hep
260	30	71.4	691	9	ABM95278	Abm95278	M. xanthu	333	29	69.0	15	9	ADU71059	Adu71059	Human hep
261	30	71.4	718	4	AAU38443	Aau38443	Salmonell	334	29	69.0	15	9	ADU70969	Adu70969	Human hep
262	30	71.4	718	6	ABU47985	Abu47985	Protein e	335	29	69.0	15	9	ADU71060	Adu71060	Human hep
263	30	71.4	726	6	ABU47211	Abu47211	Protein e	336	29	69.0	15	9	ADU71114	Adu71114	Human hep
264	30	71.4	761	6	ADH71230	Adh71230	Human pro	337	29	69.0	15	9	ADU71272	Adu71272	Human hep
265	30	71.4	762	6	ABU46305	Abu46305	Protein e	338	29	69.0	15	9	ADU70927	Adu70927	Human hep
266	30	71.4	810	3	AAH81733	Aay81733	Streptoco	339	29	69.0	15	9	ADY27047	Ady27047	Hepaxanas
267	30	71.4	810	4	AAU38043	Aau38043	Streptoco	340	29	69.0	31	4	AAU28217	Aau28217	Novel hum
268	30	71.4	810	6	ABU02725	Abu02725	S. pneumo	341	29	69.0	71	8	ABO55752	Abos55752	Human gen
269	30	71.4	810	6	ADK47837	Adk47837	Streptoco	342	29	69.0	76	4	ABG03005	Abg03005	Novel hum
270	30	71.4	810	8	ADT50162	Adt50162	S. pneumo	343	29	69.0	86	4	AAW99674	Aaw99674	Human exc
271	30	71.4	816	8	ADR95869	Adr95869	Novel S.	344	29	69.0	86	4	AAW42489	Aaw42489	Human kid
272	30	71.4	816	9	AEA59739	Aea59739	Streptoco	345	29	69.0	97	7	ADP59507	Adp59507	Human pol
273	30	71.4	823	8	ADH71228	Adh71228	Human pro	346	29	69.0	128	4	AAU28029	Aau28029	Novel hum
274	30	71.4	823	8	ADH71226	Adh71226	Human pro	347	29	69.0	128	8	ADP78618	Adp78618	Human his
275	30	71.4	826	8	ADH71222	Adh71222	Human pro	348	29	69.0	128	8	ADP04825	Adp04825	Sea squir
276	30	71.4	826	8	ADH71270	Adh71270	Human pro	349	29	69.0	128	8	ABM80576	Abm80576	Tumour-as
277	30	71.4	826	8	ADH71276	Adh71276	Human pro	350	29	69.0	128	8	ADU46847	Adu46847	H2A histo
278	30	71.4	826	8	ADH71260	Adh71260	Human pro	351	29	69.0	134	3	AAH43577	Aah43577	Human can
279	30	71.4	826	8	ADH71278	Adh71278	Human pro	352	29	69.0	134	4	AAW81862	Aaw81862	Human hae
280	30	71.4	826	8	ADH71280	Adh71280	Human pro	353	29	69.0	134	4	AAW81621	Aaw81621	Human hae
281	30	71.4	832	8	ADH71224	Adh71224	Human pro	354	29	69.0	134	4	AAW80842	Aaw80842	Human hae
282	30	71.4	847	6	ADA55477	Ada55477	Human pro	355	29	69.0	141	4	ABH61586	Abh61586	Drosophi
283	30	71.4	870	5	AAO14287	Aao14287	Fungal he	356	29	69.0	142	4	AAE07110	Aae07110	Human gen
284	30	71.4	1059	5	ABU12111	Abu12111	Human pro	357	29	69.0	143	8	ADX72297	Adx72297	Plant ful
285	30	71.4	1114	5	ABM09150	Abm09150	Bombyx mo	358	29	69.0	149	7	ABO83324	Abos83324	Pseudomon
286	30	71.4	1274	5	AAU75578	Aau75578	Human hea	359	29	69.0	151	3	AAH40417	Aah40417	Human ORF
287	30	71.4	1274	7	ADU70043	Adj70043	Human ubi	360	29	69.0	153	2	AAW44911	Aaw44911	Amino aci
288	30	71.4	1274	7	ADU62297	Adu62297	Novel bro	361	29	69.0	156	4	AAW90343	Aaw90343	C glucam
289	30	71.4	1292	7	ADU30915	Adu30915	Human nov	362	29	69.0	158	8	ABO55420	Abos55420	Human gen
290	30	71.4	1317	5	ABG32160	Abg32160	Novel hum	363	29	69.0	178	8	ADR98841	Adr98841	Lung spec
291	30	71.4	1317	6	ADT05836	Adt05836	Human ubi	364	29	69.0	208	9	ADW18307	Adw18307	Eucalyptu
292	30	71.4	1351	6	AAO29571	Aao29571	Human pro	365	29	69.0	226	6	ABU19065	Abu19065	Pathogen
293	30	71.4	1482	3	AAH84727	Aay84727	Amino aci	366	29	69.0	226	6	ABU15964	Abu15964	Protein e
294	30	71.4	1488	3	AAH84725	Aay84725	Amino aci	367	29	69.0	227	5	AAE25757	Aae25757	Soybean A
295	30	71.4	1509	3	AAH84728	Aay84728	Amino aci	368	29	69.0	227	8	ADR04283	Adr04283	Soybean A
296	30	71.4	1517	3	AAH84726	Aay84726	Amino aci	369	29	69.0	235	4	AAU33959	Aau33959	Stearylloc
297	30	71.4	1517	3	AAH84730	Aay84730	Amino aci	370	29	69.0	235	4	AAU37091	Aau37091	Staphylloc
298	30	71.4	1574	3	AAH84729	Aay84729	Amino aci	371	29	69.0	235	7	ADU72729	Adu72729	Human nov
299	30	71.4	1578	3	AAH84732	Aay84732	Amino aci	372	29	69.0	256	7	ABO72729	Abos72729	Pseudomon
300	30	71.4	1588	3	AAH84731	Aay84731	Amino aci	373	29	69.0	263	4	AAU15069	Aau15069	Human pro
301	30	71.4	1604	5	AAU82715	Aau82715	Amino aci	374	29	69.0	263	5	ABP73266	Abp73266	Candida a
302	30	71.4	1605	3	AAH84733	Aay84733	Amino aci	375	29	69.0	267	8	ADS27272	Ads27272	Bacterial
303	30	71.4	1737	8	ADK52107	Adk52107	Human ato	376	29	69.0	267	8	ADS26533	Ads26533	Bacterial
304	30	71.4	2144	8	ADQ19484	Adq19484	Human sof	377	29	69.0	267	8	ADS26966	Ads26966	Bacterial
305	30	71.4	2333	8	ADH71274	Adh71274	Human pro	378	29	69.0	267	8	ADK66621	Adk66621	Plant ful
306	30	71.4	2551	6	ABR58317	Abt58317	BCU0205A	379	29	69.0	274	6	ABM72542	Abm72542	Staphylloc
307	30	71.4	2633	6	ABR58318	Abt58318	BCU0205B	380	29	69.0	275	9	ADX40443	Adx40443	HIV vif p
308	30	71.4	2662	8	ADH71218	Adh71218	Human pro	381	29	69.0	289	9	AEH36205	Aeh36205	L. pneumo
309	30	71.4	2724	4	AAU08681	Aau08681	Human FCT	382	29	69.0	289	9	AEH39627	Aeh39627	L. pneumo
310	30	71.4	2724	7	ADH32029	Adh32029	Human FCT	383	29	69.0	301	8	ADS44675	Ads44675	Bacterial
311	30	71.4	2724	8	ADH71252	Adh71252	Human FCT	384	29	69.0	316	3	AAW35251	Aaw35251	Zea may's
312	30	71.4	2733	4	AAU08680	Aau08680	Human FCT	385	29	69.0	327	6	ABU40757	Abu40757	Protein e
313	30	71.4	2733	7	ADH32024	Adh32024	Human FCT	386	29	69.0	327	8	ADN20407	Adn20407	Bacterial
314	30	71.4	2733	8	ADH71250	Adh71250	Human pro	387	29	69.0	352	5	AAU99395	Aau99395	Human nuc
315	30	71.4	2733	8	ADH71254	Adh71254	Human pro	388	29	69.0	352	6	AAW79681	Aaw79681	Human ENZ
316	30	71.4	2733	8	ADH71240	Adh71240	Human pro	389	29	69.0	356	7	ADP07041	Adp07041	Bacterial

390	29	69.0	371.3	AAg35250	AAg35250	Zea mays	463	29	69.0	570.9	ADZ19008	Adz19008	Hepareanas
391	29	69.0	374.8	ADY12252	Ady12252	Plant ful	464	29	69.0	574.8	ADX72882	Adx72882	Plant ful
392	29	69.0	375.4	ABi18145	Abi18145	Plasmodiu	465	29	69.0	588.2	AAy30124	Aay30124	A human p
393	29	69.0	379.4	AAm58318	Aam58318	Human bra	466	29	69.0	592.2	AAy02346	Aay02346	A human h
394	29	69.0	384.8	ADY09458	Ady09458	Plant ful	467	29	69.0	592.2	AAb08850	Aab08850	Amino aci
395	29	69.0	386.8	ADr888207	Adr888207	Human mat	468	29	69.0	592.7	ADg888804	Adg888804	Human SK-
396	29	69.0	386.8	AdT78174	Adt78174	45kDa sub	469	29	69.0	592.8	ADL16383	Adl16383	Human hep
397	29	69.0	386.9	ADY27057	Ady27057	Hepareanas	470	29	69.0	592.8	ADm48720	Adm48720	Human SK-
398	29	69.0	386.9	ADZ18995	Adz18995	Human hep	471	29	69.0	592.9	AEa42461	Aea42461	Human hep
399	29	69.0	386.9	AEa42423	Aea42423	Human mat	472	29	69.0	592.9	AAW79280	Aaw79280	Arabidops
400	29	69.0	388.3	AAg35249	Aag35249	Zea mays	473	29	69.0	608.4	AAE01911	Aae01911	Arabidops
401	29	69.0	432.6	ABm70350	Abm70350	Phototrab	474	29	69.0	608.4	AAE01889	Aae01889	Arabidops
402	29	69.0	459.8	ADJ50191	Adj50191	Oil-assoc	475	29	69.0	608.4	AAE02563	Aae02563	A. thalia
403	29	69.0	460.8	ADl04200	Adl04200	A. sunn p	476	29	69.0	608.7	ADJ31063	Adj31063	Plant yie
404	29	69.0	460.8	ADY27061	Ady27061	Hepareanas	477	29	69.0	608.7	ADB31467	Adb31467	Plant yie
405	29	69.0	486.9	AEb87589	Aeb87589	Human hep	478	29	69.0	608.8	ADl41573	Adl41573	Plant tra
406	29	69.0	488.4	ABBS9574	Abbs9574	Drosophi1	479	29	69.0	608.8	AD003331	Ado03331	Thalecres
407	29	69.0	492.9	ADZ18996	Adz18996	Hep106 co	480	29	69.0	608.8	AD001715	Ado01715	Thalecres
408	29	69.0	493.9	AEb87562	Aeb87562	Human hep	481	29	69.0	608.8	ADN73979	Adn73979	Thale cre
409	29	69.0	495.9	ADZ18999	Adz18999	Hep109 co	482	29	69.0	624.7	ADm04761	Adm04761	Human pro
410	29	69.0	497.9	AEb87587	Aeb87587	Human hep	483	29	69.0	632.7	ADM26113	Adm26113	Hyperther
411	29	69.0	501.9	ADZ19000	Adz19000	HepG63 co	484	29	69.0	652.8	ADJ45503	Adj45503	LXR-ligan
412	29	69.0	507.9	ADZ19005	Adz19005	HepG6 co	485	29	69.0	662.8	ADK52124	Adk52124	Human ato
413	29	69.0	508.9	ADY27058	Ady27058	Human ina	486	29	69.0	705.5	ABP69808	Abp69808	Human pol
414	29	69.0	511.6	ABM71544	Abm71544	Staphyloc	487	29	69.0	760.6	ABU62808	Abu62808	Frog G11
415	29	69.0	515.6	ABU62801	Abu62801	Frog G11	488	29	69.0	761.2	AAW70899	Aaw70899	Protein e
416	29	69.0	525.6	ABU62803	Abu62803	Frog G11	489	29	69.0	761.3	AAy44704	Aay44704	Human tum
417	29	69.0	526.6	ADB23130	Adb23130	Environme	490	29	69.0	761.8	ADJ76177	Adj76177	Marker ge
418	29	69.0	526.6	ADZ19006	Adz19006	HepHyalur	491	29	69.0	761.8	ADJ75380	Adj75380	Marker ge
419	29	69.0	527.5	ABb07815	Abb07815	Chicken s	492	29	69.0	761.8	ADQ20487	Adq20487	Human sol
420	29	69.0	527.7	ABM02018	Abm02018	Chimeric	493	29	69.0	761.8	ADr14427	Adr14427	Human NF-
421	29	69.0	527.8	ADb063825	Adb063825	Chimeric	494	29	69.0	795.8	ADM87174	Adm87174	Human pro
422	29	69.0	527.8	ADb063827	Adb063827	Chimeric	495	29	69.0	800.6	ABM72360	Abm72360	Staphyloc
423	29	69.0	527.8	ADb063826	Adb063826	Chimeric	496	29	69.0	826.7	AD070262	Ado70262	Human mit
424	29	69.0	527.9	ADZ19004	Adz19004	HepG64 co	497	29	69.0	827.6	ABU33836	Abu33836	Protein e
430	29	69.0	533.3	AAy57590	Aay57590	Human hep	503	29	69.0	828.7	AD027073	Aao27073	GPM relA
431	29	69.0	533.3	AAb08849	Abb08849	Amino aci	504	29	69.0	828.7	ADd48017	Add48017	Human pro
432	29	69.0	543.3	AAy52990	Aay52990	Human hep	505	29	69.0	828.7	ADd48021	Add48021	Human pro
433	29	69.0	543.3	AAy97635	Aay97635	Human hep	506	29	69.0	828.7	ADb62564	Adb62564	Human pro
434	29	69.0	543.4	AAb86206	Aab86206	Human hep	507	29	69.0	828.7	ADb62562	Adb62562	Rat Prote
435	29	69.0	543.4	AAb88361	Aab88361	Human mem	508	29	69.0	828.7	ADP48019	Adp48019	Rat Prote
436	29	69.0	543.5	ABb07813	Abb07813	Human hep	509	29	69.0	828.7	ADb62566	Adb62566	Rat Prote
437	29	69.0	543.7	ADd18950	Add18950	Human hep	510	29	69.0	828.7	ADb62568	Adb62568	Human pro
438	29	69.0	543.8	ADg88800	Adg88800	Human hpa	511	29	69.0	828.7	ADb62568	Adb62568	Human pro
439	29	69.0	543.8	ADL16379	Adl16379	Human hep	512	29	69.0	828.7	ADd48015	Add48015	Rat Prote
440	29	69.0	543.8	ADK52086	Adk52086	Human ato	513	29	69.0	828.7	ADd48023	Add48023	Rat Prote
441	29	69.0	543.8	ADm48716	Adm48716	Human hpa	514	29	69.0	828.7	ADJ395202	Adj395202	Novel NOV
442	29	69.0	543.8	ADm48759	Adm48759	Human hpa	515	29	69.0	828.7	ADJ395200	Adj395200	Novel NOV
443	29	69.0	543.8	ADN05074	Adn05074	Antipsoi1	516	29	69.0	828.7	AD070270	Ado70270	Rat mitoc
444	29	69.0	543.8	ADN04902	Adn04902	Antipsoi1	517	29	69.0	831.8	ADl16106	Adl16106	Human van
445	29	69.0	543.8	ADb063831	Adb063831	Human hep	518	29	69.0	832.8	ADU02405	Adu02405	Novel hum
446	29	69.0	543.8	ADb063824	Adb063824	Human hep	519	29	69.0	841.8	ADT56233	Adt56233	Plant pol
447	29	69.0	543.8	ADb063823	Adb063823	Human hep	520	29	69.0	852.6	ABU03486	Abu03486	Angiogene
448	29	69.0	543.8	ADb063832	Adb063832	Human hep	521	29	69.0	887.4	ABG23684	Abg23684	Novel hum
449	29	69.0	543.8	ADb063822	Adb063822	Human hep	522	29	69.0	949.6	ABU31165	Abu31165	Protein e
450	29	69.0	543.8	ADQ80372	Adq80372	Hepareanas	523	29	69.0	957.7	AB064716	Ab064716	Klebsiell
451	29	69.0	543.8	ADr888210	Adr888210	Human pre	524	29	69.0	1011.1	AB065291	Ab065291	Klebsiell
452	29	69.0	543.8	ADP25079	Adp25079	PRO polyP	525	29	69.0	1024.9	ADM18493	Adm18493	Pinus rad
453	29	69.0	543.8	ADT78177	Adt78177	Human hep	526	29	69.0	1024.9	ADM17829	Adm17829	Pinus rad
454	29	69.0	543.9	ADY27036	Ady27036	Human hep	527	29	69.0	1078.5	ABP65165	Abp65165	Hypoxia-r
455	29	69.0	543.9	ADY65087	Ady65087	Human clo	528	29	69.0	1080.9	ADW48286	Adw48286	Patlial h
456	29	69.0	543.9	AEa42466	Aea42466	Human hep	529	29	69.0	1083.4	ABG04652	Abg04652	Novel hum
457	29	69.0	545.6	ABP56822	Abp56822	Human hep	530	29	69.0	1103.6	ABU62807	Abu62807	Frog G11
458	29	69.0	545.6	ABP56822	Abp56822	Human hep	531	29	69.0	1113.4	ABG06702	Abg06702	Novel hum
459	29	69.0	545.7	ADb16012	Adb16012	G-coupled	532	29	69.0	1137.9	ADM48287	Adm48287	Patlial h
460	29	69.0	545.8	ADL93951	Adl93951	Human G-c	533	29	69.0	1139.5	ABP69469	Abp69469	Human pol
461	29	69.0	556.9	ADZ19010	Adz19010	Hepareanas	534	29	69.0	1167.6	AAE32994	Aae32994	Human kin
462	29	69.0	567.4	ABG23690	Abg23690	Novel hum	535	29	69.0	1167.6	ABU63700	Abu63700	Human kin

536	29	69.0	1167	7	ADD15782	Add15782 Human MEK	609	28	66.7	120	3	AAG11673	Agg11673 Arabidops
537	29	69.0	1167	9	ADM97631	Adm97631 Human Kin	610	28	66.7	121	6	ADA48062	Ada48062 Rice prot
538	29	69.0	1178	6	ABW52976	Abw52976 Protein s	611	28	66.7	124	4	AAU63372	Aau63372 Propionib
539	29	69.0	1178	7	ADK62662	Adk62662 Disease t	612	28	66.7	124	6	ABM59891	Abm59891 Propionib
540	29	69.0	1178	8	ADS43567	Ads43567 Bacterial	613	28	66.7	126	6	ADA48736	Ada48736 Rice prot
541	29	69.0	1225	9	ADM48285	Adm48285 Partial h	614	28	66.7	128	8	ADQ66049	Adq66049 Novel hum
542	29	69.0	1253	6	ABU62802	Abu62802 Frgo G11	615	28	66.7	129	3	AAG11672	Agg11672 Arabidops
543	29	69.0	1338	4	ADM48288	Adm48288 Partial h	616	28	66.7	131	3	AAU73411	Aau73411 Human sec
544	29	69.0	1376	4	ABBS9729	Abbs9729 Drosophil	617	28	66.7	132	8	ADX74974	Adx74974 Plant ful
545	29	69.0	1388	4	ADV97882	Adv97882 Murine pr	618	28	66.7	142	8	ADR09387	Adr09387 Human pro
546	29	69.0	1781	6	ABR39830	Abrr39830 Human SCA	619	28	66.7	142	9	ADZ15013	Adz15013 Seneca Va
547	29	69.0	2136	4	AAW78695	Aaw78695 Human pro	620	28	66.7	142	9	ADZ15046	Adz15046 Seneca Va
548	29	69.0	2292	9	ADZ15034	Adz15034 EMCV-B pr	621	28	66.7	145	4	AAU61554	Aau61554 Propionib
549	29	69.0	2292	9	ADZ15035	Adz15035 EMCV-Da p	622	28	66.7	145	6	ABM58073	Abm58073 Propionib
550	29	69.0	2292	9	ADZ15032	Adz15032 EMCV-R pr	623	28	66.7	149	2	AAU10929	Aau10929 Amino aci
551	29	69.0	2292	9	ADZ15037	Adz15037 EMCV-PV2	624	28	66.7	149	7	ADP47948	Adp47948 Novel hum
552	29	69.0	2292	9	ADZ15036	Adz15036 EMCV-Db p	625	28	66.7	149	8	ADU55503	Adu55503 Novel hum
553	29	69.0	2292	9	ADZ15033	Adz15033 EMCV-PV21	626	28	66.7	152	7	ADC72803	Adc72803 HIV-1 gag
554	29	69.0	2293	5	ABG61913	Abg61913 EMCV-meng	627	28	66.7	156	4	AAU50699	Aau50699 Propionib
555	29	69.0	2725	5	ABG61913	Abg61913 Prostate	628	28	66.7	156	6	ABM47218	Abm47218 Propionib
556	29	69.0	2725	7	ADJ69881	Adj69881 Human hea	629	28	66.7	160	4	AAU30097	Aau30097 Novel hum
557	29	69.0	2725	7	ADN39610	Adn39610 Cancer/ha	630	28	66.7	164	8	ADX71678	Adx71678 Plant ful
558	29	69.0	2725	8	ADQ21282	Adq21282 Human sof	631	28	66.7	171	2	AAW07243	Aaw07243 HIV-1 gro
559	29	69.0	2758	5	ADU06625	Adu06625 Novel bro	632	28	66.7	172	2	AAW46819	Aaw46819 Endo-beta
560	29	69.0	2758	5	ABG97359	Abg97359 Human CGD	633	28	66.7	176	4	ABG20297	Abg20297 Novel hum
561	29	69.0	2769	5	ABG70388	Abg70388 Human TEN	634	28	66.7	180	8	ADU07846	Adu07846 Amino aci
562	29	69.0	2769	7	ADF74830	Adf74830 Murine NO	635	28	66.7	189	8	ADX73631	Adx73631 Plant ful
563	29	69.0	2775	7	ADF74842	Adf74842 Murine NO	636	28	66.7	189	9	ABR36510	Abrr36510 L. pneumo
564	29	69.0	2794	5	ABB98401	Abb98401 Human NOV	637	28	66.7	189	9	ABR39908	Abrr39908 L. pneumo
565	29	69.0	2802	5	AD116953	Ad116953 Chicken N	638	28	66.7	191	4	AAU65246	Aau65246 Propionib
566	29	69.0	2887	9	AEA63534	Aea63534 H. capbul	639	28	66.7	191	6	ABM61765	Abm61765 Propionib
567	28	66.7	8	ABP12559	Abp12559 HIV A02 s	640	28	66.7	198	4	ABG25693	Abg25693 Novel hum	
568	28	66.7	9	ABP12682	Abp12682 HIV A02 s	641	28	66.7	210	7	ABO79616	Abot79616 Pseudomon	
569	28	66.7	11	ABP12895	Abp12895 HIV A02 s	642	28	66.7	212	8	ADY14082	Ady14082 Plant ful	
570	28	66.7	15	ABR24569	Abpr24569 HIV DR su	643	28	66.7	218	3	AAQ40909	Aaq40909 Zee may	
571	28	66.7	15	ABP24603	Abp24603 HIV DR su	644	28	66.7	218	4	ABG28842	Abg28842 Novel hum	
572	28	66.7	26	ADB47953	Adb47953 Novel hum	645	28	66.7	229	3	AAU70509	Aau70509 Human BAG	
573	28	66.7	26	ADJ55508	Adj55508 Novel hum	646	28	66.7	229	7	ABM01307	Abm01307 Human Bcl1	
574	28	66.7	35	AAU27369	Aau27369 Novel bon	647	28	66.7	231	2	AAU04036	Aau04036 HIV-1 (BH	
575	28	66.7	50	ABP32355	Abp32355 Human ORF	648	28	66.7	231	9	ADX39486	Adx39486 HIV Gag p	
576	28	66.7	50	ADU17119	Adu17119 M. tuberc	649	28	66.7	231	9	ADX39483	Adx39483 HIV Gag p	
577	28	66.7	50	ADX79008	Adx79008 Plant ful	650	28	66.7	231	9	ADX39485	Adx39485 HIV Gag p	
578	28	66.7	51	ABP10304	Abp10304 Human ORF	651	28	66.7	231	9	ADX39482	Adx39482 HIV Gag p	
579	28	66.7	59	AAU23650	Aau23650 Novel hum	652	28	66.7	232	5	ABG75520	Abg75520 HIV-1 p24	
580	28	66.7	60	AAAG0920	Aaag0920 Human imm	653	28	66.7	232	5	ADN37729	Adn37729 Human imm	
581	28	66.7	60	AAAG1283	Agg1283 Arabidops	654	28	66.7	232	9	ADM88648	Adm88648 HIV-1 str	
582	28	66.7	62	AAAB16551	Aab16551 Bacteriop	655	28	66.7	232	9	ADM98648	Adm98648 HIV-1 str	
583	28	66.7	65	AAAB19600	Aam19600 Peptide #	656	28	66.7	232	9	ADM98645	Adm98645 HIV-1 gro	
584	28	66.7	65	AAAB39234	Abb39234 Peptide #	657	28	66.7	232	9	ADM95666	Adm95666 HIV-1 gro	
585	28	66.7	65	AAAB32735	Aam32735 Peptide #	658	28	66.7	232	9	ADY59303	Ady59303 HIV-1 gro	
586	28	66.7	65	AAAB24076	Abb24076 Protein #	659	28	66.7	232	9	ADY59915	Ady59915 HIV-1 gro	
587	28	66.7	65	AAAM72487	Aam72487 Human Don	660	28	66.7	232	9	ADY59924	Ady59924 HIV-1 gro	
588	28	66.7	65	AAAM59896	Aam59896 Human bra	661	28	66.7	232	9	ADY71147	Ady71147 HIV-1 gro	
589	28	66.7	65	ABG54178	Abg54178 Human liv	662	28	66.7	237	7	ADC72887	Adc72887 HIV-1 gag	
590	28	66.7	65	ABG42307	Abg42307 Human pep	663	28	66.7	239	7	ADC72904	Adc72904 HIV-1 gag	
591	28	66.7	69	AAAG12181	Aag12181 Arabidops	664	28	66.7	250	8	ADX73184	Adx73184 Plant ful	
592	28	66.7	69	ABJ03696	Abj03696 Human ova	665	28	66.7	252	8	ADK66494	Adk66494 Plant ful	
593	28	66.7	77	AAO05569	Aao05569 Human pol	666	28	66.7	252	8	ADY05630	Ady05630 Plant ful	
594	28	66.7	77	ABO66841	Abob6841 Klebsiell	667	28	66.7	258	8	ADY06195	Ady06195 Plant ful	
595	28	66.7	80	ADY07189	Ady07189 Plant ful	668	28	66.7	259	2	AAU35703	Aau35703 Chlamydia	
596	28	66.7	90	ABG02819	Abg02819 Novel hum	669	28	66.7	260	7	ADP05220	Adp05220 Bacterial	
597	28	66.7	99	ADJ032144	Adj032144 Mouse ant	670	28	66.7	266	4	AAAG1257	Aag1257 C. glutami	
598	28	66.7	103	ADJ78267	Adj78267 Endometri	671	28	66.7	266	4	ABG18165	Abg18165 Novel hum	
599	28	66.7	103	ADJ78266	Adj78266 Endometri	672	28	66.7	276	7	ADC72894	Adc72894 HIV-1 gag	
600	28	66.7	105	ABP04486	Abp04486 Human ORF	673	28	66.7	287	8	ADQ65847	Adq65847 Novel hum	
601	28	66.7	109	AAAM93349	Aam93349 Human pol	674	28	66.7	291	4	ABB62904	Abb62904 Drosophil	
602	28	66.7	109	ABP64434	Abp64434 Human ORF	675	28	66.7	292	6	ABU21983	Abu21983 Protein e	
603	28	66.7	109	ADL30864	Adl30864 Human pro	676	28	66.7	292	8	ADY11699	Ady11699 Plant ful	
604	28	66.7	111	ABP33176	Abp33176 Human ORF	677	28	66.7	301	4	AAAM39839	Aam39839 Human pol	
605	28	66.7	111	ABO56780	Abob56780 Human gen	678	28	66.7	304	2	AAW46807	Aaw46807 Endo-beta	
606	28	66.7	114	ABO67105	Abob67105 Klebsiell	679	28	66.7	307	3	AAAG3538	Aag3538 Arabidops	
607	28	66.7	119	AAAB25513	Aab25513 Pinus rad	680	28	66.7	311	6	ABP96401	Abp96401 Prochloro	
608	28	66.7	120	AAAB25160	Aab25160 Pinus rad	681	28	66.7	324	8	ADO63067	Adob3067 Transcrip	

682	28	66.7	327	8	ADL04904	M. catarr	755	28	66.7	459	3	AA653001	AA653001	Arabidops
683	28	66.7	331	2	AAW15563	Aspergill	756	28	66.7	459	3	AA623478	AA623478	Arabidops
684	28	66.7	331	2	AAW14596	Aspergill	757	28	66.7	459	3	AA622221	AA622221	Arabidops
685	28	66.7	331	8	ADX80115	plant ful	758	28	66.7	455	4	AA835132	AA835132	Human E2F
686	28	66.7	332	2	AAW46814	Endo beta	759	28	66.7	455	4	ABG01756	ABG01756	Human hum
687	28	66.7	332	2	AEBO0291	Endo glucu	760	28	66.7	455	8	ADQ18446	ADQ18446	Human sot
688	28	66.7	334	6	ABM66951	Phototrac	761	28	66.7	455	9	ADX08007	ADX08007	Cyclin-de
689	28	66.7	335	4	AAE12786	Talaromyc	762	28	66.7	465	9	ADY15153	ADY15153	PRO polyP
690	28	66.7	335	7	ABR63117	Thermomasc	763	28	66.7	465	9	ADY15151	ADY15151	PRO polyP
691	28	66.7	335	7	AEBO0297	Xylanase	764	28	66.7	466	7	ABO84015	ABO84015	Pseudomon
692	28	66.7	341	8	ADV81435	Streptococ	765	28	66.7	474	4	AAW79749	AAW79749	Human pro
693	28	66.7	344	8	ADV87996	Streptococ	766	28	66.7	474	4	AA866603	AA866603	Putative
694	28	66.7	344	8	ADV79249	Streptococ	767	28	66.7	480	8	ADT57249	ADT57249	Plant pol
695	28	66.7	344	8	ADY12924	Plant ful	768	28	66.7	486	4	AA839541	AA839541	Human pro
696	28	66.7	345	8	ABR62522	Drosophil	769	28	66.7	486	7	ADMO5935	ADMO5935	Human pro
697	28	66.7	346	8	ADX68736	plant ful	770	28	66.7	480	7	ADCS8031	ADCS8031	Endogluc
698	28	66.7	346	8	ADW22692	Horn fly	771	28	66.7	490	7	ADCS9465	ADCS9465	HIV Gag P
699	28	66.7	347	4	AA893168	C glutamyl	772	28	66.7	491	7	ADC72913	ADC72913	HIV-1 gag
700	28	66.7	348	4	AA882399	Horn fly	773	28	66.7	491	9	ADX39490	ADX39490	HIV Gag P
701	28	66.7	348	4	AA882401	Horn fly	774	28	66.7	491	9	ADX39534	ADX39534	HIV Gag P
702	28	66.7	348	4	AA882396	Horn fly	775	28	66.7	491	9	ADX39570	ADX39570	HIV-1 non
703	28	66.7	348	4	AA882400	Horn fly	776	28	66.7	492	3	AA869268	AA869268	HIV-1 non
704	28	66.7	348	4	AA882402	Horn fly	777	28	66.7	492	9	ADX39448	ADX39448	HIV Gag P
705	28	66.7	348	4	AA882398	Horn fly	778	28	66.7	492	9	ADX39426	ADX39426	HIV Gag P
706	28	66.7	348	4	AA882397	Horn fly	779	28	66.7	492	9	ADX39571	ADX39571	HIV Gag P
707	28	66.7	348	8	ADJ66056	C. carnea	780	28	66.7	492	9	ADX39425	ADX39425	HIV Gag P
708	28	66.7	348	8	ADJ66054	C. carnea	781	28	66.7	492	9	ADZ07879	ADZ07879	HIV CON 1
709	28	66.7	348	8	ADM36322	Chrysoper	782	28	66.7	493	7	ADC72881	ADC72881	HIV-1 gag
710	28	66.7	348	8	ADM22694	Common gr	783	28	66.7	493	9	ADX39489	ADX39489	HIV Gag P
711	28	66.7	350	3	AA643537	Arabidops	784	28	66.7	494	3	AB869275	AB869275	HIV-1 non
712	28	66.7	351	8	ABO68553	Pseudomon	785	28	66.7	494	7	ADC72896	ADC72896	HIV-1 gag
713	28	66.7	355	8	ADSI0840	Human the	786	28	66.7	495	9	ADX39585	ADX39585	HIV Gag P
714	28	66.7	356	8	ADM98630	Geranylge	787	28	66.7	495	9	ADX39517	ADX39517	HIV Gag P
715	28	66.7	362	5	ABR90626	Chlamydia	788	28	66.7	495	9	ADX39584	ADX39584	HIV Gag P
716	28	66.7	376	2	AA137122	Protein w	789	28	66.7	495	9	ADX39484	ADX39484	HIV Gag P
717	28	66.7	378	7	ADB65544	Human pro	790	28	66.7	495	9	ADZ07859	ADZ07859	HIV CON_K
718	28	66.7	379	4	ABG24734	Novel hum	791	28	66.7	496	7	ADC72900	ADC72900	HIV-1 gag
719	28	66.7	388	9	AEBO0295	Endogluc	792	28	66.7	496	7	ADC72878	ADC72878	HIV-1 gag
720	28	66.7	390	4	ABBS9276	Drosophila	793	28	66.7	496	9	ADX39574	ADX39574	HIV Gag P
721	28	66.7	390	4	AAW78765	Human pro	794	28	66.7	496	9	ADX39575	ADX39575	HIV Gag P
722	28	66.7	390	4	AA867786	Amino aci	795	28	66.7	496	9	ADX39450	ADX39450	HIV Gag P
723	28	66.7	393	8	ABM82311	Tumour-as	796	28	66.7	496	9	ADX39453	ADX39453	HIV Gag P
724	28	66.7	393	8	ADU06339	Novel bro	797	28	66.7	497	2	AA104971	AA104971	Mycobacte
725	28	66.7	398	6	ABP75478	Human sec	798	28	66.7	497	5	ABP35713	ABP35713	Fungal ZB
726	28	66.7	403	4	AAW41625	Human pol	799	28	66.7	497	7	ADC72899	ADC72899	HIV-1 gag
727	28	66.7	403	8	ADSI12099	Human the	800	28	66.7	497	9	ADV85640	ADV85640	HIV Gag P
728	28	66.7	403	8	ADSI12089	Human the	801	28	66.7	497	9	ADX39583	ADX39583	HIV Gag P
729	28	66.7	406	3	AA623480	Arabidops	802	28	66.7	497	9	ADX39582	ADX39582	HIV Gag P
730	28	66.7	413	8	ADN20544	Bacterial	803	28	66.7	497	9	ADX39589	ADX39589	HIV Gag P
731	28	66.7	414	4	AA678989	Escherich	804	28	66.7	497	9	ADX39590	ADX39590	HIV Gag P
732	28	66.7	418	8	ADX66356	Plant ful	805	28	66.7	498	4	ABG09680	ABG09680	Novel hum
733	28	66.7	419	3	AA623479	Arabidops	806	28	66.7	498	8	ADOS2543	ADOS2543	HIV-1 rec
734	28	66.7	423	4	AA892579	Human pro	807	28	66.7	498	8	ADOS2538	ADOS2538	HIV-1 rec
735	28	66.7	423	4	AA667125	Amino aci	808	28	66.7	498	9	ADX39539	ADX39539	HIV Gag P
736	28	66.7	423	6	AAE33211	Human mit	809	28	66.7	498	9	ADX39540	ADX39540	HIV Gag P
737	28	66.7	423	7	ADJ70415	Human hea	810	28	66.7	498	9	ADX39481	ADX39481	HIV Gag P
738	28	66.7	423	8	ABM82310	Tumour-as	811	28	66.7	498	9	ADZ07837	ADZ07837	HIV CON_A
739	28	66.7	423	8	ADSI10839	Human the	812	28	66.7	498	9	ADZ07839	ADZ07839	HIV CON_A
740	28	66.7	423	9	ADY17442	PRO polyP	813	28	66.7	499	9	ADX39488	ADX39488	HIV Gag P
741	28	66.7	431	7	ABM85743	Human pro	814	28	66.7	499	9	ADY99891	ADY99891	Human con
742	28	66.7	434	6	ABO00772	Polypepti	815	28	66.7	500	8	ADOS2524	ADOS2524	HIV-1 rec
743	28	66.7	441	3	AA653003	Arabidops	816	28	66.7	500	8	ADOS2550	ADOS2550	HIV-1 gag
744	28	66.7	441	3	AA622223	Arabidops	817	28	66.7	500	8	ADOS2533	ADOS2533	HIV-1 rec
745	28	66.7	442	3	AA643536	Arabidops	818	28	66.7	500	9	ADX39523	ADX39523	HIV Gag P
746	28	66.7	446	3	AA653002	Arabidops	819	28	66.7	500	9	ADX39514	ADX39514	HIV Gag P
747	28	66.7	446	3	AA622222	Arabidops	820	28	66.7	500	9	ADX39524	ADX39524	HIV Gag P
748	28	66.7	452	3	AA882512	Streptococ	821	28	66.7	500	9	ADX39442	ADX39442	HIV Gag P
749	28	66.7	457	2	AA630348	A. suppres	822	28	66.7	500	9	AE810580	AE810580	Clade B g
750	28	66.7	457	3	AA670516	Human BAG	823	28	66.7	501	6	ABU29962	ABU29962	Protein e
751	28	66.7	457	7	ABW01314	Human Bcl	824	28	66.7	501	9	ADC72906	ADC72906	HIV-1 gag
752	28	66.7	457	7	ADF69136	Human Mps	825	28	66.7	501	9	ADX39559	ADX39559	HIV Gag P
753	28	66.7	457	8	AD88153	Human pro	826	28	66.7	501	9	ADX39566	ADX39566	HIV Gag P
754	28	66.7	457	9	ADV94801	Human eph	827	28	66.7	502	9	ADX39558	ADX39558	HIV Gag P

828	28	66.7	503	4	ABB61708	Abb61708 Drosophila	901	27	64.3	58	9	AD273458	Ad273458 Human inc
829	28	66.7	503	7	ADB67082	ADB67082 Atrialine-1	902	27	64.3	63	4	AAU86604	AAU86604 Novel hum
830	28	66.7	503	8	ADL199353	ADL199353 Nanosrtruc	903	27	64.3	63	7	ADB59938	ADB59938 Connectiv
831	28	66.7	504	8	ADX39471	Adx39471 HIV Gag p	904	27	64.3	65	4	AAU16299	AAU16299 Peptide #
832	28	66.7	508	7	ADC72875	Adc72875 HIV-1 gag	905	27	64.3	65	4	ABB35290	ABB35290 Peptide #
833	28	66.7	509	5	ABP51651	Abp51651 Potato ID	906	27	64.3	65	4	AAU28791	AAU28791 Peptide #
834	28	66.7	512	7	ADC97621	Adc97621 E. faeciu	907	27	64.3	65	4	ABB30118	ABB30118 Peptide #
835	28	66.7	513	6	AAE35753	AAE35753 Human SEC	908	27	64.3	65	4	ABB20735	ABB20735 Protein #
836	28	66.7	517	4	AAE14345	AAE14345 Human pro	909	27	64.3	65	4	AAU68491	AAU68491 Human bon
837	28	66.7	517	5	AAU82718	AAU82718 Human aci	910	27	64.3	65	4	AAU55690	AAU55690 Propionib
838	28	66.7	523	5	ABX95781	Abx95781 Plant ful	911	27	64.3	65	4	AAU44673	AAU44673 Propionib
839	28	66.7	524	6	ABM70614	Abm70614 Photorhab	912	27	64.3	65	3	AAU52209	AAU52209 Propionib
840	28	66.7	527	4	AAE04826	AAE04826 Herpida	913	27	64.3	71	5	AAU45510	AAU45510 Propionib
841	28	66.7	528	2	AAE04826	AAE04826 Human imm	914	27	64.3	75	6	AAU60099	AAU60099 Propionib
842	28	66.7	534	8	ABM64912	ABM64912 Human dia	915	27	64.3	79	4	AAU55690	AAU55690 Propionib
843	28	66.7	534	8	ADU07849	ADU07849 Amino aci	916	27	64.3	79	4	AAU44673	AAU44673 Propionib
844	28	66.7	534	8	ABU49054	ABU49054 Protein e	917	27	64.3	79	6	AAU52209	AAU52209 Propionib
845	28	66.7	630	5	ABB92462	ABB92462 Herpida	918	27	64.3	79	6	AAU45510	AAU45510 Propionib
846	28	66.7	633	4	ADQ65752	ADQ65752 Novel hum	919	27	64.3	84	4	AAU45510	AAU45510 Propionib
847	28	66.7	677	8	ADQ65752	ADQ65752 Novel hum	920	27	64.3	84	5	ABP08439	ABP08439 Human ORF
848	28	66.7	699	7	AD121211	Ad121211 Novel hum	921	27	64.3	84	5	ABM42029	ABM42029 Propionib
849	28	66.7	716	6	ABU35392	ABU35392 Protein e	922	27	64.3	89	5	ABU01134	ABU01134 Ovary cel
850	28	66.7	731	7	ADG42371	Adg42371 P. syring	923	27	64.3	97	4	AAU90849	AAU90849 Human imm
851	28	66.7	736	9	ADY77374	Ady77374 Foot-and-	924	27	64.3	98	7	ABO79790	ABO79790 Pseudomon
852	28	66.7	808	7	ADFO4710	Adfo4710 Bacterial	925	27	64.3	103	4	AAU00901	AAU00901 Human pol
853	28	66.7	841	4	ABB68767	ABB68767 Drosophila	926	27	64.3	105	8	ADX93023	ADX93023 Plant ful
854	28	66.7	841	4	ADSB24015	ADSB24015 Bacterial	927	27	64.3	108	5	AAU80318	AAU80318 Anti-huma
855	28	66.7	891	8	ADS20997	ADS20997 Bacterial	928	27	64.3	109	8	ADQ31869	ADQ31869 Humanized
856	28	66.7	891	8	ADQ66974	ADQ66974 Novel hum	929	27	64.3	109	8	ADQ31871	ADQ31871 Humanized
857	28	66.7	942	8	ADQ66974	ADQ66974 Novel hum	930	27	64.3	109	8	ADQ31868	ADQ31868 Humanized
858	28	66.7	973	4	ADG73085	ADG73085 Pseudomon	931	27	64.3	109	8	ADQ31867	ADQ31867 Humanized
859	28	66.7	1146	7	ADL12140	ADL12140 Pseudomon	932	27	64.3	109	8	ADQ31870	ADQ31870 Humanized
860	28	66.7	1176	3	AAU18280	AAU18280 Plasmedin	933	27	64.3	109	8	ADQ31870	ADQ31870 Humanized
861	28	66.7	1185	5	AAU80135	AAU80135 Chimeric	934	27	64.3	109	8	ADT77630	ADT77630 Human the
862	28	66.7	1185	5	AAU80135	AAU80135 Chimeric	935	27	64.3	109	8	ADT77630	ADT77630 Human the
863	28	66.7	1220	6	AAE33407	AAE33407 Chimeric	936	27	64.3	109	8	ADT77629	ADT77629 1 VL pept
864	28	66.7	1273	5	ABP62888	ABP62888 Human pol	937	27	64.3	109	8	ADT77629	ADT77629 1 VL pept
865	28	66.7	1278	5	ABP62888	ABP62888 Human pol	938	27	64.3	109	8	ADT77627	ADT77627 2 VL pept
866	28	66.7	1308	4	ABG26018	ABG26018 Novel hum	939	27	64.3	109	8	ADT77628	ADT77628 3 VL pept
867	28	66.7	1437	6	ABP98857	ABP98857 Human str	940	27	64.3	109	8	ADT77625	ADT77625 ITA1 VL p
868	28	66.7	1445	4	AAE04828	AAE04828 Human imm	941	27	64.3	109	9	AEBS1146	AEBS1146 Humanized
869	28	66.7	1508	9	ADY99915	ADY99915 Human cod	942	27	64.3	109	9	AEBS1145	AEBS1145 Humanized
870	28	66.7	1736	9	ADY99919	ADY99919 Human cod	943	27	64.3	109	9	AEBS1144	AEBS1144 Humanized
871	28	66.7	1819	7	ADBE6309	ADBE6309 Human pro	944	27	64.3	109	9	AEBS1147	AEBS1147 Humanized
872	28	66.7	1890	9	ADZ15011	ADZ15011 Seneca Va	945	27	64.3	109	9	AEBS1149	AEBS1149 Humanized
873	28	66.7	2332	8	ADY94875	ADY94875 O-cype fo	946	27	64.3	110	3	AAU53240	AAU53240 Human col
874	28	66.7	2427	8	ADN24081	ADN24081 Bacterial	947	27	64.3	112	5	ABG70739	ABG70739 Variabla
875	28	66.7	2560	9	ADY99921	ADY99921 Human cod	948	27	64.3	119	8	ADY23074	ADY23074 Plant ful
876	28	66.7	2748	4	ABBS6843	ABBS6843 Drosophila	949	27	64.3	125	3	AAU52519	AAU52519 Arabidops
877	28	66.7	3011	2	AAE66995	AAE66995 Hepatitis	950	27	64.3	125	4	ABG00193	ABG00193 Novel hum
878	28	66.7	3011	2	AAE66995	AAE66995 Hepatitis	951	27	64.3	127	9	ADY66082	ADY66082 S. mansoni
879	28	66.7	3011	5	AAU80316	AAU80316 Anti-huma	952	27	64.3	128	3	AAU59774	AAU59774 Arabidops
880	27	64.3	12	8	ADQ08516	ADQ08516 IgG detec	953	27	64.3	130	8	ADQ31877	ADQ31877 Antibody
881	27	64.3	12	8	ADQ08541	ADQ08541 IgG purif	954	27	64.3	130	8	ADQ31866	ADQ31866 Murine an
882	27	64.3	12	8	ADQ28541	ADQ28541 IgG purif	955	27	64.3	130	8	ADQ31866	ADQ31866 Murine an
883	27	64.3	12	8	ADQ28541	ADQ28541 IgG purif	956	27	64.3	130	8	ADQ31866	ADQ31866 Murine an
884	27	64.3	12	8	ADQ28516	ADQ28516 IgG purif	957	27	64.3	130	8	ADQ31881	ADQ31881 Antibody
885	27	64.3	12	8	ADQ07231	ADQ07231 IgG purif	958	27	64.3	130	8	ADT77640	ADT77640 Antibody
886	27	64.3	12	8	ADQ07236	ADQ07236 IgG purif	959	27	64.3	130	8	ADT77636	ADT77636 Antibody
887	27	64.3	16	2	AAU18292	AAU18292 Human tes	960	27	64.3	130	9	AEBS1155	AEBS1155 Chimeric
888	27	64.3	18	2	AAU18293	AAU18293 Testis-sp	961	27	64.3	130	9	AEBS1155	AEBS1155 Chimeric
889	27	64.3	21	2	AAU18294	AAU18294 Testis-sp	962	27	64.3	133	7	ABG14584	ABG14584 Novel hum
890	27	64.3	23	9	ADY66580	ADY66580 S. mansoni	963	27	64.3	139	9	ADY64668	ADY64668 S. mansoni
891	27	64.3	25	8	ADJ67672	ADJ67672 Human ova	964	27	64.3	144	8	ADN92852	ADN92852 Novel hum
892	27	64.3	36	5	AAE26867	AAE26867 Helicobac	965	27	64.3	147	4	AAU75739	AAU75739 Human col
893	27	64.3	41	4	ABG25932	ABG25932 Novel hum	966	27	64.3	150	4	AAU95213	AAU95213 Human rep
894	27	64.3	42	2	AAU13198	AAU13198 Human tes	967	27	64.3	152	6	ABM69660	ABM69660 Photorhab
895	27	64.3	42	2	ADY18356	ADY18356 PRO polyp	968	27	64.3	156	5	AAU83215	AAU83215 Novel sec
896	27	64.3	53	4	AAU73718	AAU73718 Human col	969	27	64.3	159	6	ABM69668	ABM69668 Photorhab
897	27	64.3	57	3	AAU18291	AAU18291 Human tes	970	27	64.3	160	8	ADU67548	ADU67548 Human ova
898	27	64.3	57	3	AAU18291	AAU18291 Human tes	971	27	64.3	171	3	AAU52518	AAU52518 Arabidops
899	27	64.3	58	3	AAU64903	AAU64903 Human 5'	972	27	64.3	171	3	ADX73663	ADX73663 Plant ful
900	27	64.3	58	8	ADU72467	ADU72467 Signal pe	973	27	64.3	171	8	ADX73663	ADX73663 Plant ful

974	27	64.3	175	4	AAG82390
975	27	64.3	176	4	AAB93439
976	27	64.3	181	3	AAG25217
977	27	64.3	186	3	AAG25578
978	27	64.3	186	3	AAG54030
979	27	64.3	188	6	ABM69918
980	27	64.3	189	3	AAG59395
981	27	64.3	189	3	AAG55184
982	27	64.3	189	3	ABU51992
983	27	64.3	212	8	ADL04319
984	27	64.3	212	8	ADY24428
985	27	64.3	212	8	ADX90780
986	27	64.3	215	8	ADQ31885
987	27	64.3	215	8	ADQ31891
988	27	64.3	215	8	ADT51708
989	27	64.3	215	8	ADT77644
990	27	64.3	215	9	ABE51163
991	27	64.3	215	9	ABE51169
992	27	64.3	221	4	AAE01220
993	27	64.3	221	9	ADX07868
994	27	64.3	222	8	ADH71948
995	27	64.3	223	3	ABO64201
996	27	64.3	227	3	AAG59394
997	27	64.3	227	3	AAG55183
998	27	64.3	228	2	AAM62649
999	27	64.3	230	2	AAG59393
1000	27	64.3	230	3	AAG55182

ALIGNMENTS

RESULT 1
ADO32090 standard; peptide: 8 AA.

AC ADO32090;
12-AUG-2004 (first entry)

DE Mouse anti-CD3 antibody My9-6 light chain CDR3 SEQ ID NO:6.

XX anti-CD3 antibody; epitope-binding fragment;
KM complementarity-determining region; CDR; immunoglobulin; cytostatic;
KW antibody; myelodysplastic syndrome; acute myeloid leukaemia;
KM chronic myeloid leukaemia; pro-myelocytic leukaemia; mouse; My9-6;
light chain.

XX Mus musculus;
OS WO2004043344-A2.

PN 27-MAY-2004.

XX 05-NOV-2003; 2003WO-US032737.

PF 07-NOV-2002; 2002US-0424332P.

XX (IMMU-) IMMUNOGEN INC.

PA Hoffee MG, Tavares D, Lutz RJ;
WPI; 2004-41619/38.

DR WPI; 2004-41619/38.

XX New antibodies that bind to CD33, useful for treating a disease
PT associated with CD33 expression, such as myelodysplastic syndrome, acute
PT or chronic myeloid leukemia.

XX Claim 1; SEQ ID NO 6; 124pp; English.

XX The present invention describes an isolated anti-CD33 antibody or its
CC epitope-binding fragment comprising: (a) at least one complementarity-
CC determining region (CDR); or (b) at least heavy chain variable region

CC comprising 3 CDRs, and at least one light chain variable region, where
CC the CDR has the ability to bind CD33. Also described: (1) an
CC immunoglobulin comprising the antibody or its epitope-binding fragment
CC linked to a drug or prodrug; (2) a composition comprising the antibody or
CC epitope-binding fragment and a drug or prodrug; (3) a pharmaceutical
CC composition comprising the immunoglobulin, composition or the antibody
CC defined above, or its epitope-binding fragment, and a pharmaceutical
CC agent; (4) a diagnostic reagent comprising the antibody defined above,
CC where the antibody or antibody fragment is labelled; (5) inhibiting the
CC growth of a cell expressing CD33 by contacting the cell with the above
CC defined antibody or its epitope-binding fragment, immunoglobulin, or
CC (pharmaceutical) composition; (6) determining whether a biological sample
CC contains a myelogenous cancer cell; (7) an improved antibody or its
CC epitope-binding fragment that specifically binds to CD33; (8) an isolated
CC polynucleotide encoding the antibody or its epitope-binding fragment
CC defined above; (9) an isolated polynucleotide encoding a light or heavy
CC chain of the antibody defined above or its epitope-binding fragment; (10)
CC a recombinant vector comprising the polynucleotide; (11) a host cell
CC transformed with the recombinant vector; (12) producing an antibody or
CC its epitope-binding fragment having the ability to bind CD33; and (13)
CC obtaining CD33 from a biological material. The anti-CD33 antibody has
CC cytostatic activity. The antibody or its epitope-binding fragment
CC immunoglobulin, composition can be used for treating a subject having a
CC disease where CD33 is expressed, such as myelodysplastic syndrome, acute
CC myeloid leukaemia, chronic myeloid leukaemia or pro-myelocytic leukaemia.
CC It can also be used for inhibiting the growth of cells expressing CD33,
CC and for in vivo imaging or as affinity purification agents. The present
CC sequence represents the mouse anti-CD33 antibody My9-6 light chain CDR3,
CC which is used in an example from the present invention.

XX Sequence 8 AA;

Qy Query Match 100.0%; Score 42; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 HOYLSRT 8
1 HOYLSRT 8

RESULT 2
ADO32094 standard; protein: 113 AA.

AC ADO32094;
12-AUG-2004 (first entry)

DE Humanised mouse anti-CD3 antibody My9-6 light chain SEQ ID NO:10.

XX anti-CD3 antibody; epitope-binding fragment;
KM complementarity-determining region; CDR; immunoglobulin; cytostatic;
KW antibody; myelodysplastic syndrome; acute myeloid leukaemia;
KM chronic myeloid leukaemia; pro-myelocytic leukaemia; mouse; humanised;
My9-6; light chain.

XX Mus musculus;
OS Homo sapiens.
OS Synthetic.

PN WO2004043344-A2.

PD 27-MAY-2004.

XX 05-NOV-2003; 2003WO-US032737.

PF 07-NOV-2002; 2002US-0424332P.

XX (IMMU-) IMMUNOGEN INC.

PA Hoffee MG, Tavares D, Lutz RJ;

DR WPI; 2004-411619/38.
 XX
 PT New antibodies that bind to CD33, useful for treating a disease
 PT associated with CD33 expression, such as myelodysplastic syndrome, acute
 PR or chronic myeloid leukemia.
 XX
 PS Claim 14; SEQ ID NO 10; 124pp; English.
 XX
 CC The present invention describes an isolated anti-CD33 antibody or its
 CC epitope-binding fragment comprising: (a) at least one complementarity-
 CC determining region (CDR); or (b) at least one heavy chain variable region
 CC comprising 3 CDRs, and at least one light chain variable region, where
 CC the CDR has the ability to bind CD33. Also described: (1) an
 CC immunocombinate comprising the antibody or its epitope-binding fragment
 CC linked to a drug or prodrug; (2) a composition comprising the antibody or
 CC epitope-binding fragment and a drug or prodrug; (3) a pharmaceutical
 CC composition comprising the immunocombinate, composition or the antibody
 CC defined above, or its epitope-binding fragment, and a pharmaceutical
 CC agent; (4) a diagnostic reagent comprising the antibody defined above,
 CC where the antibody or antibody fragment is labelled; (5) inhibiting the
 CC growth of a cell expressing CD33 by contacting the cell with the above
 CC defined antibody or its epitope-binding fragment, immunocombinate, or
 CC (pharmaceutical) composition; (6) determining whether a biological sample
 CC contains a myelogenous cancer cell; (7) an improved antibody or its
 CC epitope-binding fragment that specifically binds to CD33; (8) an isolated
 CC polynucleotide encoding the antibody or its epitope-binding fragment
 CC defined above; (9) an isolated polynucleotide encoding a light or heavy
 CC chain of the antibody defined above or its epitope-binding fragment; (10)
 CC a recombinant vector comprising the polynucleotide; (11) a host cell
 CC transformed with the recombinant vector; (12) producing an antibody or
 CC its epitope-binding fragment having the ability to bind CD33; and (13)
 CC obtaining CD33 from a biological material. The anti-CD33 antibody has
 CC cytostatic activity. The antibody or its epitope-binding fragment,
 CC immunocombinate, composition can be used for treating a subject having a
 CC disease where CD33 is expressed, such as myelodysplastic syndrome, acute
 CC myeloid leukaemia, chronic myeloid leukaemia or pro-myelocytic leukaemia.
 CC It can also be used for inhibiting the growth of cells expressing CD33,
 CC and for in vivo imaging or as affinity purification agents. The present
 CC sequence represents a humanised mouse anti-CD33 antibody My9-6 light
 CC chain variable region, which is used in an example from the present
 CC invention.
 CC
 XX
 SQ Sequence 113 AA;
 XX
 QY 1 HOYLSRT 8
 Db 95 HOYLSRT 102
 XX
 Query Match 100.0%; Score 42; DB 8; Length 113;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PD 27-MAY-2004.
 XX
 PF 05-NOV-2003; 2003WO-US032737.
 XX
 PR 07-NOV-2002; 2002US-0424332P.
 XX
 PA (IMMU-) IMMUNOGEN INC.
 XX
 PI Hoffee MG, Tavares D, Lutz RJ;
 XX
 XX WPI; 2004-411619/38.
 DR N-PSDB; ADO32139.
 DR
 XX
 XX New antibodies that bind to CD33, useful for treating a disease
 PT associated with CD33 expression, such as myelodysplastic syndrome, acute
 PT or chronic myeloid leukemia.
 XX
 PS Claim 8; SEQ ID NO 8; 124pp; English.
 XX
 CC The present invention describes an isolated anti-CD33 antibody or its
 CC epitope-binding fragment comprising: (a) at least one complementarity-
 CC determining region (CDR); or (b) at least one heavy chain variable region
 CC comprising 3 CDRs, and at least one light chain variable region, where
 CC the CDR has the ability to bind CD33. Also described: (1) an
 CC immunocombinate comprising the antibody or its epitope-binding fragment
 CC linked to a drug or prodrug; (2) a composition comprising the antibody or
 CC epitope-binding fragment and a drug or prodrug; (3) a pharmaceutical
 CC composition comprising the immunocombinate, composition or the antibody
 CC defined above, or its epitope-binding fragment, and a pharmaceutical
 CC agent; (4) a diagnostic reagent comprising the antibody defined above,
 CC where the antibody or antibody fragment is labelled; (5) inhibiting the
 CC growth of a cell expressing CD33 by contacting the cell with the above
 CC defined antibody or its epitope-binding fragment, immunocombinate, or
 CC (pharmaceutical) composition; (6) determining whether a biological sample
 CC contains a myelogenous cancer cell; (7) an improved antibody or its
 CC epitope-binding fragment that specifically binds to CD33; (8) an isolated
 CC polynucleotide encoding the antibody or its epitope-binding fragment
 CC defined above; (9) an isolated polynucleotide encoding a light or heavy
 CC chain of the antibody defined above or its epitope-binding fragment; (10)
 CC a recombinant vector comprising the polynucleotide; (11) a host cell
 CC transformed with the recombinant vector; (12) producing an antibody or
 CC its epitope-binding fragment having the ability to bind CD33; and (13)
 CC obtaining CD33 from a biological material. The anti-CD33 antibody has
 CC cytostatic activity. The antibody or its epitope-binding fragment,
 CC immunocombinate, composition can be used for treating a subject having a
 CC disease where CD33 is expressed, such as myelodysplastic syndrome, acute
 CC myeloid leukaemia, chronic myeloid leukaemia or pro-myelocytic leukaemia.
 CC It can also be used for inhibiting the growth of cells expressing CD33,
 CC and for in vivo imaging or as affinity purification agents. The present
 CC sequence represents the mouse anti-CD33 antibody My9-6 light chain
 CC variable region, which is used in an example from the present invention.
 CC
 XX
 SQ Sequence 113 AA;
 XX
 QY 1 HOYLSRT 8
 Db 95 HOYLSRT 102
 XX
 Query Match 100.0%; Score 42; DB 8; Length 113;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3
 ADO32092 standard; protein; 113 AA.
 XX
 AC ADO32092;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Mouse anti-CD33 antibody My9-6 light chain variable region SEQ ID NO:8.
 XX
 KM anti-CD33 antibody; epitope-binding fragment;
 KM complementarity-determining region; CDR; immunocombinate; cytostatic;
 KM antibody; myelodysplastic syndrome; acute myeloid leukaemia;
 KM chronic myeloid leukaemia; pro-myelocytic leukaemia; mouse; My9-6;
 XX light chain.
 XX
 OS Mus musculus.
 XX
 PN WO2004043344-A2.
 XX

RESULT 4
 ADO32146 standard; protein; 114 AA.
 XX
 AC ADO32146;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Mouse anti-CD33 antibody light chain homologous protein SEQ ID NO:62.
 XX

KW	anti-CD33 antibody; epitope-binding fragment;
KW	complementarity-determining region; CDR; immunoglobulin; cytosolic;
KW	antibody; myelodysplastic syndrome; acute myeloid leukaemia;
KW	chronic myeloid leukaemia; pro-myelocytic leukaemia; mouse; light chain.
XX	
OS	Mus musculus,
XX	
PN	WO2004043344-A2.
XX	
PD	27-MAY-2004.
XX	
PF	05-NOV-2003; 2003WO-US032737.
XX	
PR	07-NOV-2002; 2002US-0424332P.
XX	
PA	(IMMU-) IMMUNOGEN INC.
XX	
P1	Hofree MG, Tavares D, Iutz RJ;
XX	
DR	WPI; 2004-411619/38.
XX	
PT	New antibodies that bind to CD33, useful for treating a disease
PT	associated with CD33 expression, such as myelodysplastic syndrome, acute
FT	or chronic myeloid leukemia.
XX	
PS	Example 3; SEQ ID NO 62; 124pp; English.

XX The present invention describes an isolated anti-CD33 antibody or its
CC epitope-binding fragment comprising: (a) at least one complementarity-
CC determining region (CDR); or (b) at least one heavy chain variable region
CC comprising 3 CDRs, and at least one light chain variable region, where
CC the CDR has the ability to bind CD33. Also described: (1) an
CC immunocongugate comprising the antibody or its epitope-binding fragment
CC linked to a drug or prodrug; (2) a composition comprising the antibody or
CC epitope-binding fragment and a drug or prodrug; (3) a pharmaceutical
CC composition comprising the immunocongugate, composition or the antibody
CC defined above, or its epitope-binding fragment, and a pharmaceutical
CC agent; (4) a diagnostic reagent comprising the antibody defined above,
CC where the antibody or antibody fragment is labelled; (5) inhibiting the
CC growth of a cell expressing CD33 by contacting the cell with the above
CC defined antibody or its epitope-binding fragment, immunocongugate, or
CC (pharmaceutical) composition; (6) determining whether a biological sample
CC contains a myelogenous cancer cell; (7) an improved antibody or its
CC epitope-binding fragment that specifically binds to CD33; (8) an isolated
CC polynucleotide encoding the antibody or its epitope-binding fragment
CC defined above; (9) an isolated polynucleotide encoding a light or heavy
CC chain of the antibody defined above or its epitope-binding fragment; (10)
CC a recombinant vector comprising the polynucleotide; (11) a host cell
CC transformed with the recombinant vector; (12) producing an antibody or
CC its epitope-binding fragment having the ability to bind CD33; and (13)
CC obtaining CD33 from a biological material. The anti-CD33 antibody has
CC cytostatic activity. The antibody or its epitope-binding fragment,
CC immunocongugate, composition can be used for treating a subject having a
CC disease where CD33 is expressed, such as myelodysplastic syndrome, acute
CC myeloid leukaemia, chronic myeloid leukaemia or pro-myelocytic leukemia.
CC It can also be used for inhibiting the growth of cells expressing CD33,
CC and for in vivo imaging or as affinity purification agents. The present
CC sequence represents a mouse anti-CD33 antibody light chain homologous
CC amino acid sequence, which is used in an example from the present
XX invention.

XX Sequence 114 AA;

Query Match

Query Match	100.0%	Score 42;	DB 8;	Length 114;
Best Local Similarity	100.0%;	Pred. No. 1;		
Matches 8; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1 HQYLSSRT 8
D6	95 HQYLSSRT 102

RESULT 5

ADE85813
ID ADE85813 standard; peptide; 25 AA.

AC ADE85813;

DT 29-JAN-2004 (first entry)

Human interleukin-21 peptide fragment.

Human; interleukin-21; immunosuppressive; antiarthritic; antiarthritic;

KM antiinflammatory; dermatological; ophthalmological; uropathic;
KM muscular-gen.; vasotropic; antidiabetic; antithyroid; thyromimetic;
KM neuroprotective; gastrointestinal-gen.; antipsoriatic; gene therapy.

Homo sapiens

PN WO2003087320-A2

PD 23-OCT-2003.

08-APR-2003; 2003WO-US010736.

AA 09-APR-2002; 2002US-0371038P
PR

AA
PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.

AA, Mol1 T, Strom TB, Zheng XX, PI

DR WPI; 2003-845317/78.

PT New substantially pure interleukin-21 polypeptide, useful for diagnosing,

PT disease, type I diabetes, Graves disease, multiple sclerosis, psoriasis

XX 3-11-1900

PS Disclosure; SEQ ID NO 6; 65bp; English.

XX The present sequence is that of a peptide fragment of human interleukin-21 (IL-21) ADB8508, including the Q19 residue important for gamma chain interaction. The invention provides antagonists of the IL-21 receptor.

CC These include mutants of IL-21 in which the Gln residue at position 119
CC of the mature polypeptide is substituted by Asp or in which the Gln
CC residues at positions 114 and 119 of the mature polypeptide are both
CC replaced by Asp. The mutant IL-21 polypeptides inhibit or suppress T-cell
CC activation. They preferably comprise a sequence that increases

CC circulating half-life, such as the FC region of an IgG molecule and may
CC further comprise an antigenic tag. Such antigens inhibit cellular
CC proliferation in response to either anti-CD3 monoclonal antibodies or
CC anti-CD3 antibodies applied together with IL-2 and/or IL-15 together with

CC IL-21. A claimed method of suppressing the immune response in a patient
CC comprises administering the IL-21 antagonist or a nucleic acid encoding
CC it. The method is used to treat an autoimmune disease such as rheumatic
CC disease, including systemic lupus erythematosus, Sjogren's syndrome,
CC

CC scleroderma, mixed connective tissue disease, dermatomyositis,
CC polymyositis, Reiter's syndrome, or Behcet's disease, or rheumatoid
CC arthritis, type I diabetes, autoimmune disease of the thyroid such as
CC Hashimoto's thyroiditis or Graves disease, an autoimmune disease of the

central nervous system such as multiple sclerosis, myasthenia gravis, or encephalomyelitis, or an autoimmune disease selected from pemphigus vulgaris, pemphigus vegetans, pemphigus foliaceus, Senechal-Usher syndrome, Crohn's disease, ulcerative colitis, Sjögren's syndrome, rheumatoid arthritis, psoriasis or inflammatory bowel disease; all

CC Brazilian Penitentiary System (not
CC claimed).

AA Sequence 25 AA;
SQ

Seq	Sequence	25	AA;
Query Match	88.1%	Score 37;	DB 7; Length 25;

Matches	7; Conserva
QY	1 HQYLSRT 8

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Db      12 HQLSSRT 19

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100


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RESULT 6
AAE29264
ID AAE29264 standard; protein; 112 AA.
XX
AC AAE29264;
XX
DT 27-JAN-2003 (first entry)
DE
S. aureus ClfA specific monoclonal antibody 13-2VLA-1 protein.
XX
KM Clumping factor A; ClfA; fibrinogen; fibrin; Clf40; Clf33; N3 protein;
KM immunological; staphylococcal infection; impetigo; pneumonia; furuncle;
KM septic arthritis; sepsis; endocarditis; antibacterial; wound; therapy.
XX
OS Staphylococcus aureus.
XX
FH Key Location/Qualifiers
FT Region 24..40
FT /note= "CDR1"
FT Region 56..62
FT /note= "CDR2"
FT Region 95..102
FT /note= "CDR3"
XX
MO200272600-A2.
XX
PD 19-SEP-2002.
XX
PF 28-JAN-2002; 2002WO-US002296.
XX
PR 26-JAN-2001; 2001US-0264072P.
PR 12-MAR-2001; 2001US-0274611P.
PR 18-JUN-2001; 2001US-0286413P.
PR 30-JUL-2001; 2001US-0308116P.
XX
PA (INH1-) INHIBITEX INC.
XX
PI Patti JM, Hutchins JT, Domanski P, Patel P, Hall A;
XX
WPI; 2002-759834/82.
DR N-PSDB; AAD46863.
XX
PT New anti-clumping factor A (ClfA) monoclonal antibody, useful for
PT treating or preventing Staphylococcus aureus infection e.g. wound
PT infections, impetigo, furuncles, pneumonia, septic arthritis or sepsis in
PT a human or animal.
XX
PS Claim 11; Page 34; 80pp; English.
XX
CC The invention relates to monoclonal antibody which binds the clumping
CC factor A (ClfA) protein from Staphylococcus aureus. The anti-ClfA
CC monoclonal antibody is useful for treating or preventing S. aureus
CC infection in a human or animal, and for inhibiting the binding of
CC staphylococcal bacteria to fibrinogen or fibrin. The immunogenic fragment
CC S. aureus Clf40 protein, S. aureus Clf33 protein, or the S. aureus N3
CC protein is useful for inducing an immunological response in a human or
CC animal. These staphylococcal infections include wound infections, sepsis,
CC impetigo, furuncles, pneumonia, septic arthritis or endocarditis. The
CC present sequence is Staphylococcus aureus ClfA specific monoclonal
CC antibody 13-2VLA-1 (variable light sequence) protein
XX
SQ Sequence 112 AA;
Query Match 88.1%; Score 37; DB 5; Length 112;
Best Local Similarity 87.5%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 HOYLSRT 8
DB 95 HOYLSRT 102
```

```
RESULT 7
ADSI9023
ID ADSI9023 standard; protein; 131 AA.
XX
AC ADSI9023;
XX
DT 30-DEC-2004 (first entry)
DE
Mature human interleukin-21 (IL-21) protein SeqID 2.
XX
KM immunological disorder; human; cytokine; interleukin-21; IL-21;
KM multiple sclerosis; IL-10 deficiency; neuroprotective; gene therapy.
XX
OS Homo sapiens.
XX
PN WO2004084835-A2.
XX
PD 07-OCT-2004.
XX
PF 22-MAR-2004; 2004WO-US008833.
XX
PR 21-MAR-2003; 2003US-0456920P.
XX
PA (AMHP ) WYETH.
XX
PI Collins M, Chin EY, Senices M, Young DA;
XX
WPI; 2004-710265/69.
DR N-PSDB; ADSI9022.
XX
PT Treating, preventing or ameliorating symptoms associated with
PT immunological disorders of the nervous system, e.g. multiple sclerosis,
PT comprises administering agonists of an interleukin (IL)-21 or IL-21
PT receptor.
XX
PS Claim 4; SEQ ID NO 2; 83pp; English.
XX
CC This invention relates to a novel method for treating an immunological
CC disorder of the nervous system by modulating the human cytokine
CC interleukin-21 (IL-21) or the IL-21 receptor, also known as IL-21R or MU-
CC 1. Specifically, it refers to a method for ameliorating a symptom of
CC multiple sclerosis where the agonist is selected from an IL-21
CC polypeptide, an agonistic anti-IL21R antibody or an antigen-binding
CC fragment of an agonistic anti-IL21R antibody and can modulate a disorder
CC associated with IL-10 deficiency. The present invention describes a
CC pharmaceutical composition comprising an IL-21/IL-21R agonist cited above
CC and an antiinflammatory agent or protein that stimulates myelin basic
CC protein in order to affect an IL-10 deficiency or disorder associated
CC thereof. Accordingly, these compositions exhibit neuroprotective activity
CC and can be used for gene therapy purposes. This polypeptide sequence is
CC the human IL-21 protein sequence of the invention.
XX
SQ Sequence 131 AA;
Query Match 88.1%; Score 37; DB 8; Length 131;
Best Local Similarity 87.5%; Pred. No. 13;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
RESULT 8
ADM43670
ID ADM43670 standard; protein; 131 AA.
XX
AC ADM43670;
XX
DT 24-MAR-2005 (first entry)
XX
DE Human interleukin-21analogue 1.
XX
```

KM Interleukin-21; mutein; Antiallergic; Antiasthmatic; Antiparasitic;
KM Antinflammatory; Neuroprotective; Cytostatic; Antimicrobial; allergy;
KM Immune disorder; asthma; parasitic infection; inflammation;
KM multiple sclerosis; cancer; neoplasm; infection.
XX Homo sapiens,
OS Synthetic.

XX Key Location/Qualifiers

PH Misc-difference 1 /note= "Wild-type Gln substituted by Asn"
FT Misc-difference 10 /note= "Wild-type Gln substituted by Glu"
FT Misc-difference 14 /note= "Wild-type Ile substituted by Val"
FT Misc-difference 28 /note= "Wild-type Gln substituted by Glu"
FT Misc-difference 36 /note= "Wild-type Val substituted by Ile"
FT Misc-difference 46 /note= "Wild-type Ser substituted by Thr"
FT Misc-difference 57 /note= "Wild-type Asn substituted by Gln"
FT Misc-difference 66 /note= "Wild-type Asn substituted by Gln"
FT Misc-difference 78 /note= "Wild-type Ser substituted by Thr"
FT Misc-difference 85 /note= "Wild-type Gln substituted by Asn"
FT Misc-difference 96 /note= "Wild-type Ser substituted by Thr"
FT Misc-difference 105 /note= "Wild-type Phe substituted by Tyr"
FT Misc-difference 109 /note= "Wild-type Phe substituted by Tyr"
FT Misc-difference 117 /note= "Wild-type Ile substituted by Val"
FT Misc-difference 130..131 /note= "Wild-type Asp-Ser substituted by Glu-Thr"
FT Misc-difference 130..131 /note= "Wild-type Asp-Ser substituted by Glu-Thr"
XX
PN W02004112703-A2.
XX
XX 29-DEC-2004.
XX
XX 15-JUN-2004; 2004WO-US018903.
XX
XX 19-JUN-2003; 2003US-0479772P.
XX
XX (CENZ) CENTOCOR INC.
XX
XX Cunningham MR, Heavner GA, Luo J, Song XR;
PI WPI; 2005-048751/05.
XX
XX N-PSDB; ADW43677.

XX New polynucleotides encoding interleukin-21 analogs, useful for treating
PT allergic diseases as well as asthma, parasitic diseases, inflammatory
PT diseases (e.g. multiple sclerosis), cancer, or infectious diseases.

XX Claim 3; SEQ ID NO 2; 28pp; English.

XX The invention relates to an isolated polynucleotide encoding interleukin
CC -21 analogs. Also included are the interleukin-21 analog proteins, a
CC vector comprising the polynucleotide, an isolated host cell comprising
CC the vector and a process for producing a polypeptide comprising culturing
CC the host cell under conditions for production of the polypeptide. The
XX polynucleotides and polypeptides, composition and method are useful for
CC treating allergic diseases as well as asthma, parasitic diseases,
CC inflammatory diseases such as multiple sclerosis, cancer, or infectious
CC diseases. The present sequence represents an IL-21 analog of the
XX invention.

XX Sequence 131 AA;
SQ

Query Match 88.1%; Score 37; DB 9; Length 131;
Best Local Similarity 87.5%; Pred. No. 13;
Matches 7; Conservative 1; Mismatches 0; Gaps 0;

QY 1 HOYLSRT 8
||:||||
Db 118 HQHLSRT 125

RESULT 9
ADW43678
ID ADW43678 standard; protein; 131 AA.
XX

AC ADW43678;

DT 24-MAR-2005 (first entry)

XX Human interleukin-21analog 10A.

KM Interleukin-21; mutein; Antiallergic; Antiasthmatic; Antiparasitic;
KM Antinflammatory; Neuroprotective; Cytostatic; Antimicrobial; allergy;
KM Immune disorder; asthma; parasitic infection; inflammation;
XX multiple sclerosis; cancer; neoplasm; infection.

OS Homo sapiens.
XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1 /note= "Wild-type Gln substituted by Asn"
FT Misc-difference 10 /note= "Wild-type Gln substituted by Glu"
FT Misc-difference 14 /note= "Wild-type Ile substituted by Val"
FT Misc-difference 24 /note= "Wild-type Asp substituted by Glu"
FT Misc-difference 36 /note= "Wild-type Val substituted by Ile"
FT Misc-difference 46 /note= "Wild-type Ser substituted by Thr"
FT Misc-difference 54 /note= "Wild-type Lys substituted by Arg"
FT Misc-difference 66 /note= "Wild-type Asn substituted by Gln"
FT Misc-difference 78 /note= "Wild-type Ser substituted by Thr"
FT Misc-difference 85 /note= "Wild-type Gln substituted by Asn"
FT Misc-difference 96 /note= "Wild-type Ser substituted by Thr"
FT Misc-difference 109 /note= "Wild-type Phe substituted by Tyr"
FT Misc-difference 117 /note= "Wild-type Ile substituted by Val"
FT Misc-difference 130 /note= "Wild-type Asp substituted by Glu"
XX

PN W02004112703-A2.

XX 29-DEC-2004.

XX 15-JUN-2004; 2004WO-US018903.

XX 19-JUN-2003; 2003US-0479772P.

XX (CENZ) CENTOCOR INC.

PI Cunningham MR, Heavner GA, Luo J, Song XR;

XX WPI; 2005-048751/05.

XX N-PSDB; ADW43677.
XX

PT New polynucleotides encoding interleukin-21 analogs, useful for treating
 PT allergic diseases as well as asthma, parasitic diseases, inflammatory
 PT diseases (e.g. multiple sclerosis), cancer, or infectious diseases.
 XX
 PS Claim 3; SEQ ID NO 10; 28pp; English.
 XX
 CC The invention relates to an isolated polynucleotides encoding interleukin
 CC -21 analogs. Also included are the interleukin-21 analog proteins, a
 CC vector comprising the polynucleotide, an isolated host cell comprising
 CC the vector and a process for producing a polypeptide comprising culturing
 CC the host cell under conditions for production of the polypeptide. The
 CC polynucleotides and polypeptides, composition and method are useful for
 CC treating allergic diseases as well as asthma, parasitic diseases,
 CC inflammatory diseases such as multiple sclerosis, cancer, or infectious
 CC diseases. The present sequence represents an IL-21 analog of the
 CC invention.
 XX
 SQ Sequence 131 AA;
 XX
 Query Match 88.1%; Score 37; DB 9; Length 131;
 Best Local Similarity 87.5%; Pred. No. 13;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HOYLSRT 8
 DB 118 HOHLSRT 125
 RESULT 10
 ADM43674
 ID ADM43674 standard; protein; 131 AA.
 XX
 AC ADM43674;
 XX
 DT 24-MAR-2005 (first entry)
 XX
 DE Human interleukin-21analog 3.
 XX
 KW Interleukin-21; mutein; Antiallergic; Antiasthmatic; Antiparasitic;
 KW Antinflammatory; Neuroprotective; Cytostatic; Antimicrobial; allergy;
 KW immune disorder; asthma; parasitic infection; inflammation;
 KW multiple sclerosis; cancer; neoplasm; infection.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PH Key Location/Qualifiers
 FT Misc-difference 1 /note= "wild-type Gln substituted by Asn"
 FT Misc-difference 10 /note= "wild-type Gln substituted by Glu"
 FT Misc-difference 14 /note= "wild-type Ile substituted by Val"
 FT Misc-difference 28 /note= "wild-type Glu substituted by Gln"
 FT Misc-difference 36 /note= "wild-type Val substituted by Ile"
 FT Misc-difference 46 /note= "wild-type Ser substituted by Thr"
 FT Misc-difference 57 /note= "wild-type Asn substituted by Gln"
 FT Misc-difference 66 /note= "wild-type Asn substituted by Gln"
 FT Misc-difference 78 /note= "wild-type Ser substituted by Thr"
 FT Misc-difference 85 /note= "wild-type Gln substituted by Asn"
 FT Misc-difference 96 /note= "wild-type Ser substituted by Thr"
 FT Misc-difference 105 /note= "wild-type Phe substituted by Tyr"
 FT Misc-difference 117 /note= "wild-type Ile substituted by Val"

FT Misc-difference 130. 131
 FT /note= "wild-type Asp-Ser substituted by Glu-Thr"
 XX
 XX W02004112703-A2.
 XX
 PD 29-DEC-2004.
 XX
 PF 15-JUN-2004; 2004WO-US018903.
 XX
 PR 19-JUN-2003; 2003US-0479772P.
 XX
 PA (CENZ) CENTOCOR INC.
 XX
 PI Cunningham MR, Heavner GA, Luo J, Song XR;
 XX WPI; 2005-048751/05.
 DR N-PSDB; ADM43673.
 DR
 XX
 PT New polynucleotides encoding interleukin-21 analogs, useful for treating
 PT allergic diseases as well as asthma, parasitic diseases, inflammatory
 PT diseases (e.g. multiple sclerosis), cancer, or infectious diseases.
 XX
 PS Claim 3; SEQ ID NO 6; 28pp; English.
 XX
 CC The invention relates to an isolated polynucleotides encoding interleukin
 CC -21 analogs. Also included are the interleukin-21 analog proteins, a
 CC vector comprising the polynucleotide, an isolated host cell comprising
 CC the vector and a process for producing a polypeptide comprising culturing
 CC the host cell under conditions for production of the polypeptide. The
 CC polynucleotides and polypeptides, composition and method are useful for
 CC treating allergic diseases as well as asthma, parasitic diseases,
 CC inflammatory diseases such as multiple sclerosis, cancer, or infectious
 CC diseases. The present sequence represents an IL-21 analog of the
 CC invention.
 XX
 SQ Sequence 131 AA;
 XX
 Query Match 88.1%; Score 37; DB 9; Length 131;
 Best Local Similarity 87.5%; Pred. No. 13;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HOYLSRT 8
 DB 118 HOHLSRT 125
 RESULT 11
 ADM43676
 ID ADM43676 standard; protein; 131 AA.
 XX
 AC ADM43676;
 XX
 DT 24-MAR-2005 (first entry)
 XX
 DE Human interleukin-21analog 4.
 XX
 KW Interleukin-21; mutein; Antiallergic; Antiasthmatic; Antiparasitic;
 KW Antinflammatory; Neuroprotective; Cytostatic; Antimicrobial; allergy;
 KW immune disorder; asthma; parasitic infection; inflammation;
 KW multiple sclerosis; cancer; neoplasm; infection.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PH Key Location/Qualifiers
 FT Misc-difference 1 /note= "wild-type Gln substituted by Asn"
 FT Misc-difference 10 /note= "wild-type Gln substituted by Glu"
 FT Misc-difference 14 /note= "wild-type Ile substituted by Val"
 FT Misc-difference 22 /note= "wild-type Val substituted by Ile"

```
FT Misc-difference 28 /note= "Wild-type Gln substituted by Gln"
FT Misc-difference 36 /note= "Wild-type Val substituted by Ile"
FT Misc-difference 46 /note= "Wild-type Ser substituted by Thr"
FT Misc-difference 57 /note= "Wild-type Asn substituted by Gln"
FT Misc-difference 66 /note= "Wild-type Asn substituted by Gln"
FT Misc-difference 78 /note= "Wild-type Asn substituted by Gln"
FT Misc-difference 85 /note= "Wild-type Ser substituted by Thr"
FT Misc-difference 96 /note= "Wild-type Gln substituted by Asn"
FT Misc-difference 109 /note= "Wild-type Ser substituted by Thr"
FT Misc-difference 117 /note= "Wild-type Phe substituted by Tyr"
FT Misc-difference 130.131 /note= "Wild-type Ile substituted by Val"
FT Misc-difference 130.131 /note= "Wild-type Asp-Ser substituted by Gln-Thr"
PN WO2004112703-A2.
PD 29-DEC-2004.
PF 15-JUN-2004; 2004MO-US018903.
PR 19-JUN-2003; 2003US-0479772P.
XX (CENZ ) CENTOCOR INC.
XX Cunningham MR, Heavner GA, Luo J, Song XR;
XX WPI; 2005-048751/05.
DR N-PSDB; ADW43675.
XX New polynucleotides encoding interleukin-21 analogs, useful for treating
PT allergic diseases as well as asthma, parasitic diseases, inflammatory
PT diseases (e.g. multiple sclerosis), cancer, or infectious diseases.
XX
XX Claim 3; SEQ ID NO 8; 28bp; English.
PS
XX The invention relates to an isolated polynucleotides encoding interleukin
CC -21 analogs. Also included are the interleukin-21 analog proteins, a
CC vector comprising the polynucleotide, an isolated host cell comprising
CC the vector and a process for producing a polypeptide comprising culturing
CC the host cell under conditions for production of the polypeptide. The
CC polynucleotides and polypeptides, composition and method are useful for
CC treating allergic diseases as well as asthma, parasitic diseases,
CC inflammatory diseases such as multiple sclerosis, cancer, or infectious
CC diseases. The present sequence represents an IL-21 analog of the
CC invention.
XX
SQ Sequence 131 AA;
Query Match 88.1%; Score 37; DB 9; Length 131;
Best Local Similarity 87.5%; Pred. No. 13;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
XX Predicted mature human interleukin-21.
DE Interleukin-21; Antiallergic; Antiasthmatic; Antiparasitic;
XX Antiinflammatory; Neuroprotective; Cytostatic; Antimicrobial; allergy;
XX Immune disorder; asthma; parasitic infection; inflammation;
XX multiple sclerosis; cancer; neoplasm; infection.
XX Homo sapiens.
XX WO2004112703-A2.
PN
XX
XX 29-DEC-2004.
PD
XX
XX 15-JUN-2004; 2004MO-US018903.
XX
XX 19-JUN-2003; 2003US-0479772P.
XX
XX (CENZ ) CENTOCOR INC.
XX
XX Cunningham MR, Heavner GA, Luo J, Song XR;
XX WPI; 2005-048751/05.
DR
XX
XX New polynucleotides encoding interleukin-21 analogs, useful for treating
PT allergic diseases as well as asthma, parasitic diseases, inflammatory
PT diseases (e.g. multiple sclerosis), cancer, or infectious diseases.
XX
XX Disclosure; SEQ ID NO 16; 28bp; English.
PS
XX
XX The invention relates to an isolated polynucleotides encoding interleukin
CC -21 analogs. Also included are the interleukin-21 analog proteins, a
CC vector comprising the polynucleotide, an isolated host cell comprising
CC the vector and a process for producing a polypeptide comprising culturing
CC the host cell under conditions for production of the polypeptide. The
CC polynucleotides and polypeptides, composition and method are useful for
CC treating allergic diseases as well as asthma, parasitic diseases,
CC inflammatory diseases such as multiple sclerosis, cancer, or infectious
CC diseases. The present sequence represents the predicted mature human IL-
CC 21.
XX
XX Sequence 131 AA;
SQ
Query Match 88.1%; Score 37; DB 9; Length 131;
Best Local Similarity 87.5%; Pred. No. 13;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

1 HOYLSRT 8
118 HQHLSRT 125

RESULT 13
ADW43672 standard; protein; 131 AA.
ADW43672;
24-MAR-2005 (first entry)
Human interleukin-21analog 2.

Interleukin-21; mutein; Antiallergic; Antiasthmatic; Antiparasitic;
Antiinflammatory; Neuroprotective; Cytostatic; Antimicrobial; allergy;
Immune disorder; asthma; parasitic infection; inflammation;
multiple sclerosis; cancer; neoplasm; infection.
Homo sapiens.
Synthetic.
Key Location/Qualifiers
FT Misc-difference 1 /note= "Wild-type Gln substituted by Asn"

```

FT Misc-difference 14 /note= "Wild-type Ile substituted by Val"
FT Misc-difference 28 /note= "Wild-type Glu substituted by Gln"
FT Misc-difference 36 /note= "Wild-type Val substituted by Ile"
FT Misc-difference 46 /note= "Wild-type Ser substituted by Thr"
FT Misc-difference 57 /note= "Wild-type Asn substituted by Gln"
FT Misc-difference 66 /note= "Wild-type Asn substituted by Gln"
FT Misc-difference 78 /note= "Wild-type Ser substituted by Thr"
FT Misc-difference 85 /note= "Wild-type Gln substituted by Asn"
FT Misc-difference 96 /note= "Wild-type Ser substituted by Thr"
FT Misc-difference 105 /note= "Wild-type Phe substituted by Tyr"
FT Misc-difference 109 /note= "Wild-type Phe substituted by Tyr"
FT Misc-difference 117 /note= "Wild-type Ile substituted by Val"
FT Misc-difference 130. /note= "Wild-type Asp-Ser substituted by Glu-Thr"
FT Misc-difference 130. /note= "Wild-type Asp-Ser substituted by Glu-Thr"
XX
XX WO2004112703-A2.
XX
XX 29-DEC-2004.
XX
XX 15-JUN-2004; 2004WO-US018903.
XX
XX 19-JUN-2003; 2003US-0479772P.
XX
XX (CENZ ) CENTOCOR INC.
XX
XX Cunningham NR, Heavner GA, Luo J, Song XR;
XX
XX WPI; 2005-048751/05.
XX
XX N-PSDB; ADM43671.
XX
XX New polynucleotides encoding interleukin-21 analogs, useful for treating
XX allergic diseases as well as asthma, parasitic diseases, inflammatory
XX diseases (e.g. multiple sclerosis), cancer, or infectious diseases.
XX
XX Claim 3; SEQ ID NO 4; 28bp; English.
XX
XX The invention relates to an isolated polynucleotides encoding interleukin
XX -21 analogs. Also included are the interleukin-21 analog proteins, a
XX vector comprising the polynucleotide, an isolated host cell comprising
XX the vector and a process for producing a polypeptide comprising culturing
XX the host cell under conditions for production of the polypeptide. The
XX polynucleotides and polypeptides, composition and method are useful for
XX treating allergic diseases as well as asthma, parasitic diseases,
XX inflammatory diseases such as multiple sclerosis, cancer, or infectious
XX diseases. The present sequence represents an IL-21 analog of the
XX invention.
XX
XX Sequence 131 AA;
SQ
XX
Query Match 88.1%; Score 37; DB 9; Length 131;
Best Local Similarity 87.5%; Pred. No. 13;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 HOYLSRT 8
Db 118 HQHLSRT 125

```

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XX
XX ADM43687;
XX
XX 24-MAR-2005 (first entry)
XX
XX Mature human interleukin-21.
XX
XX Interleukin-21; Antiallergic; Antiasthmatic; Antiparasitic;
XX Antiinflammatory; Neutroprotective; Cytostatic; Antimicrobial; allergy;
XX immune disorder; asthma, parasitic infection; inflammation;
XX multiple sclerosis; cancer; neoplasm; infection.
XX
XX Homo sapiens.
XX
XX WO2004112703-A2.
XX
XX 29-DEC-2004.
XX
XX 15-JUN-2004; 2004WO-US018903.
XX
XX 19-JUN-2003; 2003US-0479772P.
XX
XX (CENZ ) CENTOCOR INC.
XX
XX Cunningham NR, Heavner GA, Luo J, Song XR;
XX
XX WPI; 2005-048751/05.
XX
XX N-PSDB; ADM43686.
XX
XX New polynucleotides encoding interleukin-21 analogs, useful for treating
XX allergic diseases as well as asthma, parasitic diseases, inflammatory
XX diseases (e.g. multiple sclerosis), cancer, or infectious diseases.
XX
XX Claim 4; SEQ ID NO 19; 28bp; English.
XX
XX The invention relates to an isolated polynucleotides encoding interleukin
XX -21 analogs. Also included are the interleukin-21 analog proteins, a
XX vector comprising the polynucleotide, an isolated host cell comprising
XX the vector and a process for producing a polypeptide comprising culturing
XX the host cell under conditions for production of the polypeptide. The
XX polynucleotides and polypeptides, composition and method are useful for
XX treating allergic diseases as well as asthma, parasitic diseases,
XX inflammatory diseases such as multiple sclerosis, cancer, or infectious
XX diseases. The present sequence represents the wild-type mature human IL-
XX 21.
XX
XX Sequence 133 AA;
SQ
XX
Query Match 88.1%; Score 37; DB 9; Length 133;
Best Local Similarity 87.5%; Pred. No. 13;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 HOYLSRT 8
Db 120 HQHLSRT 127

```

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RESULT 14
ADM43687
ID ADM43687 standard; protein; 133 AA.

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RESULT 15
ADM43682
ID ADM43682 standard; protein; 133 AA.
XX
XX ADM43682;
XX
XX 24-MAR-2005 (first entry)
XX
XX Human interleukin-21 analog 4A.
XX
XX Interleukin-21; muten; Antiallergic; Antiasthmatic; Antiparasitic;
XX Antiinflammatory; Neutroprotective; Cytostatic; Antimicrobial; allergy;
XX immune disorder; asthma, parasitic infection; inflammation;
XX multiple sclerosis; cancer; neoplasm; infection.
XX
XX Homo sapiens.

```

```
OS Synthetic.
XX Key Location/Qualifiers
FH Misc-difference 3 /note= "Wild-type Gln substituted by Asn"
FT Misc-difference 12 /note= "Wild-type Gln substituted by Glu"
FT Misc-difference 16 /note= "Wild-type Ile substituted by Val"
FT Misc-difference 30 /note= "Wild-type Glu substituted by Gln"
FT Misc-difference 38 /note= "Wild-type Val substituted by Ile"
FT Misc-difference 48 /note= "Wild-type Ser substituted by Thr"
FT Misc-difference 59 /note= "Wild-type Asn substituted by Gln"
FT Misc-difference 68 /note= "Wild-type Asn substituted by Gln"
FT Misc-difference 80 /note= "Wild-type Asn substituted by Gln"
FT Misc-difference 87 /note= "Wild-type Ser substituted by Thr"
FT Misc-difference 98 /note= "Wild-type Gln substituted by Asn"
FT Misc-difference 98 /note= "Wild-type Ser substituted by Thr"
FT Misc-difference 107 /note= "Wild-type Phe substituted by Tyr"
FT Misc-difference 111 /note= "Wild-type Phe substituted by Tyr"
FT Misc-difference 119 /note= "Wild-type Ile substituted by Tyr"
FT Misc-difference 132.133 /note= "Wild-type Ile substituted by Val"
FT Misc-difference 132.133 /note= "Wild-type Asp-Ser substituted by Glu-Thr"
XX
XX W02004112703-A2.
XX
XX 29-DEC-2004.
XX
XX 15-JUN-2004; 2004WO-US018903.
XX
XX 19-JUN-2003; 2003US-0479772P.
XX
XX (CENZ ) CENTOCOR INC.
XX
XX Cunningham MR, Heavner GA, Luo J, Song XR;
XX WPI; 2005-048751/05.
XX N-PSDB; ADW43681.
XX
XX New polynucleotides encoding interleukin-21 analogs, useful for treating
XX allergic diseases as well as asthma, parasitic diseases, inflammatory
XX diseases (e.g. multiple sclerosis), cancer, or infectious diseases.
XX
XX Claim 3; SEQ ID NO 14; 28pp; English.
XX
XX The invention relates to an isolated polynucleotides encoding interleukin
XX -21 analogs. Also included are the interleukin-21 analog proteins, a
XX vector comprising the polynucleotide, an isolated host cell comprising
XX the vector and a process for producing a polypeptide comprising culturing
XX the host cell under conditions for production of the polypeptide. The
XX polynucleotides and polypeptides, composition and method are useful for
XX treating allergic diseases as well as asthma, parasitic diseases,
XX inflammatory diseases such as multiple sclerosis, cancer, or infectious
XX diseases. The present sequence represents an IL-21 analog of the
XX invention.
XX
XX Sequence 133 AA;
XX
XX Query Match 88.1%; Score 37; DB 9; Length 133;
XX Best Local Similarity 87.5%; Pred. No. 13;
XX Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 HOYLSRT 8
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DB 120 HOYLSRT 127
|||||
RESULT 16
ADW43680
ID ADW43680 standard; protein; 133 AA.
XX
XX AC ADW43680;
XX
XX 24-MAR-2005 (first entry)
XX
XX Human interleukin-21analog 10B.
XX
XX Interleukin-21; mutein; Antiallergic; Antihistaminic; Antiparasitic;
XX Antiinflammatory; Neutroprotective; Cytostatic; Antimicrobial; allergy;
XX Immune disorder; asthma; parasitic infection; inflammation;
XX multiple sclerosis; cancer; neoplasm; infection.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Misc-difference 3 /note= "Wild-type Gln substituted by Asn"
FT Misc-difference 12 /note= "Wild-type Gln substituted by Glu"
FT Misc-difference 16 /note= "Wild-type Ile substituted by Val"
FT Misc-difference 26 /note= "Wild-type Asp substituted by Glu"
FT Misc-difference 38 /note= "Wild-type Val substituted by Ile"
FT Misc-difference 48 /note= "Wild-type Ser substituted by Thr"
FT Misc-difference 56 /note= "Wild-type Lys substituted by Arg"
FT Misc-difference 68 /note= "Wild-type Asn substituted by Gln"
FT Misc-difference 80 /note= "Wild-type Ser substituted by Thr"
FT Misc-difference 87 /note= "Wild-type Gln substituted by Asn"
FT Misc-difference 98 /note= "Wild-type Ser substituted by Thr"
FT Misc-difference 111 /note= "Wild-type Phe substituted by Tyr"
FT Misc-difference 119 /note= "Wild-type Ile substituted by Val"
FT Misc-difference 132 /note= "Wild-type Asp substituted by Glu"
XX
XX W02004112703-A2.
XX
XX 29-DEC-2004.
XX
XX 15-JUN-2004; 2004WO-US018903.
XX
XX 19-JUN-2003; 2003US-0479772P.
XX
XX (CENZ ) CENTOCOR INC.
XX
XX Cunningham MR, Heavner GA, Luo J, Song XR;
XX WPI; 2005-048751/05.
XX N-PSDB; ADW43679.
XX
XX New polynucleotides encoding interleukin-21 analogs, useful for treating
XX allergic diseases as well as asthma, parasitic diseases, inflammatory
XX diseases (e.g. multiple sclerosis), cancer, or infectious diseases.
XX
XX Claim 3; SEQ ID NO 12; 28pp; English.
XX
```

CC The invention relates to an isolated polynucleotides encoding interleukin
CC -21 analogs. Also included are the interleukin-21 analog proteins, a
CC vector comprising the polynucleotide, an isolated host cell comprising
CC the vector and a process for producing a polypeptide comprising culturing
CC the host cell under conditions for production of the polypeptide. The
CC polynucleotides and polypeptides, composition and method are useful for
CC treating allergic diseases as well as asthma, parasitic diseases,
CC inflammatory diseases such as multiple sclerosis, cancer, or infectious
CC diseases. The present sequence represents an IL-21 analog of the
CC invention.
XX
SQ Sequence 133 AA;
QY
Query Match 88.1%; Score 37; DB 9; Length 133;
Best Local Similarity 87.5%; Pred. No. 13;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db 120 HOHLSSRT 127
1 HOYLSRT 8
||:|||||
ADP70485
ID ADP70485 standard; protein; 134 AA.
XX
AC ADP70485;
XX
DT 23-SEP-2004 (first entry)
XX
DE Codon optimised interleukin 21 (IL-21) protein SEQ ID NO:28.
XX
KM interleukin 21; IL-21; human; codon optimised.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO2004055168-A2.
XX
PD 01-JUL-2004.
XX
PF 12-DEC-2003; 2003WO-US039764.
XX
PR 13-DEC-2002; 2002US-0433448P.
PR 13-DEC-2002; 2002US-0433452P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Chang C, Zamost BL, Covert DC, Liu HY, De Jongh KS, Meyer JD;
PI Holderman SD;
XX
DR WPI: 2004-500211/47.
DR N-PSDB; ADP70484.
XX
PT New expression vectors for the large-scale production of IL-21 proteins
PT comprises a prokaryotic origin of replication, a transcriptional
PT initiation DNA element, a polynucleotide sequence and a transcriptional
PT terminator.
XX
XX Claim 13; SEQ ID NO 28; 90pp; English.
XX
CC The present invention describes an expression vector for producing
CC interleukin 21 (IL-21) protein. The expression vector comprises the
CC following operably linked elements: (a) a prokaryotic origin of
CC replication; (b) a transcriptional initiation DNA element; (c) an IL-21
CC polynucleotide sequence having the 405 base pair sequence given in SEQ ID
CC NO:27 (ADP70484); and (d) a transcriptional terminator. Also described:
CC (1) a prokaryotic host cell transformed with the expression vector
CC described above; (2) producing IL-21 proteins; (3) isolating insoluble IL-
CC -21 protein; and (4) a composition comprising an IL-21 protein comprising
CC amino acids residues of the 134 amino acid sequence given in SEQ ID NO:28
CC (ADP70485) at a concentration of about 10 mg/ml IL-21 protein in 10 mM
CC histidine, and 4.7 % mannitol at pH 5.3. The composition and methods are

CC useful for the large-scale production of IL-21 in prokaryotic hosts. The
CC present sequence represents a human IL-21 protein which has been codon
CC optimised for prokaryotic expression, which is used in an example from
CC the present invention.
XX
SQ Sequence 134 AA;
QY
Query Match 88.1%; Score 37; DB 8; Length 134;
Best Local Similarity 87.5%; Pred. No. 14;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db 121 HOHLSSRT 128
1 HOYLSRT 8
||:|||||
AEA52828
ID AEA52828 standard; protein; 160 AA.
XX
AC AEA52828;
XX
DT 11-AUG-2005 (first entry)
XX
DE Human interleukin-21 (IL-21) amino acid sequence - SEQ ID 1.
XX
KM cell differentiation; bone marrow transplantation; immune stimulation;
XX interleukin-21.
XX
OS Homo sapiens.
XX
PN WO2005052139-A2.
XX
PD 09-JUN-2005.
XX
PF 18-NOV-2004; 2004WO-US039135.
XX
PR 19-NOV-2003; 2003US-0523754P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Leonard WJ, Lipski P, Morse HC, Ettlinger CR, Spolski R;
XX
DR WPI: 2005-405375/41.
XX
PT Inducing B cell progenitor differentiation into memory B cell and a
PT plasma cell, useful for treating immunodeficiency, by contacting cell
PT population of B cell progenitor with an activator of e.g. Janus activated
PT kinase 1 (JAK1).
XX
PS Disclosure; SEQ ID NO 1; 75pp; English.
XX
XX The invention comprises a method of inducing differentiation of a B cell
XX progenitor into a memory B cell and/or a plasma cell. The method involves
XX contacting a population of cells which contain a B cell progenitor with
XX an agent that activates at least one of the following: Janus activated
XX kinase 1 (JAK1), JAK3, signal transducer and activator, transcription 5A
XX (STAT5A), or STAT5B. The method of the invention is useful for treating a
XX subject with a either a memory B cell or plasma cell deficiency, such as
XX treating a subject who has undergone a bone marrow transplant. The method
XX of the invention is useful for enhancing an immune response in a subject.
XX
XX The present amino acid sequence represents a human interleukin-21 (IL-
XX 21).
SQ Sequence 160 AA;
QY
Query Match 88.1%; Score 37; DB 9; Length 160;
Best Local Similarity 87.5%; Pred. No. 17;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db 149 HOHLSSRT 156
1 HOYLSRT 8
||:|||||

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RESULT 19
AAB18623
ID AAB18623 standard; protein; 162 AA.
XX
XX AAB18623;
AC
XX 22-JAN-2001 (first entry)
DT
XX A human zalphall ligand polypeptide.
DE
XX zalphall ligand; cytokine; haematopoietic cell proliferation; lymphoma;
KM tumourigenesis; leukaemia; hematopoiesis; B cell tumour.
XX
XX Homo sapiens.
OS
XX WO200053761-A2.
PN
XX 14-SEP-2000.
PD
XX 09-MAR-2000; 2000WO-US006067.
PF
XX 09-MAR-1999; 99US-00264908.
PR 11-MAR-1999; 99US-00265992.
PR 01-JUL-1999; 99US-0142013P.
XX
XX (ZYMO) ZYMOGENETICS INC.
PA
XX Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;
PI Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
XX
XX WPI: 2000-565600/52.
DR N-PSDB; AAA75552.
XX
XX New human cytokine, designated zalphall ligand, useful for stimulating
PT the proliferation and/or development of hematopoietic cells in vitro and
PT in vivo, and for treating tumorigenesis.
XX
XX Disclosure; Page 205-206; 256pp; English.
PS
XX
XX The present sequence represents a human zalphall ligand polypeptide,
CC which is a cytokine. The zalphall ligand is useful for stimulating the
CC proliferation and development of haematopoietic cells in vitro and in
CC vivo. Zalphall ligand polynucleotides can be used as primers or probes
CC for cloning the zalphall gene. The zalphall ligand is useful for treating
CC tumourigenesis. A zalphall ligand-saporin fusion toxin may be used for
CC treating leukaemias and lymphomas. Antagonists against zalphall ligand
CC are useful as research reagents for characterizing ligand-receptor
CC interaction. Antagonists are also useful for inhibiting expansion,
CC proliferation, activation and differentiation of cells involved in
CC regulating hematopoiesis. The zalphall ligand may also be used to
CC stimulate an immune response against B cell tumour, a virus, a parasite
CC or a bacterium. The zalphall polypeptides, polynucleotides, antagonists,
CC agonists and antibodies are also useful for the detection, diagnosis,
CC prevention, and treatment of diseases associated with a zalphall ligand
CC genetic defect
XX
XX Sequence 162 AA;
SQ
XX
XX Query Match 88.1%; Score 37; DB 3; Length 162;
XX Best Local Similarity 87.5%; Pred. No. 17;
XX Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 HOYLSSRT 8
XX ||:|||||
Db 149 HQHLSRT 156

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```

AC AAE13729;
XX
XX 26-FEB-2002 (first entry)
DT
XX
XX Human soluble Zalphall cytokine receptor ligand protein.
DE
XX
XX Human; Zalphall; cytokine receptor; immunosuppressive; cytostatic;
KM inflammatory disorder; haemostatic; cell proliferation; immune disorder;
KM autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;
KM myasthenia gravis; systemic lupus erythematosus (SLE); diabetes; asthma;
KM ulcerative colitis; inflammatory bowel disease; Crohn's disease; sepsis;
XX viral infection.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 1..31
FT Peptide /label= Signal_peptide
FT 32..162
FT Protein /label= Mature_zalphall_ligand
FT 41..56
FT Region /label= Helix_A
FT 69..84
FT Region /label= Helix_B
FT 92..105
FT Region /label= Helix_C
FT 135..148
FT Region /label= Helix_D
FT 136..138
FT Region /note="Conserved region"
XX
XX WO200177171-A2.
PN
XX
XX 18-OCT-2001.
PD
XX
XX 03-APR-2001; 2001WO-US010872.
PF
XX 05-APR-2000; 2000US-0194731P.
PR 28-JUL-2000; 2000US-0222121P.
XX
XX (ZYMO) ZYMOGENETICS INC.
PA
XX Sprecher CA, Novak JE, West JW, Presnell SR, Holly RD, Nelson AJ;
PI WPI: 2002-025898/03.
XX N-PSDB; AAD22923.
DR
XX Novel soluble receptor polypeptides and polynucleotides used as cytokine
PT antagonist for stimulating ligand activity-induced proliferation of
PT hematopoietic cells and for suppressing immune response in a mammal.
XX
XX Claim 1; Page 181; 243pp; English.
PS
XX
XX The invention relates to an isolated soluble zalphall cytokine receptor
XX polypeptide and their cDNA molecules. Zalpha proteins are useful for
XX inhibiting or antagonising the ligand activity-induced proliferation of
XX haematopoietic cells and haematopoietic cell progenitors preferably
XX lymphoid cells which are natural killer cells or cytotoxic T cells.
XX Zalpha is useful for treating immune and inflammatory disorders, for
XX reducing proliferation of neoplastic B or T cells, for suppressing an
XX immune response in a mammal exposed to an antigen or pathogen. Zalpha is
XX useful for treating diseases that require immune regulation including
XX autoimmune diseases such as rheumatoid arthritis, multiple sclerosis,
XX myasthenia gravis, systemic lupus erythematosus (SLE) and diabetes;
XX asthma, ulcerative colitis, inflammatory bowel disease, Crohn's disease,
XX sepsis, viral infection (dengue virus infection) and cancer. The present
XX sequence is human soluble Zalphall cytokine receptor ligand
SQ
XX
XX Query Match 88.1%; Score 37; DB 5; Length 162;
XX Best Local Similarity 87.5%; Pred. No. 17;
XX Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```


QY 1 HOYLSRT 8
DB 149 HQHLSRT 156

RESULT 21
AAU11965
ID AAU11965 standard; protein, 162 AA.
XX
AC AAU11965;
XX
DT 09-APR-2002 (first entry)
XX
DE Human zalphall ligand polypeptide.
XX
KW Cytokine; zalphall ligand; zalphall receptor; NK cell progenitor;
KW natural killer cell proliferation; T-cell proliferation;
KW B-cell proliferation; anti-tumour response; immune system;
KW immunostimulant; cytoskeletal; human; hPBCS;
KW activated human peripheral blood cell.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1. .31
FT /label= Signal_peptide
FT Protein 32. .162
FT /label= Mature_zalphall_ligand
XX
XX US6307024-B1.
XX
PD 23-OCT-2001.
XX
PF 09-MAR-2000; 2000US-00522217.
XX
XX 09-MAR-1999; 99US-0123547P.
XX 11-MAR-1999; 99US-0123904P.
PR 01-JUL-1999; 99US-0142013P.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
PI Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD,
PI Grose JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK,
XX
XX WPI; 2002-040208/05.
XX N-PSDB; AAS20637.
XX
XX New zalphall ligand polypeptides and polynucleotides, useful for
PT stimulating proliferation, activation, differentiation and/or induction
PT of inhibition of specialized cell function, or for stimulating an
PT antigenic response.
XX
XX Claim 7; Col 125-126; 105pp; English.
XX
XX The present invention relates to the isolation of a novel cytokine,
CC zalphall ligand and the polynucleotide encoding it. The invention also
CC gives the sequence for the zalphall receptor and the polynucleotide
CC encoding it. The zalphall ligand polypeptide stimulates proliferation of
CC natural killer (NK) cells or NK cell progenitors, the activation of NK
CC cells, proliferation of T-cells, proliferation of B-cells stimulated with
CC anti-CD40 antibodies, stimulates an antigenic response in a mammal, and
CC reduces proliferation of B-cells stimulated with anti-IGM antibodies. The
CC zalphall ligand polypeptide is also useful in preparing antibodies that
CC bind to zalphall ligand epitopes. The zalphall ligand polynucleotides can
CC be used as probes or primers to clone regions of a zalphall ligand gene,
CC and in gene therapy. Zalphall ligand may also be used to identify
CC inhibitors of its activity, to enhance the generation of anti-tumour
CC responses with or without the infusion of donor lymphocytes, and to
CC activate or stimulate the immune system. The present sequence represents
CC human zalphall ligand polypeptide. The cDNA encoding this is isolated
CC from a cDNA library from activated human peripheral blood cells (hPBCS)
XX

SQ Sequence 162 AA;
Query Match 88.1%; Score 37; DB 5; Length 162;
Best Local Similarity 87.5%; Pred. No. 17;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
DB 149 HQHLSRT 156

RESULT 22
ABR61407
ID ABR61407 standard; protein, 162 AA.
XX
AC ABR61407;
XX
DT 12-AUG-2003 (first entry)
XX
DE Human IL-21 SEQ ID NO.19.
XX
KW arthritic disorder; interleukin-21; IL-21; IL-21 receptor; IL-21R;
KW immune cell activity; cancer; infectious disorder; antirheumatic;
KW antiarthritic; osteopathic; antipsoriatic; cytoskeletal; antibacterial;
KW virucide; antiparasitic; immunosuppressive; antidiabetic; dermatological;
KW neuroprotective; analgesic; antiallergic; antinausea; hepatotropic;
KW antihypertensive; antidiabetic; immune response; immune disorder;
KW autoimmune disease; human.
XX
XX Homo sapiens.
XX
XX WO2003028630-A2.
XX
XX 10-APR-2003.
XX
XX 04-OCT-2002; 2002WO-US029839.
XX
XX 04-OCT-2001; 2001US-00972218.
PR 17-APR-2002; 2002US-0373746P.
XX
XX (AMHP) WYETH.
XX
XX Carter U, Whitters MJ, Collins M, Young DA, Larsen G,
PI Donaldson DD, Lowe LD, Dunnett K, Ma M, Wittek US, Kasarian MR,
PI Ungar M;
XX
XX WPI; 2003-430146/40.
XX N-PSDB; ACC80873.
XX
XX Treating or preventing arthritic disorder, cancer or infectious disorders
PT in a subject, involves administering a modulator of interleukin-21 or its
PT receptor which modulate immune cell activity.
XX
XX Disclosure; Page 37; 176pp; English.
XX
XX The invention relates to a novel method for treating or preventing an
CC arthritic disorder in a subject. The method involves administering to the
CC subject an interleukin-21 (IL-21)/IL-21 receptor (IL-21R) antagonist
CC optionally in combination with another therapeutic agent, to inhibit or
CC reduce immune cell activity in the subject. The method is also useful for
CC treating or preventing cancer or an infectious disorder, in a subject, by
CC administering IL-21/IL-21R agonist, to increase immune cell activity. The
CC method of the invention has antirheumatic, antiarthritic, osteopathic,
CC antipsoriatic, cytoskeletal, antibacterial, virucide, antiparasitic,
CC immunosuppressive, antidiabetic, neuroprotective, dermatological,
CC antitumor, antinausea, antiallergic, antinausea, hepatotropic,
CC antihypertensive, and antidiabetic activity. The method is useful for
CC treating or preventing an arthritic disorder such as rheumatoid
CC arthritis, juvenile rheumatoid arthritis, osteoarthritis, psoriatic
CC arthritis or ankylosing spondylitis, and also cancer such as solid
CC tumor, soft tissue tumor or metastatic lesion, or an infectious
CC disorder such as bacterial, viral or parasitic infection in a mammal,
CC preferably human. A method of the invention is also useful for

increasing the ability of a vaccine composition containing an antigen to elicit a protective immune response in a subject against the antigen. The antigen is from a pathogen such as virus, bacterium or protozoan, or from cancer or tumor cell antigen, or expressed on the surface of cancer cell. An alternative method of the invention is useful for modulating the activity of immune or haematopoietic cells and thus to treat or prevent a variety of immune disorders, such as autoimmune diseases, for example diabetes mellitus, multiple sclerosis, myasthenia gravis, systemic lupus erythematosus, dermatitis, ulcer, asthma, allergic asthma, anaemia, hepatitis, Graves's disease, graft versus host disease, and scleroderma. The present sequence is used in an exemplification of the invention

Sequence 162 AA:

Query Match 88.1%; Score 37; DB 6; Length 162;
Best Local Similarity 87.5%; Pred. No. 17;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 HOYLSRT 8
149 HQHLSRT 156

Db

RESULT 23
AAE14934
ID AAE14934 standard; protein; 162 AA.
XX
AC AAE14934;
XX
DT 27-AUG-2003 (first entry)
XX
DE Human interleukin-21 (IL-21) antagonist #2.
XX
KW Interleukin-21; IL-21; antagonist; cancer; inflammatory;
KW autoimmune disorder; rheumatoid arthritis; multiple sclerosis;
KW systemic lupus erythematosus; myasthenia gravis; diabetes; human;
KW zalphall ligand; mutant; mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 145
FT /note= "Wild-type Gln substituted with Asp"
FT Misc-difference 148
FT /note= "Wild-type Ile substituted with Asp"
XX
PN WO2003040313-A2.
XX
PD 15-MAY-2003.
XX
PF 28-OCT-2002; 2002WO-US034502.
XX
PR 05-NOV-2001; 2001US-0337586P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Presnell SR, West JW, Novak JE;
XX
DR WPI; 2003-441547/41.
DR N-PSDB; AAD47854.
XX
XX New IL-21 polypeptide and encoding polynucleotide, useful for diagnosing
PT and treating disorders with aberrant expression or activity of the IL-21
PT polypeptide, such as cancer, rheumatoid arthritis, multiple sclerosis and
PT diabetes.
XX
PS Claim 3; Page 58; 71pp; English.
XX
CC The invention relates to polynucleotides and polypeptides of interleukin-
CC 21 (IL-21) antagonists, that bind with specificity and exhibit an EC50
CC that is not detectable in receptor binding studies. The antagonists of
CC the invention have mutations in the D helix of the IL-21 molecule, and

can be used to inhibit the activity of IL-21 with its cognate receptor. The IL-21 antagonists are useful for diagnosing and treating disorders CC involving the aberrant expression or activity of the IL-21 polypeptide, CC such as cancer, inflammatory and autoimmune disorders, including CC rheumatoid arthritis, multiple sclerosis, systemic lupus erythematosus, CC myasthenia gravis and diabetes. The polypeptides can also be used to CC prepare antibodies that bind IL-21 epitopes, peptides or polypeptides, CC and for enhancing in vivo killing of target tissues. The present sequence CC is human IL-21 antagonist. The antagonist molecule is a mutant of IL-21 CC polypeptide, with Gln145Asp and Ile148Asp substitutions. The resulting CC mutant was designated zalphall ligand Q135D/I156D

Sequence 162 AA:

Query Match 88.1%; Score 37; DB 7; Length 162;
Best Local Similarity 87.5%; Pred. No. 17;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 HOYLSRT 8
149 HQHLSRT 156

Db

RESULT 24
AAE14932
ID AAE14932 standard; protein; 162 AA.
XX
AC AAE14932;
XX
DT 27-AUG-2003 (first entry)
XX
DE Human interleukin-21 (IL-21) .
XX
KW Interleukin-21; IL-21; antagonist; cancer; inflammatory;
KW autoimmune disorder; rheumatoid arthritis; multiple sclerosis;
KW systemic lupus erythematosus; myasthenia gravis; diabetes; human;
KW zalphall ligand.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 41..56
FT /label= Helix_A
FT Binding-site 44
FT /note= "Important for IL-21 binding to its receptor"
FT Binding-site 47
FT /note= "Important for IL-21 binding to its receptor"
FT Region 57..68
FT /label= A/B_loop
FT Region 69..84
FT /label= Helix_B
FT Region 85..91
FT /label= B/C_loop
FT Region 92..105
FT /label= Helix_C
FT Region 106..134
FT /label= C/D_loop
FT Region 135..148
FT /label= Helix_D
FT Binding-site 135
FT /note= "Important for IL-21 binding to its receptor"
XX
PN WO2003040313-A2.
XX
PD 15-MAY-2003.
XX
PF 28-OCT-2002; 2002WO-US034502.
XX
PR 05-NOV-2001; 2001US-0337586P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Presnell SR, West JW, Novak JE;

```

XX MPI: 2003-441547/41.
DR N-PSDB; RMD47852.
XX
XX New IL-21 polypeptide and encoding polynucleotide, useful for diagnosing
PT and treating disorders with aberrant expression or activity of the IL-21
PT polypeptide, such as cancer, rheumatoid arthritis, multiple sclerosis and
XX diabetes.
XX
PS Disclosure; Page 53-54; 71pp; English.
XX
CC The invention relates to polynucleotides and polypeptides of interleukin-
CC 21 (IL-21) antagonists, that bind with specificity and exhibit an EC50
CC that is not detectable in receptor binding studies. The antagonists of
CC the invention have mutations in the D helix of the IL-21 molecule, and
CC can be used to inhibit the activity of IL-21 with its cognate receptor.
CC The IL-21 antagonists are useful for diagnosing and treating disorders
CC involving the aberrant expression or activity of the IL-21 polypeptide,
CC such as cancer, inflammatory and autoimmune disorders, including
CC rheumatoid arthritis, multiple sclerosis, systemic lupus erythematosus,
CC myasthenia gravis and diabetes. The polypeptides can also be used to
CC prepare antibodies that bind IL-21 epitopes, peptides or polypeptides,
CC and for enhancing in vivo killing of target tissues. The present sequence
CC is human IL-21 (originally designated zalpball 11gand)
XX
SQ Sequence 162 AA;
XX
Query Match 88.1%; Score 37; DB 7; Length 162;
Best Local Similarity 87.5%; Pred. No. 17;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0.
Qy 1 HOYLSST 8
||:|||||
Db 149 HQHLSST 156
XX
RESULT 25
ABU62893
ID ABU62893 standard; protein; 162 AA.
XX
XX ABU62893;
AC
XX
XX 15-SEP-2003 (first entry)
DT
XX
XX Human interleukin 21 (IL-21).
DE
XX
XX Human; MU-1; haematopoietin receptor superfamily chain; immunomodulator;
KW cytosolic; antibacterial; virucide; antianemic; gene therapy;
KW haematopoiesis; anaemias; immune response; cancer; infection;
KW transplanted organ; cytokine; receptor; interleukin 21; IL21.
XX
XX Homo sapiens.
OS
XX
XX US2003049798-A1.
FN
XX
XX 13-MAR-2003.
PD
XX
XX 04-OCT-2001; 2001US-00972218.
PF
XX
XX 17-MAR-1998; 98US-00040005.
PR 28-APR-2000; 2000US-00560766.
PR 11-MAY-2000; 2000US-00569384.
XX
XX (CART/) CARTER L.
PA (WHIT/) WHITTERS M J.
PA (COLL/) COLLINS M.
PA (YOUN/) YOUNG D A.
PA (DONA/) DONALDSON D D.
PA (LOME/) LOWE L D.
XX (UNGE/) UNGER M.
XX
XX Carter L, Whitters MJ, Collins M, Young DA, Donaldson DD;
PI Lowe LD, Unger M;

```

[illegible]

CC 21). The invention provides antagonists of the IL-21 receptor. These
CC include mutants of murine IL-21 in which the Gln residue at position 119
CC of the mature polypeptide is substituted by Asp or in which the Gln
CC residues at positions 114 and 119 of the mature polypeptide are both
CC replaced by Asp. The mutant IL-21 polypeptides inhibit or suppress T-cell
CC activation. They preferably comprise a sequence that increases
CC circulating half-life, such as the Fc region of an IgG molecule and may
CC further comprise an antigenic tag. Such antagonists inhibit cellular
CC proliferation in response to either anti-CD3 monoclonal antibodies or
CC anti-CD3 antibodies applied together with IL-2 and/or IL-15 together with
CC IL-21. A claimed method of suppressing the immune response in a patient
CC comprises administering the IL-21 antagonist or a nucleic acid encoding
CC it. The method is used to treat an autoimmune disease such as rheumatic
CC disease, including systemic lupus erythematosus, Sjogren's syndrome,
CC scleroderma, mixed connective tissue disease, dermatomyositis,
CC polymyositis, Reiter's syndrome, or Behcet's disease, or rheumatoid
CC arthritis, type I diabetes, autoimmune disease of the thyroid such as
CC Hashimoto's thyroiditis or Graves' disease, an autoimmune disease of the
CC central nervous system such as multiple sclerosis, myasthenia gravis, or
CC encephalomyelitis, or an autoimmune disease selected from pemphigus
CC vulgaris, pemphigus vegetans, pemphigus foliaceus, Senear-Usher syndrome,
CC Brazilian pemphigus, psoriasis or inflammatory bowel disease (all
CC claimed).
CC
XX Sequence 162 AA;
SQ

Query Match 88.1%; Score 37; DB 7; Length 162;
Best Local Similarity 87.5%; Pred. No. 17;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HQYLSSRT 8
||:|||||
Db 149 HQHLSRT 156

RESULT 27

ADFI7046
ID ADFI7046 standard; protein; 162 AA.

AC ADFI7046;

DT 12-FEB-2004 (first entry)

DE Human albumin fusion protein-related protein SegID2177.

XX albumin fusion protein; albumin activity; human serum albumin;
KW serum osmotic pressure; shelf-life; stability; antidiabetic;
KW gene therapy/ diabetes mellitus; human; gene; ds.
XX

OS Homo sapiens.

PN WO2003060071-A2.

PD 24-JUL-2003.

PF 23-DEC-2002; 2002WO-US040891.

PR 21-DEC-2001; 2001US-0341811P.

PR 24-JAN-2002; 2002US-0350358P.

PR 28-JAN-2002; 2002US-0351360P.

PR 26-FEB-2002; 2002US-0359370P.

PR 28-FEB-2002; 2002US-0360000P.

PR 27-MAR-2002; 2002US-0367500P.

PR 08-APR-2002; 2002US-0370227P.

PR 10-MAY-2002; 2002US-0378950P.

PR 24-MAY-2002; 2002US-0382617P.

PR 28-MAY-2002; 2002US-0385123P.

PR 05-JUN-2002; 2002US-0385708P.

PR 10-JUL-2002; 2002US-0398008P.

PR 24-JUL-2002; 2002US-0402131P.

PR 09-AUG-2002; 2002US-0402708P.

PR 13-AUG-2002; 2002US-0411355P.

PR 18-SEP-2002; 2002US-0411355P.

PR 18-SEP-2002; 2002US-0411426P.
PR 02-OCT-2002; 2002US-0414984P.
PR 11-OCT-2002; 2002US-0417611P.
PR 23-OCT-2002; 2002US-0420246P.
PR 05-NOV-2002; 2002US-0423623P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (DELZ) DELTA BIOTECHNOLOGY LTD.
PA (PRIN-) PRINCIPIA PHARM CORP.
XX
PI Ballance DJ, Turner AJ, Rosen CA, Haseltine WA;
XX WPI; 2003-598517/56.
DR N-PSDB; ADFI7040.
XX

PT New albumin fusion protein, useful for preparing a composition for
PT treating diabetes mellitus.

Example 4; SEQ ID NO 2177; 24pp; English.

CC This invention relates to a novel albumin fusion protein having albumin
CC or biological activity. Human serum albumin is responsible for a
CC significant proportion of the osmotic pressure of serum and also
CC functions as a carrier of endogenous and exogenous ligands. The fusion of
CC albumin to a therapeutic protein may increase shelf-life and stability of
CC the therapeutic protein. The albumin fusion protein of the invention may
CC allow production of compositions with antidiabetic activity whilst the
CC nucleotide sequence which encodes it may be useful for gene therapy. The
CC albumin fusion protein is useful for preparing a composition for treating
CC diabetes mellitus. The present sequence is that of a therapeutic protein
CC which was fused with human albumin to create a novel albumin fusion
CC protein of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
CC format directly from WIPO at ftp.wipo.int/pub/publichepct_sequences
XX

SQ Sequence 162 AA;

Query Match 88.1%; Score 37; DB 7; Length 162;
Best Local Similarity 87.5%; Pred. No. 17;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HQYLSSRT 8
||:|||||
Db 149 HQHLSRT 156

RESULT 28

ADH44572
ID ADH44572 standard; protein; 162 AA.

AC ADH44572;

DT 25-MAR-2004 (first entry)

DE Human Zalphall1 ligand protein.

XX Human; Zalphall1 ligand; Zalphall1 receptor; immune response;
KW tumour progression; metastasis; tumour stasis; hematopoietic tumour;
KW lymphoma; B cell tumour; systemic lupus erythematosus;
KW rheumatoid arthritis; myasthenia gravis; diabetes; infectious disease;
KW immunocompromised patient; HIV infection; vaccine; chromosome 4q27.
XX

OS Homo sapiens.

PN US6605272-B2.

PD 12-AUG-2003.

FT Key

FT Peptide

FT Protein

FT US6605272-B2.

PD 12-AUG-2003.

Location/Qualifiers
1..31
/note="Signal peptide"
32..162
/note="Mature Zalphall1, claimed in claim 1"

XX 03-AUG-2001; 2001US-00923246.
 PF
 XX 09-MAR-1999; 99US-0123547P.
 PR 11-MAR-1999; 99US-0123904P.
 PR 01-JUL-1999; 99US-0142013P.
 PR 09-MAR-2000; 2000US-00522217.
 XX
 XX (ZYMO) ZYMOGENETICS INC.
 PI Novak JE, Preenell SR, Sprecher CA, Foster DC, Holly RD;
 PI Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
 XX
 DR WPI; 2003-895283/82.
 XX
 PT Stimulating an immune response in a mammal exposed to an antigen or
 PT pathogen, useful for enhancing anti-tumor activity resulting in reduced
 PT tumor progression or metastasis, comprises administering zalphall ligand
 PT polypeptide.
 PS Claim 1; SEQ ID NO 2; 103pp; English.
 XX
 CC The invention relates to stimulating an immune response in a mammal
 CC exposed to an antigen or pathogen comprising administering a composition
 CC comprising mature zalphall ligand polypeptide comprising residues 32-162
 CC of ADH44572 in a pharmaceutical vehicle. Also included are stimulating an
 CC immune response in a mammal exposed to an antigen or pathogen
 CC (comprising: (a) determining (in)directly the level of antigen or
 CC pathogen present in the mammal; (b) administering a composition
 CC comprising zalphall ligand polypeptide in a pharmaceutical vehicle; (c)
 CC determining (in)directly the level of antigen or pathogen in the mammal;
 CC and (d) comparing the antigen or pathogen level in (a) with (b), where a
 CC change in the level indicates stimulation of immune response), and
 CC stimulating an immune response in a mammal exposed to an antigen or
 CC pathogen (comprising: (a) determining a level of antigen- or pathogen-
 CC specific antibody; (b) administering a composition comprising zalphall
 CC ligand polypeptide in a pharmaceutical vehicle; (c) determining a post
 CC administration level of the antigen- or pathogen-specific antibody; and
 CC (d) comparing the level of the antibody in (a) with (b), where an
 CC increase in the antibody level indicates stimulation of immune response).
 CC The method is useful for stimulating an immune response in a mammal
 CC exposed to an antigen or pathogen, and for enhancing anti-tumor activity
 CC resulting in a reduction in tumor progression, decrease in metastasis,
 CC or tumor strasis. The tumor may be a haematopoietic tumour, a lymphoma
 CC or a B cell tumour. The zalphall ligand is useful for treating a wide
 CC range of diseases arising from defects in the immune system, e.g.
 CC systemic lupus erythematosus, rheumatoid arthritis, myasthenia gravis, or
 CC diabetes, for boosting immunity to infectious diseases, treating
 CC immunocompromised patients, such as HIV+ patients and in improving
 CC vaccines. The present sequence is a human zalphall ligand protein.
 XX
 SQ Sequence 162 AA;
 QY
 DB 1 HOYLSRT 8
 149 HQHLSRT 156
 RESULT 29
 ADI00908
 ID ADI00908 standard; protein; 162 AA.
 AC ADI00908;
 XX
 XX 22-APR-2004 (first entry)
 DE Immunity-related human zalphall ligand protein.
 XX zalphall ligand; immunity; infectious disease; immunocompromised patient;

KM HIV; vaccine; human.
 XX
 OS Homo sapiens.
 XX
 PN US2003125524-A1.
 XX
 PD 03-JUL-2003.
 XX
 PF 15-NOV-2002; 2002US-00295723.
 XX
 PR 09-MAR-2000; 2000US-00522217.
 XX
 XX (ZYMO) ZYMOGENETICS INC.
 PI Novak JE, Preenell SR, Sprecher CA, Foster DC, Holly RD;
 PI Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
 XX
 DR WPI; 2003-811003/76.
 DR N-PSDB; ADI00907.
 XX
 PT New zalphall ligand polypeptides, useful for boosting immunity to
 PT infectious diseases, and treating immunocompromised patients, such as
 PT human immunodeficiency virus (HIV) patients, or in improving vaccines.
 PS Claim 7; SEQ ID NO 2; 113pp; English.
 XX
 CC The invention relates to a novel isolated zalphall ligand polypeptide.
 CC The polypeptide of the invention may be useful for boosting immunity to
 CC infectious diseases and treating immunocompromised patients, such as HIV
 CC patients, as well as in improving vaccines. The current sequence is that
 CC of the human zalphall ligand protein of the invention.
 XX
 SQ Sequence 162 AA;
 QY
 DB 1 HOYLSRT 8
 149 HQHLSRT 156
 RESULT 30
 ADH10501
 ID ADH10501 standard; protein; 162 AA.
 AC ADH10501;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE Human interleukin-21 (IL-21) polypeptide.
 XX
 KM IL-21; interleukin-21; cytostatic; virucide; antiinflammatory;
 KM hepatotropic; neuroprotective; muscular; respiratory; antiarthritic;
 KM antibacterial; anti-HIV; gene therapy; cancer; human.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FH Peptide
 FT 32..162
 FT /note="specifically claimed fragment"
 FT 41..148
 FT /note="specifically claimed fragment"
 XX
 PN WO2003103589-A2.
 XX
 PD 18-DEC-2003.
 XX
 PF 06-JUN-2003; 2003WO-US017808.
 XX
 PR 07-JUN-2002; 2002US-0387127P.
 XX

PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Nelson AJ, Hughes SD, Holly RD, Kindsvogel WR;
 XX
 DR WPI; 2004-062206/06.
 XX N-PSDB; ADH10500.
 XX
 PT Treating Non-Hodgkin's lymphoma, cancer or infection comprises
 PT administering to the subject a polypeptide having a functional activity
 PT of interleukin-21.
 XX
 XX
 PS Claim 9; SEQ ID NO 2; 154pp; English.
 XX
 CC The invention relates to treating Non-Hodgkin's lymphoma, cancer or
 CC infection and involves administering to the subject a polypeptide having
 CC a functional activity of interleukin-21 (IL-21). The methods are useful
 CC for treating Non-Hodgkin's lymphoma, cancer such as renal cell carcinoma,
 CC epithelial carcinoma, breast cancer, prostate cancer, ovarian cancer and
 CC colon cancer; viral infection such as AIDS, Hepatitis B or C virus,
 CC gastroenteritis, haemorrhagic diseases, enteritis, carditis,
 CC encephalitis, paralysis, bronchitis, upper or lower respiratory
 CC disease, respiratory papillomatosis, arthritis, disseminated disease,
 CC meningitis, and mononucleosis; or bacterial infection, such as an
 CC infection by a bacteria selected from chlamydiae, listeriae, helicobacter
 CC pylori, mycobacterium, mycoplasma, salmonella, and shigella, or sudden
 CC acute respiratory syndrome caused by a coronavirus, Herpes Simplex
 CC virus, Epstein-Barr virus, Cytomegalovirus, Fox viruses, Papilloma
 CC virus, Adenovirus, Poliovirus, Orthomyxoviruses, Paramyxoviruses,
 CC Influenza viruses, caliciviruses, rabies viruses, and rinderpest viruses.
 CC The present sequence represents a human IL-21 polypeptide.
 XX
 SQ Sequence 162 AA;
 XX
 QY 1 HOYLSRT 8
 ||:|||||
 Db 149 HOHLSRT 156
 XX
 RESULT 31
 ADJ25621
 ID ADJ25621 standard; protein; 162 AA.
 XX
 AC ADJ25621;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Human interleukin 21 (IL-21) protein SEQ ID NO:2.
 XX
 KW interferon gamma inhibition; IFNgamma inhibition; interleukin 21 agonist;
 KW IL-21 agonist; antiasthmatic; antiallergic; antiarthritic; antineumatic;
 KW neuroprotective; antiinflammatory; dermatological; immunosuppressive;
 KW muscular; antiporiatic; T helper; Th1; Th2; asthma; allergy;
 KW rheumatoid arthritis; multiple sclerosis; lupus; diabetes;
 KW Crohn's disease; psoriasis; myasthenia gravis; human; IL-21.
 XX
 XX
 OS Homo sapiens.
 XX
 PN WO2004007682-A2.
 XX
 PD 22-JAN-2004.
 XX
 PF 15-JUL-2003; 2003WO-US021975.
 XX
 PR 15-JUL-2002; 2002US-039616P.
 PR 12-AUG-2002; 2002US-0403001P.
 XX
 PA (AMHP) WYETH.
 PA (HARD) HARVARD COLLEGE.
 XX

PI Grusby M, Wurster A, Young DA, Collins M, Witters MJ;
 XX
 DR WPI; 2004-122921/12.
 XX N-PSDB; ADJ25620.
 XX
 PT Inhibiting interferon gamma (IFNgamma) levels and T helper cell
 PT development and function in a T cell or cell population using IL-21
 PT modulators, useful for the preventing and/or treating asthma, allergy,
 PT arthritis, lupus and diabetes.
 XX
 XX
 PS Claim 1; SEQ ID NO 2; 59pp; English.
 XX
 CC The present invention describes a method for inhibiting interferon gamma
 CC (IFNgamma) levels in a T cell population by contacting the T cell or cell
 CC population with an interleukin 21 (IL-21) agonist in an amount sufficient
 CC to inhibit IFNgamma in the T cell or cell population, wherein the agonist
 CC is an IL-21 polypeptide comprising an amino acid sequence at least 85%
 CC identical to the 162 amino acids (SEQ ID NO: 2, ADJ25621), and which is
 CC capable of binding to an IL-21R. An IL-21 agonist has antiasthmatic,
 CC antiallergic, antirheumatic, antineumatic, neuroprotective,
 CC antiinflammatory, dermatological, immunosuppressive, muscular and
 CC antiporiatic activities. The methods and compositions of the present
 CC invention are useful for the diagnosis, prevention and/or treatment of
 CC diseases or conditions associated with aberrant expression or activity of
 CC IL-21, T helper 1 (Th1) and/or Th2, such as asthma, allergy, rheumatoid
 CC arthritis, multiple sclerosis, lupus, diabetes, Crohn's disease,
 CC psoriasis and myasthenia gravis. The present sequence represents human IL
 CC -21, which is used in the exemplification of the present invention.
 XX
 SQ Sequence 162 AA;
 XX
 QY 1 HOYLSRT 8
 ||:|||||
 Db 149 HOHLSRT 156
 XX
 RESULT 32
 ADM41017
 ID ADM41017 standard; protein; 162 AA.
 XX
 AC ADM41017;
 XX
 DT 15-JUL-2004 (first entry)
 XX
 DE Human IL-21 amino acid sequence, seq id 2.
 XX
 KW Antiallergic; antiasthmatic; antipariatic; antiinflammatory;
 KW antineumatic; dermatological; immunomodulator; interleukin; IL-21;
 KW eosinophil; allergic; parasitic; asthma; allergic rhinitis;
 KW helminthic infection.
 XX
 OS Homo sapiens.
 XX
 FT Key Location/Qualifiers
 FT Region 30..162
 FT /note="region specifically referred to in claims"
 XX
 PN WO2004032953-A1.
 XX
 PD 22-APR-2004.
 XX
 PF 13-OCT-2003; 2003WO-DK000691.
 XX
 PR 11-OCT-2002; 2002DK-00001546.
 PR 16-OCT-2002; 2002DK-00001587.
 PR 17-OCT-2002; 2002US-0419225P.
 XX
 XX
 PA (NOVO) NOVO NORDISK AS.
 XX

PI Romer J, Moller NP, Skak K;
 XX WPI; 2004-340821/31.
 XX
 PT Use of interleukin-21 for the treatment of diseases or conditions where
 PT eosinophils are involved in a protective response in a subject, e.g.
 PT allergic conditions and/or parasitic diseases.
 XX
 PS Claim 6; SEQ ID NO 2; 32pp; English.
 CC
 CC The invention relates to an interleukin (IL)-21 that is used for the
 CC treatment of diseases or conditions where eosinophils are involved in a
 CC protective response in a subject, e.g. allergic conditions and/or
 CC parasitic diseases. Methods of the invention are useful for the treatment
 CC of diseases or conditions where eosinophils are involved in a protective
 CC response in a subject, such as allergic conditions (e.g. asthma, allergic
 CC rhinitis or allergic diseases of the skin) and/or parasitic diseases,
 CC especially helminthic infection. The current sequence represents the DNA
 CC sequence encoding IL-21. Note: This sequence is not encoded by that of
 CC ADM41016, which we are told in the specification is the IL-21 encoding
 CC nucleotide.
 CC
 SQ Sequence 162 AA;
 CC
 QY
 DB 1 HOYLSRT 8
 149 HOYLSRT 156
 RESULT 33
 ADP12563
 ID ADP12563 standard; protein; 162 AA.
 XX
 AC ADP12563;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Protein encoded by mRNA of the invention #173.
 XX
 XX transplacent rejection; immune system; rheumatoid arthritis; lupus;
 KM inflammatory bowel disease; multiple sclerosis; HIV; AIDS.
 XX
 OS Homo sapiens.
 PN WO2004042346-A2.
 XX
 PD 21-MAY-2004.
 XX
 PF 24-APR-2003; 2003WO-US012946.
 XX
 PR 24-APR-2002; 2002US-00131831.
 PR 20-DEC-2002; 2002US-00325899.
 XX
 PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
 XX
 PI Wohlgemuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M,
 PI Rosenbery S;
 XX
 DR WPI; 2004-400724/37.
 XX
 PT Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
 PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
 PT rejection, in an individual, comprises detecting the expression level of
 PT the genes.
 XX
 PS Claim 65; SEQ ID NO 2572; 1762pp; English.
 CC
 CC The present invention relates to diagnosing or monitoring transplant
 CC rejection, e.g. cardiac or kidney transplant rejection, in an individual

CC comprises detecting the expression level of one or more genes. The
 CC methods, system and kits are useful in diagnosing or monitoring
 CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
 CC islet, lung, bone marrow or stem cell transplant rejection.
 CC xenotransplant rejection or mechanical organ replacement rejection, in an
 CC individual. The method is also useful in assessing the immune status of
 CC an individual. The methods are also useful in diagnosing and monitoring
 CC diseases that involve the immune system, e.g. rheumatoid arthritis,
 CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
 CC viral, bacterial or fungal infection. The present sequence represents a
 CC protein that is encoded by the mRNA of the invention.
 CC
 SQ Sequence 162 AA;
 CC
 QY
 DB 1 HOYLSRT 8
 149 HOYLSRT 156
 RESULT 34
 ADP19731
 ID ADP19731 standard; protein; 162 AA.
 XX
 AC ADP19731;
 XX
 DT 26-AUG-2004 (first entry)
 XX
 DE Human zalphall ligand.
 XX
 XX Cytostatic; zalphall ligand; pharmaceutical; cancer; immune response;
 KM melanoma; tumour; solid tumour; haematopoietic tumour; lymphoma; human;
 KM chromosome 4.
 XX
 OS Homo sapiens.
 PN US2004110932-A1.
 XX
 PD 10-JUN-2004.
 XX
 PF 10-SEP-2003; 2003US-00659684.
 XX
 PR 09-MAR-1999; 99US-0123547P.
 PR 11-MAR-1999; 99US-0123804P.
 PR 01-JUL-1999; 99US-0142013P.
 PR 09-MAR-2000; 2000US-00522217.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Novak JE, Preenell SR, Sprecher CA, Foster DC, Holly RD,
 PI Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
 XX
 DR N-PSDB; ADP19730, ADP19732.
 XX
 PT New zalphall ligand polynucleotide and polypeptide molecules, useful for
 PT treating cancer, e.g. melanoma, solid tumor, hematopoietic tumor, or
 PT lymphoma.
 XX
 PS Claim 1; SEQ ID NO 2; 111pp; English.
 CC
 CC The invention describes an isolated polypeptide comprising a sequence of
 CC amino acid residues that is at least 90 or 95% identical to residues 41
 CC (Gln to 148 (Ile), or 32 (Gln) to 148 (Ile) of a sequence of 162 amino
 CC acids (SEQ ID NO:2, human zalphall ligand), fully defined in the
 CC specification. Also described are: a pharmaceutical composition
 CC comprising the polypeptide, and a vehicle; a method of treating cancer in
 CC a mammal; a method of stimulating an immune response in a mammal with
 CC melanoma; a method of stimulating an immune response in a mammal bearing
 CC a tumour; an isolated polynucleotide comprising a sequence of nucleotides

CC that encode amino acid residues cited above, where the polynucleotide
CC encodes a polypeptide that binds a receptor comprising 538 amino acids,
CC fully defined in the specification; a pharmaceutical composition
CC comprising the polynucleotide encoding, in a pharmaceutically acceptable
CC vehicle; an expression vector comprising the following operably linked
CC elements a control element; and a DNA segment comprising the
CC polynucleotide; and an isolated polynucleotide molecule comprising at
CC least 10 nucleotides of the polynucleotide sequence of 642 bp, fully
CC defined in the specification. The molecules, compositions and methods are
CC useful for treating cancer, e.g. melanoma, solid tumour, hematopoietic
CC tumour, or lymphoma. This is the amino acid sequence of novel human
CC cytokine zalphall ligand.

XX
XX
SQ Sequence 162 AA;

Query Match 88.1%; Score 37; DB 8; Length 162;
Best Local Similarity 87.5%; Pred. No. 17;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
||:|||||
Db 149 HQHLSRT 156

RESULT 35

ID ADP70459 standard; protein; 162 AA.

AC ADP70459;

DT 23-SEP-2004 (first entry)

DE Human interleukin 21 (IL-21) protein SEQ ID NO:2.

XX interleukin 21; IL-21; human.

KW Homo sapiens.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..29 /label= signal

FT Protein 30..161

XX /note= "interleukin 21 (IL-21)"

PN WO2004055168-A2.

XX 01-JUL-2004.

PD 12-DEC-2003; 2003WO-US039764.

XX 13-DEC-2002; 2002US-0433448P.

PR 13-DEC-2002; 2002US-0433452P.

XX (ZYMO) ZYMOGENETICS INC.

PA Chang C, Zamost BL, Covert DC, Liu HY, De Jongh KS, Meyer JD;

PI Holderman SD,

XX WPI, 2004-500211/47.

DR N-PSDB; ADP70458.

XX New expression vectors for the large-scale production of IL-21 proteins

PT comprises a prokaryotic origin of replication, a transcriptional

PT initiation DNA element, a polynucleotide sequence and a transcriptional

PT terminator.

XX Disclosure; SEQ ID NO 2; 90pp; English.

CC NO:27 (ADP70484); and (d) a transcriptional terminator. Also described:
CC (1) a prokaryotic host cell transformed with the expression vector
CC described above; (2) producing IL-21 proteins; (3) isolating insoluble IL
CC -21 protein; and (4) a composition comprising an IL-21 protein comprising
CC amino acids residues of the 134 amino acid sequence given in SEQ ID NO:28
CC (ADP70485) at a concentration of about 10 mg/ml IL-21 protein in 10 mM
CC histidine, and 4.7 % mannitol at pH 5.3. The composition and methods are
CC useful for the large-scale production of IL-21 in prokaryotic hosts. The
CC present sequence represents human IL-21, which is used in an example from
CC the present invention.

XX
XX
SQ Sequence 162 AA;

Query Match 88.1%; Score 37; DB 8; Length 162;
Best Local Similarity 87.5%; Pred. No. 17;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
||:|||||
Db 149 HQHLSRT 156

RESULT 36

ID ADS19031 standard; protein; 162 AA.

AC ADS19031;

DT 30-DEC-2004 (first entry)

DE Full length human interleukin-21 (IL-21) protein SegID 10.

XX immunological disorder; human; cytokine; interleukin-21; IL-21;

KW multiple sclerosis; IL-10 deficiency; neuroprotective; gene therapy.

OS Homo sapiens.

XX WO2004084835-A2.

XX 07-OCT-2004.

PD 22-MAR-2004; 2004WO-US008833.

PR 21-MAR-2003; 2003US-0456920P.

XX (AMHP) WYETH.

PA Collins M, Chin EY, Senices M, Young DA;

PI WPI, 2004-710265/69.

DR N-PSDB; ADS19022.

XX Treating, preventing or ameliorating symptoms associated with

PT immunological disorders of the nervous system, e.g. multiple sclerosis,

PT comprises administering agonists of an interleukin (IL)-21 or IL-21

PT receptor.

XX Disclosure; SEQ ID NO 10; 83pp; English.

XX This invention relates to a novel method for treating an immunological

CC disorder of the nervous system by modulating the human cytokine

CC interleukin-21 (IL-21) or the IL-21 receptor, also known as IL-21R or MU-

CC 1. Specifically, it refers to a method for ameliorating a symptom of

CC multiple sclerosis where the agonist is selected from an IL-21

CC polypeptide, an agonistic anti-IL21R antibody and an antigen-binding

CC fragment of an agonistic anti-IL21R antibody and can modulate a disorder

CC associated with IL-10 deficiency. The present invention describes a

CC pharmaceutical composition comprising an IL-21/IL-21R agonist cited above

CC and an antiinflammatory agent or protein that stimulates myelin basic

CC protein in order to affect an IL-10 deficiency or disorder associated

CC thereof. Accordingly, these compositions exhibit neuroprotective activity

CC and can be used for gene therapy purposes. This polypeptide sequence is

CC the full length human IL-21 protein sequence of the invention.


```

RESULT 39
ADY17792
ID ADY17792 standard; protein; 162 AA.
XX
XX ADY17792;
AC
XX
XX 05-MAY-2005 (first entry)
DT
XX
XX PRO polypeptide SEQ ID NO 3598.
DE
XX
XX Antiinflammatory; Immune disorder; Dermatological; Immunosuppressive;
XX Antithyroidic; Antiarthritic; Osteopathic; Hemostatic; Antianemic;
XX Antithyroidic; Antidiabetic; Nephrotropic; CNS-gen.; Hepatotropic;
XX Virocidic; Gastrointestinal-Gen.; Antipsoriatic; Antiasthmatic;
XX Allergic; diagnosis.
XX
XX Homo sapiens.
OS
XX
XX WO2005016962-A2.
PN
XX
XX 24-FEB-2005.
PD
XX
XX 11-AUG-2004; 2004WO-US026249.
PF
XX
XX 11-AUG-2003; 2003US-0493546P.
PR
XX
XX (GETH ) GENENTECH INC.
PA
XX
XX Abbas A, Clark H, Ouyang W, Williams MP, Wood WT, Wu TD;
PI
XX
XX WPI; 2005-182330/19.
DR
XX
XX New nucleic acid encoding PRO polypeptide, useful for diagnosing and
PT treating an immune related disorder, e.g. systemic lupus erythematosus,
PT rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.
XX
XX Claim 8; SEQ ID NO 3598; 158pp; English.
XX
XX The invention relates to an isolated nucleic acid encoding a PRO
XX polypeptide. The polypeptide, agonist or an antagonist, antibody,
XX composition, and method are useful for diagnosing and treating an immune
XX related disorder, e.g. systemic lupus erythematosus, rheumatoid
XX arthritis. The present sequence represents a PRO polypeptide.
XX
XX Sequence 162 AA:
SQ
XX
XX Query Match 88.1%; Score 37; DB 9; Length 162;
XX Best Local Similarity 87.5%; Pred. No. 17;
XX Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 HOYLSRT 8
OY ||:|||||
Db 149 HQHLSRT 156
XX
XX
XX RESULT 40
XX ADZ20501
ID ADZ20501 standard; protein; 162 AA.
XX
XX ADZ20501;
AC
XX
XX 16-JUN-2005 (first entry)
DT
XX
XX Human interleukin-21 (IL-21) protein.
DE
XX
XX immune inhibition; pharmaceutical; interleukin-21; IL-21;
XX autoimmune disease; multiple sclerosis; rheumatoid arthritis;
XX systemic lupus erythematosus; psoriasis; ankylosing spondylitis;
XX scleroderma; insulin dependent diabetes; psoriatic arthritis;
XX osteoarthritis; inflammatory bowel disease; atopic dermatitis; asthma;
XX immunosuppressive; neuroprotective; antirheumatic; antiarthritic;
XX antiinflammatory; dermatological; antipsoriatic; antidiabetic;
XX gastrointestinal-gen.; antiasthmatic.

```

```

XX OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..29
XX Protein /label= Signal_peptide
XX /label= Mature_IL-21_protein
XX /note= "Specifically claimed in Claims 1, 2, 7, and 8"
XX
XX Region 41..56
XX /note= "Helix A"
XX
XX Region 57..68
XX /note= "A/B Loop"
XX
XX Region 69..84
XX /note= "Helix B"
XX
XX Region 85..91
XX /note= "B/C Loop"
XX
XX Region 92..105
XX /note= "Helix C"
XX
XX Region 106..134
XX /note= "C/D Loop"
XX
XX Region 135..148
XX /note= "Helix D"
XX
XX WO2005030196-A2.
PN
XX
XX 07-APR-2005.
PD
XX
XX 27-SEP-2004; 2004WO-US031710.
PF
XX
XX 25-SEP-2003; 2003US-0505919P.
PR
XX
XX (ZYMO ) ZYMOGENETICS INC.
PA
XX
XX Sivakumar PV, Nelson AJ;
PI
XX
XX WPI; 2005-262904/27.
DR
XX
XX N-PSDB; ADZ20500.
DR
XX
XX Decreasing an autoimmune response in a mammal for treating e.g. multiple
PT sclerosis or rheumatoid arthritis, comprises administering a
PT pharmaceutical composition comprising an interleukin-21 polypeptide.
XX
XX Claim 1; SEQ ID NO 2; 59pp; English.
XX
XX The invention relates to a method of decreasing an autoimmune response in
XX a mammal. The method comprises administering a pharmaceutical composition
XX comprising an interleukin (IL)-21 polypeptide having amino acids 30-162
XX of SEQ ID NO: 2, in a pharmaceutically acceptable vehicle. Also described
XX is a method of treating a mammal with an autoimmune disease. The method
XX of the invention is useful in decreasing an autoimmune response in
XX a mammal. The autoimmune disease comprises multiple sclerosis, rheumatoid
XX arthritis, systemic lupus erythematosus, psoriasis, ankylosing
XX spondylitis, scleroderma, Type 1 diabetes, psoriatic arthritis,
XX osteoarthritis, inflammatory bowel disease, atopic dermatitis or asthma.
XX This sequence represents human interleukin-21 (IL-21).
XX
XX Sequence 162 AA:
SQ
XX
XX Query Match 88.1%; Score 37; DB 9; Length 162;
XX Best Local Similarity 87.5%; Pred. No. 17;
XX Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 HOYLSRT 8
OY ||:|||||
Db 149 HQHLSRT 156
XX
XX
XX RESULT 41
XX AEB26428
ID AEB26428 standard; protein; 162 AA.
XX
XX AEB26428;
AC

```

XX 06-OCT-2005 (first entry)
 DT Human interleukin-21 (IL-21) polypeptide.
 XX
 DE interleukin-21; IL-21; cytokine; T-lymphocyte; B-lymphocyte;
 KM autoimmune disease; immune disorder; rheumatoid arthritis;
 KM multiple sclerosis; insulin dependent diabetes; transplant rejection;
 KM neuroprotective; anticholesteric; antirheumatic; antidiabetic;
 KM immunosuppressive.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FT Region
 PT /note="Region specifically claimed in Claim 2"
 XX
 PN WO2005067956-A2.
 PD 28-JUL-2005.
 XX
 XX 13-JAN-2005; 2005WO-DK000015.
 PF 15-JAN-2004; 2004DK-00000043.
 PR (NOVO) NOVO NORDISK AS.
 PA
 PI Skak K;
 XX WPI; 2005-522743/53.
 DR N-PSDB; AEB26427.
 XX
 PT Use of interleukin-21, its analog, derivative, active fragment, mimetic
 PT or polynucleotide for management, treatment or prevention of
 PT diseases/conditions involving T or B cells e.g. rheumatoid arthritis.
 XX
 XX Claim 2; SEQ ID NO 2; 37pp; English.
 XX
 XX The invention relates to the use of interleukin-21 (IL-21) polypeptide
 CC (SEQ ID No:2), its analog, derivative or active fragment, IL-21 mimetic,
 CC or IL-21 polynucleotide for the management, treatment or prevention of
 CC diseases or conditions, where T or B cells are involved. Also described
 CC are: (1) a combination of IL-21, its analog, derivative or active
 CC fragment, IL-21 mimetic, or IL-21 polynucleotide, and one or more active
 CC substances involved in diseases or conditions where T or B cells are
 CC involved; (2) a method of managing, treating or preventing diseases or
 CC conditions where T or B cells are involved in a subject, by administering
 CC IL-21, its analog, derivative or active fragment, IL-21 mimetic, or IL-21
 CC polynucleotide; and (3) a pharmaceutical composition comprising a
 CC combination of IL-21, its analog, derivative or active fragment, IL-21
 CC mimetic, or IL-21 polynucleotide, and one or more active substances
 CC involved in diseases or conditions where T or B cells are involved,
 CC together with additives. The following are also disclosed: targeting IL-
 CC 21 to a dendritic cell by conjugating IL-21 to an antibody; culturing
 CC dendritic cells in vitro with IL-21 with or without other cytokines;
 CC growth factors and/or antigens to generate regulatory dendritic cells;
 CC isolated protein polypeptides that are substantially identical to IL-21;
 CC and a variety of other polypeptide fusions, IL-21 polypeptide, its
 CC analog, derivative or active fragment, IL-21 mimetic, or IL-21
 CC polynucleotide are useful for the manufacture of a medicament for the
 CC management, treatment or prevention of diseases or conditions, where T or
 CC B cells are involved, where the disease or conditions where T or B cells
 CC involved are autoimmune diseases or conditions such as rheumatoid
 CC arthritis, multiple sclerosis, type 1 diabetes, or allograft rejection.
 CC This sequence represents human IL-21.
 XX
 XX Sequence 162 AA;
 SQ

Query Match 88.1%; Score 37; DB 9; Length 162;
 Best Local Similarity 87.5%; Pred. No. 17;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HOYLSRT 8

Db 149 HOHLSRT 156
 ||:||||
 RESULT 42
 AAB18627
 ID AAB18627 standard; protein; 519 AA.
 XX
 AC AAB18627;
 XX
 DT 22-JAN-2001 (first entry)
 XX
 XX Amino acid sequence of MBP-human zalphall ligand fusion in pTAP126.
 DE zalphall ligand; cytokine; haematopoietic cell proliferation; lymphoma;
 KM tumourigenesis; leukaemia; hematopoiesis; B cell tumour.
 KM
 XX Synthetic.
 OS Homo sapiens.
 XX
 PN WO200053761-A2.
 PD 14-SEP-2000.
 XX
 XX 09-MAR-2000; 2000WO-US006067.
 PF 09-MAR-1999; 99US-00264908.
 PR 11-MAR-1999; 99US-00265992.
 PR 01-JUL-1999; 99US-0142013P.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;
 PI Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
 DR WPI; 2000-565600/52.
 DR N-PSDB; AAA75599.
 XX
 PT New human cytokine, designated zalphall ligand, useful for stimulating
 PT the proliferation and/or development of hematopoietic cells in vitro and
 PT in vivo, and for treating tumorigenesis.
 XX
 XX Example 31; Page 233-235; 256pp; English.
 XX
 XX The present sequence represents a MBP-human zalphall ligand fusion in the
 CC plasmid pTAP126. Zalphall ligand is a cytokine. The zalphall ligand is
 CC useful for stimulating the proliferation and development of
 CC hematopoietic cells in vitro and in vivo. Zalphall ligand
 CC polynucleotides can be used as primers or probes for cloning the zalphall
 CC gene. The zalphall ligand is useful for treating tumorigenesis. A
 CC zalphall ligand-saporin fusion toxin may be used for treating leukemias
 CC and lymphomas. Antagonists against zalphall ligand are useful as research
 CC reagents for characterizing ligand-receptor interaction. Antagonists are
 CC also useful for inhibiting expansion, proliferation, activation and
 CC differentiation of cells involved in regulating hematopoiesis. The
 CC zalphall ligand may also be used to stimulate an immune response against
 CC B cell tumour, a virus, a parasite or a bacterium. The zalphall
 CC polypeptides, polynucleotides, antagonists, agonists and antibodies are
 CC also useful for the detection, diagnosis, prevention, and treatment of
 CC diseases associated with a zalphall ligand genetic defect
 XX
 XX Sequence 519 AA;
 SQ

Query Match 88.1%; Score 37; DB 3; Length 519;
 Best Local Similarity 87.5%; Pred. No. 60;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HOYLSRT 8
 Db 506 HOHLSRT 513

RESULT 43

AAU11971
ID AAU11971 standard; protein; 519 AA.
XX
AC AAU11971;
XX
XX
DT 09-APR-2002 (first entry)
XX
DE MBP-human zalphall ligand fusion protein.
XX
XX Cytokine; zalphall ligand; zalphall receptor; NK cell progenitor;
KW natural killer cell proliferation; T-cell proliferation; mutant;
KW natural killer cell proliferation; anti-tumor response; immune system; MBP;
KW immunostimulant; cytostatic; human; maltose binding protein; mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US6307024-B1.
XX
PD 23-OCT-2001.
XX
PF 09-MAR-2000; 2000US-00522217.
XX
XX 09-MAR-1999; 99US-0123547P.
PR 11-MAR-1999; 99US-0123904P.
PR 01-JUL-1999; 99US-0142013P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;
PI Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
XX
DR WPI: 2002-040208/05.
DR N-PSDB; AAS20714.
XX
PT New zalphall ligand polypeptides and polynucleotides, useful for
PT stimulating proliferation, activation, differentiation and/or induction
PT of inhibition of specialized cell function, or for stimulating an
PT antigenic response.
XX
XX
PS Example 31; Col 161-166; 105pp; English.
XX
XX The present invention relates to the isolation of a novel cytokine,
CC zalphall ligand and the polynucleotide encoding it. The invention also
CC gives the sequence for the zalphall receptor and the polynucleotide
CC encoding it. The zalphall ligand polypeptide stimulates proliferation of
CC natural killer (NK) cells or NK cell progenitors, the activation of NK
CC cells, proliferation of T-cells, proliferation of B-cells stimulated with
CC anti-CD40 antibodies, stimulates an antigenic response in a mammal, and
CC reduces proliferation of B-cells stimulated with anti-IgM antibodies. The
CC zalphall ligand polypeptide is also useful in preparing antibodies that
CC bind to zalphall ligand epitopes. The zalphall ligand polynucleotides can
CC be used as probes or primers to clone regions of a zalphall ligand gene,
CC and in gene therapy. Zalphall Ligand may also be used to identify
CC inhibitors of its activity, to enhance the generation of anti-lymphocur
CC responses with or without the infusion of donor lymphocytes, and to
CC activate or stimulate the immune system. The present sequence
CC representing MBP-human zalphall ligand fusion protein is used in the
CC methods of the present invention
XX
SQ Sequence 519 AA;

Query Match 88.1%; Score 37; DB 5; Length 519;
Best Local Similarity 87.5%; Pred. No. 60;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HOVLSSRT 8
||:|||||
Db 506 HQHLSRT 513

RESULT 44
ADH44655

ADH44655 standard; protein; 519 AA.
ADH44655;
AC
XX
XX
DT 25-MAR-2004 (first entry)
XX
DE Human Zalphall ligand/MBP fusion protein.
XX
XX Human; Zalphall ligand; Zalphall receptor; immune response;
KW tumour progression; metastasis; tumour stasis; haematopoietic tumour;
KW lymphoma; B cell tumour; systemic lupus erythematosus;
KW rheumatoid arthritis; myasthenia gravis; diabetes; infectious disease;
KW immunocompromised patient; HIV infection; vaccine.
XX
XX Chimeric.
OS Homo sapiens.
OS Escherichia coli.
XX
PN US6605272-B2.
XX
PD 12-AUG-2003.
XX
PF 03-AUG-2001; 2001US-00923246.
XX
XX 09-MAR-1999; 99US-0123547P.
PR 11-MAR-1999; 99US-0123904P.
PR 01-JUL-1999; 99US-0142013P.
PR 09-MAR-2000; 2000US-00522217.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;
PI Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
XX
DR WPI: 2003-895283/82.
DR N-PSDB; ADH44654.
XX
XX Stimulating an immune response in a mammal exposed to an antigen or
PT pathogen, useful for enhancing anti-tumor activity resulting in reduced
PT tumor progression or metastasis, comprises administering zalphall ligand
PT polypeptide.
XX
XX
PS Example 31; SEQ ID NO 85; 103pp; English.
XX
XX The invention relates to stimulating an immune response in a mammal
CC exposed to an antigen or pathogen comprising administering a composition
CC comprising mature zalphall ligand polypeptide comprising residues 32-162
CC of ADH44572 in a pharmaceutical vehicle. Also included are stimulating an
CC immune response in a mammal exposed to an antigen or pathogen
CC (comprising: (a) determining (in)directly the level of antigen or
CC pathogen present in the mammal; (b) administering a composition
CC comprising zalphall ligand polypeptide in a pharmaceutical vehicle; (c)
CC determining (in)directly the level of antigen or pathogen in the mammal;
CC and (d) comparing the antigen or pathogen level in (a) with (b), where a
CC change in the level indicates stimulation of immune response), and
CC stimulating an immune response in a mammal exposed to an antigen or
CC pathogen (comprising: (a) determining a level of antigen- or pathogen-
CC specific antibody; (b) administering a composition comprising zalphall
CC ligand polypeptide in a pharmaceutical vehicle; (c) determining a post
CC administration level of the antigen- or pathogen-specific antibody; and
CC (d) comparing the level of the antibody in (a) with (b), where an
CC increase in the antibody level indicates stimulation of immune response).
CC The method is useful for stimulating an immune response in a mammal
CC exposed to an antigen or pathogen, and for enhancing anti-tumor activity
CC resulting in a reduction in tumour progression, decrease in metastasis,
CC or tumour stasis. The tumour may be a haematopoietic tumour, a lymphoma
CC or a B cell tumour. The zalphall ligand is useful for treating a wide
CC range of diseases arising from defects in the immune system, e.g.
CC systemic lupus erythematosus, rheumatoid arthritis, myasthenia gravis, or
CC diabetes, for boosting immunity to infectious diseases, treating
CC immunocompromised patients, such as HIV+ patients and in improving
CC vaccines. The present sequence is a human Zalphall fusion protein.
XX

SQ Sequence 519 AA;

Query Match 88.1%; Score 37; DB 7; Length 519;
Best Local Similarity 87.5%; Pred. No. 60;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
||:|||||
Db 506 HOHLSRT 513

RESULT 45

AD100991

ID AD100991 standard; protein; 519 AA.

XX AD100991;

XX 22-APR-2004 (first entry)

XX MBP (maltose binding protein)-human zalphallilignand fusion protein.

XX zalphall ligand; immunity; infectious disease; immunocompromised patient;

XX HIV; vaccine; human; MBP; maltose binding protein; plasmid pTAP126.

XX Homo sapiens.

XX Unidentified.

XX US2003125524-A1.

XX 03-JUL-2003.

XX 15-NOV-2002; 2002US-00295723.

XX 09-MAR-2000; 2000US-00522217.

XX (ZYMO) ZYMOGENETICS INC.

XX Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;

XX Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;

XX WPI; 2003-811003/76.

XX N-PSDB; AD100990.

XX Example 31; SEQ ID NO 85; 113pp; English.

XX The invention relates to a novel isolated zalphall ligand polypeptide.

XX CC The polypeptide of the invention may be useful for boosting immunity to

XX CC infectious diseases and treating immunocompromised patients, such as HIV

XX CC patients, as well as in improving vaccines. The current sequence is that

XX CC of the MBP (maltose binding protein)-human zalphallilignand fusion protein

XX CC of the invention.

XX SQ Sequence 519 AA;

Query Match 88.1%; Score 37; DB 7; Length 519;
Best Local Similarity 87.5%; Pred. No. 60;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
||:|||||
Db 506 HOHLSRT 513

RESULT 46

ADP19814

ID ADP19814 standard; protein; 519 AA.

XX ADP19814;

XX

DT 26-AUG-2004 (first entry)

XX Human zalphall ligand-MBP fusion protein.

XX DE Cytostatic; zalphall ligand; pharmaceutical; cancer; immune response;

XX KW melanoma; tumour; solid tumour; haematopoietic tumour; lymphoma; human;

XX MBP; maltose binding protein.

XX Homo sapiens.

XX Unidentified.

XX US2004110932-A1.

XX 10-JUN-2004.

XX 10-SEP-2003; 2003US-00659684.

XX 09-MAR-1999; 99US-0123547P.

XX 11-MAR-1999; 99US-0123904P.

XX 01-JUL-1999; 99US-0142013P.

XX 09-MAR-2000; 2000US-00522217.

XX (ZYMO) ZYMOGENETICS INC.

XX Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;

XX Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;

XX WPI; 2004-440401/41.

XX N-PSDB; ADP19813.

XX New zalphall ligand polynucleotide and polypeptide molecules, useful for

XX PT treating cancer, e.g. melanoma, solid tumor, hematopoietic tumor, or

XX PT lymphoma.

XX PS Disclosure; SEQ ID NO 85; 111pp; English.

XX CC The invention describes an isolated polypeptide comprising a sequence of

XX CC amino acid residues that is at least 90 or 95% identical to residues 41

XX CC (Gln) to 148 (Ile), or 32 (Gln) to 148 (Ile) of a sequence of 162 amino

XX CC acids (SEQ ID NO:2, human zalphall ligand), fully defined in the

XX CC specification. Also described are: a pharmaceutical composition

XX CC comprising the polynucleotide encoding; in a pharmaceutical composition

XX CC vehicle; an expression vector comprising the following operably linked

XX CC elements a control element; and a DNA segment comprising the

XX CC polynucleotide; and an isolated polynucleotide molecule comprising at

XX CC least 10 nucleotides of the polynucleotide sequence of 642 bp, fully

XX CC defined in the specification. The molecules, compositions and methods are

XX CC useful for treating cancer, e.g. melanoma, solid tumour, haematopoietic

XX CC tumour, or lymphoma. This is the amino acid sequence of a fusion protein

XX CC comprising the human zalphall ligand fused to MBP (maltose binding

XX CC protein).

QY 1 HOYLSRT 8
||:|||||
Db 506 HOHLSRT 513

RESULT 47

ADV96438

ID ADV96438 standard; protein; 519 AA.

XX

XX AC ADV96438;
 XX DT 10-MAR-2005 (first entry)
 XX DE Human zalphal1 ligand-MBP fusion protein - SEQ ID 85.
 XX KM stem cell; cell culture; zalphal1 ligand; maltose binding protein.
 XX OS Homo sapiens.
 XX OS Chimeric.
 XX OS Unidentified.
 XX PN US2004260065-A1.
 XX PD 23-DEC-2004.
 XX PF 26-FEB-2004; 2004US-00787442.
 XX PR 09-MAR-1999; 99US-0123547P.
 XX PR 11-MAR-1999; 99US-0123904P.
 XX PR 01-JUL-1999; 99US-0142013P.
 XX PR 09-MAR-2000; 2000US-00522217.
 XX PA (NOVA/) NOVAK J E.
 XX PA (PRES/) PRESNELL S R.
 XX PA (SPRE/) SPRECHER C A.
 XX PA (FOST/) FOSTER D C.
 XX PA (HOL/) HOLLY R D.
 XX PA (GROS/) GROSS J A.
 XX PA (JOHN/) JOHNSTON J V.
 XX PA (NELS/) NELSON A J.
 XX PA (DILL/) DILLON S R.
 XX PA (HAMM/) HAMMOND A K.
 XX PI Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD,
 XX PI Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
 XX WPI: 2005-038783/04.
 XX DR N-PSDB; ADV96437.
 XX PT New zalpha 11 ligand fusion protein, useful for stimulating the
 XX PT proliferation and/or development of hematopoietic cells in vitro and in
 XX PT vivo, and in autologous marrow culture.
 XX PS Example 31; SEQ ID NO 85; 110pp; English.
 XX CC The invention comprises a fusion protein that contains a zalphal1 ligand
 XX CC and a cytokine polypeptide (e.g. IL-2, IL-4, IL-15 or GM-CSF), the fusion
 XX CC protein of the invention binds to the human receptor protein. The protein
 XX CC of the invention is useful for stimulating the proliferation and/or
 XX CC development of hematopoietic cells. The protein of the invention is also
 XX CC useful in autologous marrow culture. The present amino acid sequence
 XX CC represents a fusion protein between human zalphal1 ligand and maltose
 XX CC binding protein (MBP).
 XX SQ Sequence 519 AA;
 XX
 XX Query Match 88.1%; Score 37; DB 9; Length 519;
 XX Best Local Similarity 87.5%; Pred. No. 60;
 XX Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

DT 12-FEB-2004 (first entry)
 XX DE Human albumin therapeutic fusion proteinh SeqID2167.
 XX KM albumin fusion protein; albumin activity; human serum albumin;
 XX KM serum osmotic pressure; shelf-life; stability; antidiabetic;
 XX KM gene therapy; diabetes mellitus; human.
 XX OS Chimeric.
 XX OS Homo sapiens.
 XX PN WO2003060071-A2.
 XX PD 24-JUL-2003.
 XX PF 23-DEC-2002; 2002WO-US040891.
 XX PR 21-DEC-2001; 2001US-0341811P.
 XX PR 24-JAN-2002; 2002US-0350358P.
 XX PR 28-JAN-2002; 2002US-0351360P.
 XX PR 26-FEB-2002; 2002US-0359370P.
 XX PR 28-FEB-2002; 2002US-0360000P.
 XX PR 27-MAR-2002; 2002US-0367500P.
 XX PR 08-APR-2002; 2002US-0370227P.
 XX PR 10-MAY-2002; 2002US-0378950P.
 XX PR 24-MAY-2002; 2002US-0382617P.
 XX PR 28-MAY-2002; 2002US-0383123P.
 XX PR 05-JUN-2002; 2002US-0385708P.
 XX PR 10-JUL-2002; 2002US-0394625P.
 XX PR 24-JUL-2002; 2002US-0398008P.
 XX PR 09-AUG-2002; 2002US-0402131P.
 XX PR 13-AUG-2002; 2002US-0402708P.
 XX PR 18-SEP-2002; 2002US-0411355P.
 XX PR 18-SEP-2002; 2002US-0411426P.
 XX PR 02-OCT-2002; 2002US-0414984P.
 XX PR 11-OCT-2002; 2002US-0417611P.
 XX PR 23-OCT-2002; 2002US-0420246P.
 XX PR 05-NOV-2002; 2002US-0423623P.
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX PA (DELT-) DELTA BIOTECHNOLOGY LTD.
 XX PA (PRIN-) PRINCIPLEA PHARM CORP.
 XX PI Ballance DJ, Turner AJ, Rosen CA, Haseltine WA;
 XX WPI: 2003-598517/56.
 XX PT New albumin fusion protein, useful for preparing a composition for
 XX PT treating diabetes mellitus.
 XX PS Example 4; SEQ ID NO 2167; 24pp; English.
 XX CC This invention relates to a novel albumin fusion protein having albumin
 XX CC or biological activity. Human serum albumin is responsible for a
 XX CC significant proportion of the osmotic pressure of serum and also
 XX CC functions as a carrier of endogenous and exogenous ligands. The fusion of
 XX CC albumin to a therapeutic protein may increase shelf-life and stability of
 XX CC the therapeutic protein. The albumin fusion protein of the invention may
 XX CC allow production of compositions with antidiabetic activity whilst the
 XX CC nucleotide sequence which encodes it may be useful for gene therapy. The
 XX CC albumin fusion protein is useful for preparing a composition for treating
 XX CC diabetes mellitus. The present sequence is the amino acid sequence of a
 XX CC novel full-length human albumin therapeutic fusion protein of the
 XX CC invention. Note: The sequence data for this patent did not form part of
 XX CC the printed specification, but was obtained in electronic format directly
 XX CC from WIPO at fcp.wipo.int/pub/publishedpc_sequences
 XX SQ Sequence 742 AA;
 XX
 XX Query Match 88.1%; Score 37; DB 7; Length 742;
 XX Best Local Similarity 87.5%; Pred. No. 89;
 XX Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 48
 ADP17042
 ID ADP17042 standard; protein; 742 AA.
 XX AC ADP17042;
 XX

OY 1 HOYLSRT 8
 |||||
 Db 144 HOYLSRT 151

RESULT 49
 AAE29276

ID AAE29276 standard; peptide; 8 AA.

XX AAE29276;

XX 27-JAN-2003 (first entry)

XX Anti-ClfA monoclonal antibody variable light chain CDR3.

XX Clumping factor A; ClfA; fibrinogen; fibrin; Clf40; Clf33; N3 protein;
 KM immunological; staphylococcal infection; impetigo; pneumonia; furuncle;
 KM septic arthritis; sepsis; endocarditis; antibacterial; wound; therapy;
 KM complementarity determining region; CDR.

OS Unidentified.

XX WO200272600-A2.

XX 19-SEP-2002.

XX 28-JAN-2002; 2002WO-US002296.

XX 26-JAN-2001; 2001US-0264072P.

XX 12-MAR-2001; 2001US-0274611P.

XX 18-JUN-2001; 2001US-0298413P.

XX 30-JUL-2001; 2001US-0308116P.

XX (INH1-) INHIBITEX INC.

XX Facti JM, Hutchins JT, Domanski P, Patel P, Hall A;
 WPI; 2002-759834/82.

XX New anti-clumping factor A (ClfA) monoclonal antibody, useful for
 PT treating or preventing Staphylococcus aureus infection e.g. wound
 PT infections, impetigo, furuncles, pneumonia, septic arthritis or sepsis in
 PT a human or animal.

XX Claim 31; Page 55; 80pp; English.

XX The invention relates to monoclonal antibody which binds the clumping
 CC factor A (ClfA) protein from Staphylococcus aureus. The anti-ClfA
 CC monoclonal antibody is useful for treating or preventing S. aureus
 CC infection in a human or animal, and for inhibiting the binding of
 CC staphylococcal bacteria to fibrinogen or fibrin. The immunogenic fragment
 CC S. aureus Clf40 protein, S. aureus Clf33 protein, or the S. aureus N3
 CC protein is useful for inducing an immunological response in a human or
 CC animal. These staphylococcal infections include wound infections, sepsis,
 CC impetigo, furuncles, pneumonia, septic arthritis or endocarditis. The
 CC present sequence is an anti-ClfA monoclonal antibody variable light chain
 CC complementarity determining region (CDR)

XX Sequence 8 AA;

SQ

Query Match 83.3%; Score 35; DB 5; Length 8;
 Best Local Similarity 87.5%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 HOYLSRT 8
 |||||

Db 1 HOYLSRT 8

RESULT 50
 ADL23028

ID ADL23028 standard; peptide; 8 AA.

XX

AC ADL23028;
 XX 20-MAY-2004 (first entry)

XX Myelin associated glycoprotein MAG binding antibody light chain CDR L3.

XX antibody; MAG; myelin associated glycoprotein; light chain; CDR; stroke;
 KM neurodegenerative disorder; gene therapy; vaccine.

XX Unidentified.

XX WO2004014953-A2.

XX 19-FEB-2004.

XX 05-AUG-2003; 2003WO-EP008749.

XX 06-AUG-2002; 2002GB-00018229.

XX 06-AUG-2002; 2002GB-00018230.

XX 06-AUG-2002; 2002GB-00018232.

XX 06-AUG-2002; 2002GB-00018234.

XX (GLAXO) GLAXO GROUP LTD.

XX Ellis JH, Gernaschewski V;
 WPI; 2004-180641/17.

XX N-PSDB; ADL23033.

XX New altered antibody that binds to and neutralizes myelin associated
 PT glycoprotein (MAG), useful for preparing a composition for treating or
 PT preventing stroke or other neurodegenerative disorders e.g., Alzheimer's
 PT disease.

XX Claim 1; Page 53; 67pp; English.

XX The present invention relates to a new altered antibody or its functional
 CC fragment, which binds to and neutralizes myelin associated glycoprotein
 CC (MAG) and comprises a light chain variable domain (VL) comprising
 CC complementary determining region light 1 (CDRL1), CDRL2 or CDRL3 and/or a
 CC heavy chain variable domain (VH) comprising CDRH1, CDRH2 or CDRH3. The
 CC antibody is useful for preparing a composition for treating or preventing
 CC stroke or other neurodegenerative disorders in a human, e.g., traumatic
 CC brain injury, Alzheimer's disease, dementias, peripheral neuropathy,
 CC Parkinson's disease, Huntington's disease and multiple sclerosis. The
 CC present sequence is the anti-MAG antibody light chain CDR L3 of the
 CC invention.

XX Sequence 8 AA;

Query Match 83.3%; Score 35; DB 8; Length 8;
 Best Local Similarity 87.5%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 HOYLSRT 8
 |||||

Db 1 HOYLSRT 8

Search completed: May 4, 2006, 12:56:39
 Job time: 122.111 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 4, 2006, 13:00:03 ; Search time 11.4286 Seconds
(without alignments)
67.352 Million cell updates/sec

Title: US-10-700-632-6
Perfect score: 42
Sequence: 1 HOYLSRT 8

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 1000 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	90.5	553	2 T40438	hypothetical prote
2	35	83.3	103	2 PH1054	Ig light chain V r
3	33	78.6	88	2 C82627	hypothetical prote
4	33	78.6	374	2 B82572	P-protein Xf2325 (
5	33	78.6	389	2 T32516	hypothetical prote
6	32	76.2	134	2 S53074	hypothetical prote
7	32	76.2	251	2 U01722	3b protein - canin
8	32	76.2	757	2 J80198	genome polypeptid
9	31	73.8	101	2 S26337	Ig light chain V r
10	31	73.8	112	2 S51125	genome polypeptid
11	31	73.8	112	2 S51124	genome polypeptid
12	31	73.8	112	2 A84605	hypothetical prote
13	31	73.8	318	2 S25459	ribosomal protein
14	31	73.8	326	2 S44259	sucrose operon reg
15	31	73.8	377	2 H89717	protein C18B12.2 (
16	31	73.8	443	2 T43170	probable triacylgl
17	31	73.8	443	2 T39540	triglyceride lipas
18	31	73.8	454	2 T19380	hypothetical prote
19	31	73.8	926	2 A35905	endopeptidase Clp
20	31	73.8	952	2 T52456	endopeptidase Clp
21	31	73.8	952	2 T49283	AcClpC - Arabidops
22	31	73.8	1280	2 T29021	cobra venom factor
23	31	73.8	1642	2 I51018	genome polypeptid
24	31	73.8	2210	1 GNNY89	genome polypeptid
25	31	73.8	2332	1 GNNY4F	genome polypeptid
26	31	73.8	2332	1 GNNY2F	genome polypeptid
27	31	73.8	2336	2 S37077	genome polypeptid
28	31	73.8	2336	2 S37077	genome polypeptid
29	30	71.4	79	2 AE2014	hypothetical prote

30	30	71.4	328	2 S24203	protein 1 - Neisse
31	30	71.4	385	2 G70628	probable ackA prot
32	30	71.4	409	2 S57689	hypothetical prote
33	30	71.4	511	2 S77350	hypothetical prote
34	30	71.4	528	2 T02466	probable ATP-depen
35	30	71.4	574	2 E96722	hypothetical prote
36	30	71.4	718	2 AF0835	probable type I se
37	30	71.4	762	2 E98121	hypothetical prote
38	30	71.4	805	2 S13410	chloride channel p
39	30	71.4	810	2 D95256	ATP-dependent Clp
40	30	71.4	810	2 S19725	voltage-gated chor
41	30	71.4	855	2 B89472	protein ZC35.4 (im
42	30	71.4	899	2 T16204	hypothetical prote
43	30	71.4	1114	2 T18197	reverse transcript
44	30	71.4	6420	2 T30283	polyketide synthas
45	29	69.0	104	2 T10351	hypothetical prote
46	29	69.0	107	2 T44160	hypothetical prote
47	29	69.0	107	2 T09305	EFRR1 protein - hu
48	29	69.0	107	2 T43973	hypothetical prote
49	29	69.0	128	2 A35881	histone H2A.2 - hu
50	29	69.0	128	2 S03642	histone H2A.2 - bo
51	29	69.0	128	2 S03644	histone H2A.2 - ra
52	29	69.0	141	2 S08118	histone H2A.2 - f
53	29	69.0	151	2 A72093	conserved hypotet
54	29	69.0	151	2 H86529	nitrate/nitrite re
55	29	69.0	209	2 AH0369	glucanase operon t
56	29	69.0	226	2 D90054	hypothetical prote
57	29	69.0	227	2 T21783	hypothetical prote
58	29	69.0	261	2 AH2031	hypothetical prote
59	29	69.0	301	2 B69815	CDP-glucose 4,6-de
60	29	69.0	339	2 A72211	N-acetyl-gamma-glu
61	29	69.0	367	2 C81722	conserved hypotet
62	29	69.0	375	2 A71625	rifin PFB0035c - m
63	29	69.0	405	2 AB2126	acetate kinase (im
64	29	69.0	406	2 T52626	probable mitogen-a
65	29	69.0	442	2 AE0477	hyd Family secret
66	29	69.0	459	2 T10526	cyclin B1c-11 - ye
67	29	69.0	473	2 A33652	probable keratin 1
68	29	69.0	488	2 H87614	conserved hypotet
69	29	69.0	580	2 H86189	hypothetical prote
70	29	69.0	608	2 T02684	MYB-related transc
71	29	69.0	612	2 T22586	hypothetical prote
72	29	69.0	661	2 T38176	hypothetical Myd f
73	29	69.0	721	2 A70764	probable glgX prot
74	29	69.0	761	2 T09052	hypothetical prote
75	29	69.0	800	2 G89831	hypothetical prote
76	29	69.0	827	2 A41672	glycerol-3-phospha
77	29	69.0	866	2 T48544	MAP3K delta-1 prot
78	29	69.0	900	2 GNNYMW	genome polypeptid
79	29	69.0	1178	2 S57698	regulatory protein
80	29	69.0	1360	2 T12064	DNA binding protei
81	29	69.0	1941	2 T23979	hypothetical prote
82	29	69.0	1943	2 T23986	hypothetical prote
83	29	69.0	2241	2 S09811	hypothetical prote
84	29	69.0	2292	1 GNNYEB	genome polypeptid
85	29	69.0	2292	1 GNNYEB	genome polypeptid
86	29	69.0	2292	1 GNNYED	genome polypeptid
87	29	69.0	2292	1 S54401	capsid polypeptid
88	29	69.0	2292	2 S35961	capsid polypeptid
89	29	69.0	2802	2 F97686	cyclic beta-(1-2)
90	29	69.0	2825	2 T14271	Doc4 protein, stre
91	29	69.0	2831	2 A12911	beta (1->2) glucan
92	28	66.7	136	2 A10124	probable preplilin
93	28	66.7	140	2 S58375	ketoconazole resis
94	28	66.7	161	2 E84201	hypothetical prote
95	28	66.7	166	2 B83226	aliphatic amidase
96	28	66.7	207	2 T21903	hypothetical prote
97	28	66.7	216	2 AE2548	hypothetical prote
98	28	66.7	244	1 WZBE56	gene 56 protein -
99	28	66.7	244	2 S47425	hypothetical prote
100	28	66.7	244	2 B60007	hypothetical prote
101	28	66.7	246	2 S04890	hypothetical prote
102	28	66.7	246	2 T31020	hypothetical prote

103	28	66.7	263	2	H91125	negative regulator
104	28	66.7	263	2	G85970	exu regulon regula
105	28	66.7	263	2	G65098	exu regulon regula
106	28	66.7	266	2	S59237	hypothetical prote
107	28	66.7	272	2	T26235	hypothetical prote
108	28	66.7	290	1	SYB8AT	thymidylate syntha
109	28	66.7	290	1	T42984	thymidylate syntha
110	28	66.7	294	1	SYB8S	thymidylate syntha
111	28	66.7	308	2	S22930	ubiquinol-cytochro
112	28	66.7	323	2	T27640	hypothetical prote
113	28	66.7	348	2	S35520	transposase - lacc
114	28	66.7	362	2	E72002	aromatic amino aci
115	28	66.7	362	2	C86621	hypothetical prote
116	28	66.7	368	1	H71568	hypothetical prote
117	28	66.7	388	1	JC5461	cellulase (EC 3.2.
118	28	66.7	388	1	S43920	cellulase (EC 3.2.
119	28	66.7	396	2	D81339	acetate kinase (EC
120	28	66.7	402	2	T52522	hypothetical prote
121	28	66.7	414	2	H90815	probable kinase [i
122	28	66.7	414	2	D85675	probable kinase yc
123	28	66.7	414	2	C64856	probable permease
124	28	66.7	416	2	AC0198	lipoprotein release
125	28	66.7	420	2	S67559	probable membrane
126	28	66.7	441	2	C43935	lantibiotic subfil
127	28	66.7	452	2	JC4100	hydroxyindole O-me
128	28	66.7	474	2	E75069	glutamate synthase
129	28	66.7	476	2	D71200	probable glutamate
130	28	66.7	481	2	S74934	pled-1 protein - S
131	28	66.7	497	2	T41718	hypothetical funga
132	28	66.7	500	2	S33979	gas polypeptin -
133	28	66.7	509	2	S48856	finger protein pcp
134	28	66.7	514	2	T48318	hypothetical prote
135	28	66.7	575	2	C86310	protein FIL3.2 [im
136	28	66.7	580	2	C82551	nitrogen-related term
137	28	66.7	599	2	D97818	ATP-dependent DNA
138	28	66.7	620	2	E82351	ATP-dependent DNA
139	28	66.7	629	2	T23081	hypothetical prote
140	28	66.7	642	2	C89124	protein K07C11.9 [
141	28	66.7	662	2	T28064	hypothetical prote
142	28	66.7	733	2	J01891	capsid protein - f
143	28	66.7	733	2	U01892	capsid protein - f
144	28	66.7	795	2	T21487	hypothetical prote
145	28	66.7	809	2	T38051	hypothetical prote
146	28	66.7	812	2	AE3010	Tomb-dependent rec
147	28	66.7	833	2	A96274	probable tomb-depe
148	28	66.7	888	2	E71608	ATP-dept. acyl-CoA
149	28	66.7	899	2	A83019	conserved hypotet
150	28	66.7	936	2	T06190	lipoxigenase (EC 1
151	28	66.7	1011	1	GNNYCL	genome polypeptin
152	28	66.7	1117	2	AE0075	hypothetical prote
153	28	66.7	1197	2	T39613	pyruvate (flavodox
154	28	66.7	1199	2	AD2156	pyruvate-flavodoxi
155	28	66.7	1260	2	T14276	myosin-like protei
156	28	66.7	1277	2	T30532	neural cell adhesi
157	28	66.7	1528	2	T14279	myosin-like protei
158	28	66.7	2332	1	GNNYF	genome polypeptin
159	28	66.7	2357	2	A59249	Class VII unconven
160	28	66.7	2427	2	T16613	hypothetical prote
161	28	66.7	3011	1	S40770	genome polypeptin
162	27	64.3	41	2	E69828	hypothetical prote
163	27	64.3	60	2	B82516	hypothetical prote
164	27	64.3	93	2	A33472	transcription regu
165	27	64.3	94	2	DB4117	transcription regu
166	27	64.3	105	2	C72631	hypothetical prote
167	27	64.3	109	2	S51134	genome polypeptin
168	27	64.3	109	2	S51135	genome polypeptin
169	27	64.3	130	2	G87422	hypothetical prote
170	27	64.3	132	2	S46373	Ig kappa chain V-J
171	27	64.3	147	2	G82925	hypothetical prote
172	27	64.3	151	2	S77763	hypothetical prote
173	27	64.3	180	2	T36628	hypothetical prote
174	27	64.3	189	2	T45792	hypothetical prote
175	27	64.3	197	2	D64053	segA protein - Hae
176	27	64.3	204	2	T04658	hypothetical prote
177	27	64.3	220	2	A85018	probable copper-co
178	27	64.3	223	2	F83598	cell division prot
179	27	64.3	222	2	A42095	floral homeotic pr
180	27	64.3	228	2	H83379	probable pili asse
181	27	64.3	241	2	G75081	hypothetical prote
182	27	64.3	251	2	B87674	oxidoreductase, al
183	27	64.3	292	2	A89884	hypothetical prote
184	27	64.3	294	2	E86900	transcription regu
185	27	64.3	302	2	S49809	probable membrane
186	27	64.3	310	2	AC1859	hypothetical prote
187	27	64.3	318	2	S61840	porin class P1B -
188	27	64.3	322	2	A99936	hypothetical prote
189	27	64.3	322	2	D89785	hypothetical prote
190	27	64.3	331	2	C83701	hypothetical prote
191	27	64.3	348	1	MMNHPB	outer membrane pro
192	27	64.3	348	2	A39920	outer membrane pro
193	27	64.3	350	2	S17459	outer membrane pro
194	27	64.3	352	2	S74238	probable G protein
195	27	64.3	356	2	T00881	probable PCP2-like
196	27	64.3	359	2	B83923	hypothetical prote
197	27	64.3	371	1	R6BYM7	ribosomal protein
198	27	64.3	380	2	T01706	hypothetical prote
199	27	64.3	383	2	E90285	hypothetical prote
200	27	64.3	385	2	I39826	hypothetical prote
201	27	64.3	413	2	AG2456	transposase al1520
202	27	64.3	430	2	G02673	testis calpastatin
203	27	64.3	451	2	S75569	hypothetical prote
204	27	64.3	452	2	T10527	cyclin Bld-11 - ye
205	27	64.3	454	2	T10525	cyclin Bld-11 - ye
206	27	64.3	476	2	F83286	probable glycosyla
207	27	64.3	491	2	B71957	ATP-dependent RNA
208	27	64.3	492	2	G64550	ATP-dependent RNA
209	27	64.3	496	2	B89027	protein T08H10.1 [
210	27	64.3	510	2	F86392	TLK7.7 protein - A
211	27	64.3	518	2	T23120	hypothetical prote
212	27	64.3	522	2	T31893	hypothetical prote
213	27	64.3	523	2	F90414	elongation factor
214	27	64.3	535	2	S66148	gene pipsqueak pro
215	27	64.3	543	2	A32693	steroid receptor p
216	27	64.3	554	2	S46346	gag polypeptin -
217	27	64.3	550	2	T32288	hypothetical prote
218	27	64.3	587	2	E95369	probable adenylate
219	27	64.3	590	2	D69068	methyl coenzyme M
220	27	64.3	599	2	T48450	hypothetical prote
221	27	64.3	600	2	G71682	GMP-binding protei
222	27	64.3	614	2	AB0935	vitamin B12 recept
223	27	64.3	646	2	S36586	E1 protein - human
224	27	64.3	647	2	T48902	sulfate transpor
225	27	64.3	647	2	S36557	E1 protein - human
226	27	64.3	658	2	T49069	sulfate transpor
227	27	64.3	658	2	T48901	sulfate transpor
228	27	64.3	703	2	T51161	hypothetical prote
229	27	64.3	706	2	T36176	hypothetical prote
230	27	64.3	713	1	S46838	hypothetical prote
231	27	64.3	723	1	RRMQTN	RNA-directed RNA p
232	27	64.3	746	2	B32693	steroid receptor p
233	27	64.3	770	2	T22944	hypothetical prote
234	27	64.3	784	2	T22939	hypothetical prote
235	27	64.3	784	2	AC1091	5'-nucleotidase, p
236	27	64.3	785	2	AB1455	5'-nucleotidase, p
237	27	64.3	790	1	S77032	ABC transporter s1
238	27	64.3	799	2	T02981	1,4-alpha-glucan b
239	27	64.3	799	2	T01663	1,4-alpha-glucan b
240	27	64.3	799	2	B86735	hypothetical prote
241	27	64.3	825	2	A48537	starch branching e
242	27	64.3	839	2	T04859	extensin homolog f
243	27	64.3	849	2	E83349	probable ClpA/B-cy
244	27	64.3	854	2	S65045	1,4-alpha-glucan b
245	27	64.3	856	1	F64098	endopeptidase Clp
246	27	64.3	857	2	A82290	clpB protein VC071
247	27	64.3	857	2	A10397	clp ATPase (import
248	27	64.3	858	2	B84780	starch branching e

249	27	64.3	860	1	C35905	endopeptidase C1p	322	26	61.9	251	2	C86081	CDP-diacylglycerol
250	27	64.3	874	2	T19540	hypothetical prote	323	26	61.9	251	2	AF0942	CDP-diacylglycerol
251	27	64.3	883	2	T51221	hypothetical prote	324	26	61.9	251	2	C91234	CDP-diacylglycerol
252	27	64.3	892	2	S57055	probable membrane	325	26	61.9	260	2	T26773	hypothetical prote
253	27	64.3	920	2	T10052	aminopeptidase (EC	326	26	61.9	265	2	T50569	probable membrane
254	27	64.3	922	2	T06493	1,4-alpha-glucan b	327	26	61.9	274	2	T46041	hypothetical prote
255	27	64.3	930	2	AC1980	hypothetical prote	328	26	61.9	276	2	T15909	hypothetical prote
256	27	64.3	933	2	T25600	hypothetical prote	329	26	61.9	279	2	G83626	transcription regu
257	27	64.3	1026	1	A40315	maternal effect pr	330	26	61.9	280	2	T21876	hypothetical prote
258	27	64.3	1037	2	T27345	hypothetical prote	331	26	61.9	281	2	C5519	hypothetical prote
259	27	64.3	1085	2	S66149	gene p1pqueak pro	332	26	61.9	287	2	S71182	mitosis-specific c
260	27	64.3	1142	2	A45031	cysteine-rich fibr	333	26	61.9	289	2	S55667	thymidylate synth
261	27	64.3	1175	2	S52417	E-selectin ligand	334	26	61.9	294	2	B72246	dihydrolipicolinat
262	27	64.3	1178	2	S08405	hypothetical prote	335	26	61.9	295	2	G97827	hypothetical prote
263	27	64.3	1180	2	T20773	hypothetical prote	336	26	61.9	296	2	E90700	allanoinase [limp
264	27	64.3	1226	2	H64479	protoporphyrin IX	337	26	61.9	296	2	B84527	hypothetical prote
265	27	64.3	1335	2	T30211	autolysin E - Stap	338	26	61.9	296	2	H85550	hypothetical prote
266	27	64.3	1371	2	G77521	sensory transducti	339	26	61.9	298	2	S39150	clathrin assembly
267	27	64.3	1496	2	T19833	hypothetical prote	340	26	61.9	300	1	RDBOB5	cytochrome-b5 redu
268	27	64.3	1512	2	AH0439	probable membrane	341	26	61.9	301	1	RDBUB5	cytochrome-b5 redu
269	27	64.3	1885	1	JC4086	fatty-acid synthas	342	26	61.9	301	1	RDRTB5	arginase BH3948 [i
270	27	64.3	1908	2	A86311	protein FL13.14 [i	343	26	61.9	301	2	BD4143	hypothetical prote
271	27	64.3	2179	1	GNNYH4	genome polyprotein	344	26	61.9	301	2	I54209	hypothetical prote
272	27	64.3	4549	2	T20771	hypothetical prote	345	26	61.9	306	2	T43597	yp targeting nega
273	27	64.3	4637	2	T20774	hypothetical prote	346	26	61.9	311	2	T15266	hypothetical prote
274	27	61.9	71	2	AE2358	hypothetical prote	347	26	61.9	312	2	S49612	transposase - Bac
275	26	61.9	73	2	F86877	hypothetical prote	348	26	61.9	314	2	B84518	probable spliceoso
276	26	61.9	75	2	AB1849	hypothetical prote	349	26	61.9	324	2	E83320	conserved hypotnet
277	26	61.9	81	2	S07518	gene 6.5 protein -	350	26	61.9	329	2	S73710	adhesin p1 homolog
278	26	61.9	85	2	G84684	bombyxlin A-3 homol	351	26	61.9	332	1	H69008	conserved hypotnet
279	26	61.9	98	2	JQ0906	probable membrane	352	26	61.9	333	2	A41881	collagenase Prtc (
280	26	61.9	113	2	S66936	hypothetical prote	353	26	61.9	340	2	T21805	hypothetical prote
281	26	61.9	120	2	F69934	single-strand DNA-	354	26	61.9	346	2	T33309	hypothetical prote
282	26	61.9	121	2	AC1390	single-strand DNA-	355	26	61.9	349	2	S42835	R40P12.6 protein -
283	26	61.9	123	2	AE1765	histone H2A.F/Z va	356	26	61.9	352	2	C85909	hypothetical prote
284	26	61.9	123	2	JB0093	histone H2A.F/Z va	357	26	61.9	352	2	G91064	hypothetical prote
285	26	61.9	124	2	H69745	hypothetical prote	358	26	61.9	354	2	A97224	uncharacterized con
286	26	61.9	124	2	F84052	hypothetical prote	359	26	61.9	356	2	G82523	endo-1,4-beta-gluc
287	26	61.9	125	2	S07392	histone H2A.F/Z -	360	26	61.9	356	2	A95900	probable caraboliit
288	26	61.9	125	2	T18929	hypothetical prote	361	26	61.9	359	1	RGHUCY	GMP-binding regula
289	26	61.9	128	1	HSC82F	histone H2A.F, emb	362	26	61.9	359	2	T33115	hypothetical prote
290	26	61.9	128	2	T30714	hypothetical prote	363	26	61.9	359	2	T33115	hypothetical prote
291	26	61.9	129	2	AE2087	gas vesicle protei	364	26	61.9	364	2	B84565	probable spliceoso
292	26	61.9	140	1	QQMSIG	hypothetical Ig do	365	26	61.9	370	2	T34221	lir-1 protein - Ca
293	26	61.9	140	2	T29662	hypothetical prote	366	26	61.9	370	2	G89812	conserved hypotnet
294	26	61.9	142	2	B75463	conserved hypotet	367	26	61.9	380	2	T28251	ORF MSV090 probabl
295	26	61.9	147	2	AG3113	3-dehydroquinase d	368	26	61.9	384	2	A41661	probable replicati
296	26	61.9	153	2	A60585	thymoglobulin - sl	369	26	61.9	385	2	T43085	hypothetical prote
297	26	61.9	154	2	F98173	3-dehydroquinase d	370	26	61.9	391	2	H84735	hypothetical prote
298	26	61.9	158	2	T38204	hypothetical prote	371	26	61.9	391	2	A11701	acetate kinase ack
299	26	61.9	160	2	B27793	methyl coenzyme M	372	26	61.9	393	2	T47803	hypothetical prote
300	26	61.9	163	2	T08261	hypothetical prote	373	26	61.9	394	2	T20778	mitogen-activated
301	26	61.9	166	2	T48344	hypothetical prote	374	26	61.9	395	1	A46345	hypothetical prote
302	26	61.9	167	2	F64314	methyl coenzyme M	375	26	61.9	396	2	T27946	gene III protein -
303	26	61.9	171	2	S52929	GAG protein - huma	376	26	61.9	397	2	AE1272	acetate kinase hom
304	26	61.9	184	2	S44652	heat shock transcr	377	26	61.9	397	2	AE1634	acetate kinase hom
305	26	61.9	192	2	S59537	hypothetical prote	378	26	61.9	400	1	S75775	alanine racemase (
306	26	61.9	193	2	T05475	hypothetical prote	379	26	61.9	402	2	S32565	actin-binding prot
307	26	61.9	194	2	E95375	probable acetyltra	380	26	61.9	403	2	H72397	actin-binding prote
308	26	61.9	194	2	A10241	hypothetical prote	381	26	61.9	406	1	Q3ECTD	exur-tcdc intergen
309	26	61.9	198	2	AC2478	transposase alr700	382	26	61.9	407	2	AF2497	transposase al1715
310	26	61.9	201	2	T42647	hypothetical prote	383	26	61.9	413	2	T26572	hypothetical prote
311	26	61.9	216	2	A72357	amino acid ABC tra	384	26	61.9	419	2	D45045	hypothetical prote
312	26	61.9	221	2	A70543	hypothetical prote	385	26	61.9	424	2	AC2875	phycobiliprotein h
313	26	61.9	227	2	S12378	MADS box protein d	386	26	61.9	424	2	H98307	oxidoreductase ord
314	26	61.9	221	2	AE1907	hypothetical prote	387	26	61.9	425	2	T21835	probable oxidoredu
315	26	61.9	232	2	C89938	conserved hypotet	388	26	61.9	431	2	E82766	hypothetical prote
316	26	61.9	236	2	JQ0606	acylsterase (EC 3	389	26	61.9	432	2	T11652	conserved transp
317	26	61.9	239	2	T36995	hypothetical prote	390	26	61.9	432	2	F83394	probable transp
318	26	61.9	242	2	C82575	phage-related prot	391	26	61.9	435	2	FN0290	homogentisate 1,2-
319	26	61.9	248	2	S75174	hypothetical prote	392	26	61.9	436	2	F82354	protein-tyrosine k
320	26	61.9	251	1	PSECCD	CPDdiacylglycerol	393	26	61.9	438	2	C86273	protein kinases ho
321	26	61.9	251	1	S04172	UDP-sugar hydrolas	394	26	61.9	442	1	B43362	protein-tyrosine k

395	26	61.9	442	2	A13075	glutamate synthase
396	26	61.9	442	2	H98210	glutamic protein [i
397	26	61.9	447	2	T49777	probable beta-succ
398	26	61.9	447	2	A38351	phosphoprotein pho
399	26	61.9	447	2	A41805	phosphoprotein pho
400	26	61.9	453	1	G64782	probable allantoic
401	26	61.9	453	2	A13225	pyridine nucleotid
402	26	61.9	453	2	AE0567	probable allantoic
403	26	61.9	453	2	B55543	cmat protein - Pse
404	26	61.9	460	2	T24248	hypothetical prote
405	26	61.9	462	2	C81701	hypothetical prote
406	26	61.9	468	2	S65951	[phosphorylase] ph
407	26	61.9	471	2	S51511	capsanthin/capsoru
408	26	61.9	476	2	T51492	hypothetical prote
409	26	61.9	477	2	TN0291	protein-tyrosine k
410	26	61.9	477	2	SS2162	sucrose hydrolase
411	26	61.9	477	2	C91034	sucrose-6-phosphat
412	26	61.9	477	2	D85878	sucrose hydrolase
413	26	61.9	478	1	FOVWVL	gag polyprotein -
414	26	61.9	482	1	H84539	probable homeodoma
415	26	61.9	482	1	FOJLND	gag polyprotein -
416	26	61.9	488	2	T09436	gag polyprotein -
417	26	61.9	498	2	S71511	capsanthin/capsoru
418	26	61.9	498	2	T47702	tetrahydrotolylipol
419	26	61.9	500	1	FOVWLV	gag polyprotein -
420	26	61.9	500	1	A44001	gag polyprotein -
421	26	61.9	500	1	FOVWH4	gag polyprotein -
422	26	61.9	500	2	S66350	lycopene beta-cycl
423	26	61.9	500	2	S66349	lycopene beta-cycl
424	26	61.9	500	2	S72505	lycopene beta-cycl
425	26	61.9	500	2	S72506	lycopene beta-cycl
426	26	61.9	501	2	SS4377	gag polyprotein -
427	26	61.9	502	1	FOVMA2	gag polyprotein -
428	26	61.9	504	2	AE2013	hypothetical prote
429	26	61.9	505	2	T01667	gag polyprotein -
430	26	61.9	506	1	A38068	gag polyprotein -
431	26	61.9	508	1	FOJLSI	gag polyprotein -
432	26	61.9	512	1	FOVWH3	gag polyprotein -
433	26	61.9	512	2	T00870	probable cytochrom
434	26	61.9	519	1	JS0725	cytochrome P450 AL
435	26	61.9	519	2	I38402	guanine nucleotide
436	26	61.9	524	2	F75264	hypothetical prote
437	26	61.9	528	2	A13231	hypothetical prote
438	26	61.9	528	2	C69323	conserved hypochet
439	26	61.9	535	2	T19051	hypothetical prote
440	26	61.9	543	2	T32973	hypothetical prote
441	26	61.9	544	2	UC3503	G-protein signalin
442	26	61.9	554	2	T08976	2-amino-4-hydroxy-
443	26	61.9	555	2	T00778	probable tRNA aden
444	26	61.9	561	2	B35140	hemolysin B precur
445	26	61.9	568	2	B56636	retroicid element PA
446	26	61.9	595	2	F85438	nuclioportin-like p
447	26	61.9	596	2	F88188	protein C18H9.7 [i
448	26	61.9	598	2	S39621	DNA-directed DNA p
449	26	61.9	604	2	T20769	hypothetical prote
450	26	61.9	604	2	AF0187	probable sideropho
451	26	61.9	605	2	SS9996	AMP deaminase (EC
452	26	61.9	608	2	F84114	capsular polysacch
453	26	61.9	608	2	B53295	xylanase (EC 3.2.1
454	26	61.9	609	2	T14759	hypothetical prote
455	26	61.9	613	2	A99552	oligoendopeptidase
456	26	61.9	635	2	AS4592	110k actin filamen
457	26	61.9	636	2	A12552	transposase alr801
458	26	61.9	641	2	T07668	starch synthase (E
459	26	61.9	661	2	IS2603	MPS1 protein - mou
460	26	61.9	666	1	UE0201	protein-tyrosine k
461	26	61.9	676	2	C97775	acylaminio-acid-rel
462	26	61.9	681	2	AD3045	conserved hypochet
463	26	61.9	686	2	H98240	hypothetical prote
464	26	61.9	694	2	S10632	replication initia
465	26	61.9	697	2	S62006	hypothetical prote
466	26	61.9	706	2	D84466	hypothetical prote
467	26	61.9	706	2	SS0616	hypothetical prote
468	26	61.9	707	2	T42239	probable phosphopr
469	26	61.9	710	1	XJHOFK	formaldehyde trans
470	26	61.9	717	2	T34514	hypothetical prote
471	26	61.9	722	2	T34072	hypothetical prote
472	26	61.9	723	2	I38412	receptor tyrosine
473	26	61.9	728	2	T20561	hypothetical prote
474	26	61.9	729	2	T06797	probable 1,4-alpha
475	26	61.9	739	2	AB8445	protein C26E6.10 [
476	26	61.9	749	2	T38327	hypothetical prote
477	26	61.9	760	2	A44313	AMP deaminase (EC
478	26	61.9	768	2	UC6564	cellulobiose oxidase
479	26	61.9	796	2	AG1849	serine/threonine k
480	26	61.9	800	2	AB1079	endoglucanase homo
481	26	61.9	800	2	A11436	endoglucanase homo
482	26	61.9	813	2	AF0526	ATP-dependent heli
483	26	61.9	823	2	T06574	probable 1,4-alpha
484	26	61.9	833	2	S45042	genome polyprotein
485	26	61.9	836	2	S61570	regulatory protein
486	26	61.9	856	2	IS8411	protein-tyrosine k
487	26	61.9	856	2	T22575	hypothetical prote
488	26	61.9	857	2	IS5529	potassium channel
489	26	61.9	858	2	S31761	potassium channel
490	26	61.9	862	2	B84567	probable trehalose
491	26	61.9	873	2	H84459	hypothetical prote
492	26	61.9	876	2	I49152	protein-tyrosine k
493	26	61.9	878	2	S74207	lipoygenase (EC 1
494	26	61.9	880	1	JC4166	protein-tyrosine k
495	26	61.9	880	2	B53743	protein-tyrosine k
496	26	61.9	882	2	I38912	receptor tyrosine
497	26	61.9	882	2	PC1231	hypothetical prote
498	26	61.9	890	1	AS3743	protein-tyrosine k
499	26	61.9	896	2	S36326	clathrin assembly
500	26	61.9	899	2	B38529	nib protein - Esc
501	26	61.9	901	2	A44825	phosphoprotein, sy
502	26	61.9	910	2	UC4609	chitin synthase [E
503	26	61.9	912	2	UH0563	metabotropic gluta
504	26	61.9	915	2	S36327	clathrin assembly
505	26	61.9	926	2	T39082	progestosterone recep
506	26	61.9	930	2	A25923	hypothetical prote
507	26	61.9	947	2	T00340	hypothetical prote
508	26	61.9	950	2	B87611	TonB-dependent rec
509	26	61.9	974	1	A49714	protein-tyrosine k
510	26	61.9	974	2	T30204	pglz protein - Str
511	26	61.9	974	2	S35045	bacteriophage phic
512	26	61.9	984	2	C84781	hypothetical prote
513	26	61.9	1003	2	T13951	DNA topoisomerase
514	26	61.9	1017	2	T18488	hypothetical prote
515	26	61.9	1019	1	A45341	major structural c
516	26	61.9	1025	2	T10259	RNA-directed DNA p
517	26	61.9	1035	2	S61342	sulfite reductase
518	26	61.9	1035	2	T51491	hypothetical prote
519	26	61.9	1215	2	H84513	probable disease r
520	26	61.9	1279	2	T17194	protophyrin IX
521	26	61.9	1303	1	S27396	phytochrome / prot
522	26	61.9	1352	2	G84473	hypothetical prote
523	26	61.9	1413	2	B82877	conserved hypochet
524	26	61.9	1420	2	B57062	SRB9 protein - yea
525	26	61.9	1425	2	T22493	hypothetical prote
526	26	61.9	1583	2	T00727	myosin heavy chain
527	26	61.9	1607	2	T02837	long chain fatty a
528	26	61.9	1677	2	T46095	hypothetical prote
529	26	61.9	1791	2	T24089	hypothetical prote
530	26	61.9	1802	2	H88444	protein C26E6.12 [
531	26	61.9	1941	2	T30554	ubiquitin-protein
532	26	61.9	2129	2	T27431	hypothetical prote
533	26	61.9	2150	2	T08165	RNAi polyprotein -
534	26	61.9	2175	1	GNNYBE	genome polyprotein
535	26	61.9	2182	1	GNNYB1	genome polyprotein
536	26	61.9	2182	2	T14320	calcineurin inhibi
537	26	61.9	2183	1	GNNYB4	genome polyprotein
538	26	61.9	2185	1	GNNYBT	genome polyprotein
539	26	61.9	2185	1	GNNYSV	genome polyprotein
540	26	61.9	2185	1	GNNYS3	genome polyprotein

541	26	61.9	2185	1	GNNVSH	genome polyprotein	614	25	59.5	215	2	A41681	S-crystallin 1 - g
542	26	61.9	2185	1	JQ0201	genome polyprotein	615	25	59.5	216	2	A97675	amino acid efflux
543	26	61.9	2193	2	S44251	polyprotein - echo	616	25	59.5	217	2	A98196	hypothetical prote
544	26	61.9	2193	2	S52919	polyprotein (1A, 1	617	25	59.5	218	2	T51681	myb-related transc
545	26	61.9	2193	2	S44194	polyprotein - echo	618	25	59.5	222	2	A83896	dolichyl-phosphate
546	26	61.9	2194	1	GNNVE7	genome polyprotein	619	25	59.5	223	2	S69054	probable membrane
547	26	61.9	2201	1	GNNYA9	genome polyprotein	620	25	59.5	224	2	T51875	hypothetical prote
548	26	61.9	2201	1	T18674	hypothetical prote	621	25	59.5	225	2	A86043	probable transposa
549	26	61.9	2216	2	C90538	hypothetical prote	622	25	59.5	226	1	S19715	nitrile hydratase
550	26	61.9	4436	2	E71086	hypothetical prote	623	25	59.5	234	2	AC0431	conserved hypochet
551	25.5	60.7	323	2	B83215	conserved hypochet	624	25	59.5	237	2	P95271	hypothetical prote
552	25	59.5	64	2	I38213	protein-serine/thr	625	25	59.5	239	2	D81351	hypothetical prote
553	25	59.5	76	2	A97957	hypothetical prote	626	25	59.5	241	2	B36794	hypothetical prote
554	25	59.5	87	2	J00836	bombyxin B-10 prec	627	25	59.5	242	2	B86293	FTH2.20 protein -
555	25	59.5	87	2	J00836	bombyxin B-10 - si	628	25	59.5	243	2	A13270	transcription regu
556	25	59.5	90	1	IPMTB1	bombyxin B-1 precu	629	25	59.5	244	2	G64628	CDPdiacylglycerol
557	25	59.5	90	1	IPMTB2	bombyxin B-2 precu	630	25	59.5	244	2	B71885	cdp-diacylglycerol
558	25	59.5	90	1	S69485	bombyxin B-4 precu	631	25	59.5	244	2	T50936	dehydrogenase/redu
559	25	59.5	90	2	S69485	bombyxin B-12 prec	632	25	59.5	245	2	D71554	probable adenylate
560	25	59.5	90	2	S69486	bombyxin B-6 precu	633	25	59.5	247	2	T33288	hypothetical prote
561	25	59.5	90	2	S69491	bombyxin B-3 precu	634	25	59.5	252	2	S66289	alpha 1 antichymot
562	25	59.5	90	2	S69488	bombyxin B-7 precu	635	25	59.5	252	2	B69034	hypothetical prote
563	25	59.5	96	2	H36850	A2SL protein - var	636	25	59.5	254	2	E95217	hypothetical prote
564	25	59.5	96	2	T28567	probable membrane	637	25	59.5	254	2	E98081	hypothetical prote
565	25	59.5	100	2	S48479	hypothetical prote	638	25	59.5	258	2	E95998	conserved hypochet
566	25	59.5	101	2	S69300	hypothetical prote	639	25	59.5	259	2	G97188	probable membrane
567	25	59.5	108	2	AE2199	hypothetical prote	640	25	59.5	262	2	T40554	yeast proteasome c
568	25	59.5	108	2	A84003	hypothetical prote	641	25	59.5	262	2	T18886	hypothetical prote
569	25	59.5	108	2	B71074	hypothetical prote	642	25	59.5	262	2	E86851	hypothetical prote
570	25	59.5	111	2	G30502	Ig kappa chain V r	643	25	59.5	265	2	G84434	probable phloem-sp
571	25	59.5	118	2	T27456	hypothetical prote	644	25	59.5	267	1	A46535	interleukin-2 rece
572	25	59.5	125	2	F83072	hypothetical prote	645	25	59.5	271	2	A36893	transcription acti
573	25	59.5	134	2	G72166	A6L protein - var	646	25	59.5	271	2	JQ0950	ICP 18.5 protein -
574	25	59.5	135	2	T40220	hypothetical prote	647	25	59.5	271	2	S59543	hypothetical prote
575	25	59.5	139	2	S03485	T-cell receptor be	648	25	59.5	273	1	TQ2390	MTB transcription
576	25	59.5	139	2	S63353	hypothetical prote	649	25	59.5	274	2	T10270	protein kinase (BC
577	25	59.5	142	2	B69955	hypothetical prote	650	25	59.5	276	2	E71483	probable dipeptide
578	25	59.5	149	2	B83633	3-dehydroquinat d	651	25	59.5	279	2	S67670	hypothetical prote
579	25	59.5	150	2	H82341	3-dehydroquinat d	652	25	59.5	282	2	T31088	probable rhamnosyl
580	25	59.5	152	2	B86171	hypothetical prote	653	25	59.5	286	2	H96706	probable transcrip
581	25	59.5	154	2	AB3252	cytochrome functio	654	25	59.5	286	2	S08993	signal sequence re
582	25	59.5	157	2	T35990	dehydroquinat deh	655	25	59.5	286	2	I38246	signal sequence re
583	25	59.5	160	2	G63736	conserved hypochet	656	25	59.5	287	2	T35229	hypothetical prote
584	25	59.5	164	2	C64405	methy1 coenzyme M	657	25	59.5	288	2	H70894	hypothetical prote
585	25	59.5	164	2	J01551	V3 protein - panic	658	25	59.5	290	2	B81746	peptide ABC transp
586	25	59.5	172	2	C89754	hypothetical prote	659	25	59.5	294	1	B64226	hypothetical prote
587	25	59.5	172	2	A86338	protein F5M15.24 l	660	25	59.5	294	2	AF1218	Salmonella typhimu
588	25	59.5	173	2	A31277	3-dehydroquinat d	661	25	59.5	294	2	AI1571	Regulatory protein
589	25	59.5	179	2	C60328	hypothetical prote	662	25	59.5	295	2	C72573	hypothetical prote
590	25	59.5	180	2	T09063	cytochrome c bioge	663	25	59.5	296	2	A45645	alpha-2-giardin -
591	25	59.5	181	1	B64167	cytochrome c bioge	664	25	59.5	297	1	WCBP75	gene D12 protein -
592	25	59.5	183	2	D84473	Br/Spm-like transp	665	25	59.5	297	2	H86519	hypothetical prote
593	25	59.5	184	2	B82174	cytochrome c bioge	666	25	59.5	297	2	G81565	hypothetical prote
594	25	59.5	185	2	AF0787	thiol,disulfide in	667	25	59.5	297	2	E72102	5'-methylthiodeno
595	25	59.5	185	2	A10960	thiol,disulfide in	668	25	59.5	304	2	G87291	integrase/recombin
596	25	59.5	185	2	A64989	cytochrome c bioge	669	25	59.5	305	2	C89915	hypothetical prote
597	25	59.5	185	2	B85858	thiol disulfide in	670	25	59.5	309	2	B69956	phosphate ABC tran
598	25	59.5	185	2	D91014	thiol disulfide in	671	25	59.5	316	2	T22713	hypothetical prote
599	25	59.5	186	2	G85763	spermidine NI-acet	672	25	59.5	319	2	S76960	hypothetical prote
600	25	59.5	186	2	A55345	diamine N-acetyltr	673	25	59.5	320	2	H87443	NADP-dependent qui
601	25	59.5	186	2	B90915	spermidine NI-acet	674	25	59.5	321	2	A55090	cathpsin O (EC 3.
602	25	59.5	189	2	H70875	hypothetical prote	675	25	59.5	322	1	WMV21U	A-type inclusion p
603	25	59.5	189	2	AB0361	probable iron-nulp	676	25	59.5	322	2	AF6023	hypothetical prote
604	25	59.5	191	2	A72752	hypothetical prote	677	25	59.5	324	2	H85989	probable dehydroge
605	25	59.5	192	2	S42990	viral infectivity	678	25	59.5	324	2	E91144	probable dehydroge
606	25	59.5	193	2	E69469	hypothetical prote	679	25	59.5	324	2	US0688	hypothetical 35k p
607	25	59.5	198	1	A57987	myb protein - Bsc	680	25	59.5	324	2	A71346	probable chromosom
608	25	59.5	204	1	T51669	myb-related transc	681	25	59.5	327	2	A82187	hypothetical prote
609	25	59.5	205	2	T21737	hypothetical prote	682	25	59.5	328	2	AF0075	lacI-family regula
610	25	59.5	206	2	T33064	hypothetical prote	683	25	59.5	328	2	T29002	hypothetical prote
611	25	59.5	206	2	B72236	hypothetical prote	684	25	59.5	330	2	AD2854	conserved hypochet
612	25	59.5	206	2	B82563	hexon-associated p	685	25	59.5	333	1	C69812	ferrichrome ABC tr
613	25	59.5	215	1	SXADMS		686	25	59.5	333	2	D95283	probable AtrAc-cype

687	25	59.5	336	2	B90071	ornithine transcar	760	25	59.5	468	2	E81924	probable two-compo
688	25	59.5	336	2	H96554	probable protein k	761	25	59.5	470	2	F70406	conserved hypothet
689	25	59.5	336	2	E96874	hypothetical prote	762	25	59.5	468	2	AD2101	hypothetical prote
690	25	59.5	338	2	A61383	NADH oxidase homol	763	25	59.5	473	2	B84366	hypothetical prote
691	25	59.5	338	2	G85547	adhesin/invasin-11	764	25	59.5	474	2	E90165	hypothetical prote
692	25	59.5	338	2	D90697	adhesin/invasin-11	765	25	59.5	474	2	S31712	beta-1,3-glucanase
693	25	59.5	340	2	B70781	hypothetical prote	766	25	59.5	475	2	B75024	glutamate synthase
694	25	59.5	343	2	T32334	hypothetical prote	767	25	59.5	476	2	T19786	hypothetical prote
695	25	59.5	355	2	F83914	hypothetical prote	768	25	59.5	476	2	JC7189	tubulointerstitial
696	25	59.5	362	2	A12159	hypothetical prote	769	25	59.5	479	2	D84129	4-hydroxyphenylace
697	25	59.5	364	2	T20843	hypothetical prote	770	25	59.5	481	2	A41339	xylokinase (EC 2
698	25	59.5	367	2	A81367	probable GTP-bindi	771	25	59.5	481	2	JQ1147	N-acetylneuramoyl-L
699	25	59.5	370	2	T47504	mitogen-activated	772	25	59.5	482	2	A39285	calcitonin recepto
700	25	59.5	370	2	S40469	mitogen-activated	773	25	59.5	483	2	H90210	hypothetical prote
701	25	59.5	370	2	F87638	conserved hypothet	774	25	59.5	489	2	T41241	oxysterol-binding
702	25	59.5	371	2	T32692	hypothetical prote	775	25	59.5	490	2	A45623	Antra 11.17 varian
703	25	59.5	373	2	T52593	equamosa promoter	776	25	59.5	491	2	T19505	hypothetical prote
704	25	59.5	374	2	A84783	hypothetical prote	777	25	59.5	492	2	C83592	calcitonin recepto
705	25	59.5	375	2	T00929	equamosa-promoter	778	25	59.5	498	2	I47130	hypothetical prote
706	25	59.5	375	2	AD3432	A/G-specific adeni	779	25	59.5	504	2	C86470	hypothetical prote
707	25	59.5	376	2	T24223	hypothetical prote	780	25	59.5	505	2	T19037	hypothetical prote
708	25	59.5	377	2	AD2922	altonate oxidored	781	25	59.5	509	2	T21512	hypothetical prote
709	25	59.5	377	2	E97696	altonate oxidored	782	25	59.5	510	2	G86430	T518.1 protein - A
710	25	59.5	381	1	A47327	selenoprotein P pr	783	25	59.5	512	2	A53219	hypothetical prote
711	25	59.5	384	1	BVECCX	membrane protein c	784	25	59.5	512	2	A53219	singed protein - f
712	25	59.5	384	2	B90678	membrane protein c	785	25	59.5	513	2	A85697	Na+/H+ antiporter
713	25	59.5	384	2	F85528	cyante transport	786	25	59.5	513	2	A99839	Na+/H+ antiporter
714	25	59.5	384	2	S73429	glycerol-3-phosphat	787	25	59.5	513	2	T38866	conserved hypothet
715	25	59.5	385	2	S22620	hypothetical prote	788	25	59.5	513	2	G64864	Na+/H+-exchangng
716	25	59.5	386	2	AE0576	probable aminotran	789	25	59.5	515	2	I49154	calctonin recepto
717	25	59.5	386	2	F64793	probable aminotran	790	25	59.5	522	2	AF0893	methy1-accepting c
718	25	59.5	386	2	C85559	probable aminotran	791	25	59.5	524	2	S38539	disintegrin-like m
719	25	59.5	386	2	G90708	probable aminotran	792	25	59.5	527	2	T15606	hypothetical prote
720	25	59.5	386	2	A97631	hypothetical 37.4k	793	25	59.5	531	2	S57752	hal3 protein - yea
721	25	59.5	394	2	D83541	probable acetate k	794	25	59.5	531	2	T08456	hypothetical prote
722	25	59.5	396	2	C98143	hypothetical prote	795	25	59.5	545	2	S28117	gas-vesicle operon
723	25	59.5	401	2	AC2113	alanine racemase l	796	25	59.5	547	2	T06758	probable galactose
724	25	59.5	402	2	B81075	nicotinate phospho	797	25	59.5	552	2	T11161	NADH2 dehydrogenas
725	25	59.5	402	2	AH0896	propionate kinase	798	25	59.5	553	2	S53080	hypothetical prote
726	25	59.5	403	2	T44737	probable membrane	799	25	59.5	558	2	S61604	probable membrane
727	25	59.5	406	2	B81391	zinc proteinase-11	800	25	59.5	565	2	S44330	malate oxidoreduct
728	25	59.5	413	2	E90226	hypothetical prote	801	25	59.5	567	2	A84748	hypothetical prote
729	25	59.5	416	2	D95231	diaminopimelate de	802	25	59.5	567	2	S25521	dymein intermediat
730	25	59.5	416	2	F98095	diaminopimelate de	803	25	59.5	570	1	HNNZAV	hemagglutinin-neur
731	25	59.5	416	2	B83271	conserved hypothet	804	25	59.5	571	1	I46328	hemagglutinin-neur
732	25	59.5	416	2	S33473	interleukin-1 rece	805	25	59.5	571	1	A36829	hemagglutinin-neur
733	25	59.5	416	2	A43561	homeotic protein m	806	25	59.5	571	1	B36829	hemagglutinin-neur
734	25	59.5	419	2	B81866	nicotinate phospho	807	25	59.5	571	1	C36829	hemagglutinin-neur
735	25	59.5	419	2	D86785	diaminopimelate de	808	25	59.5	571	1	D36829	hemagglutinin-neur
736	25	59.5	420	2	I51667	thrombin receptor	809	25	59.5	571	2	S40164	hemagglutinin-neur
737	25	59.5	421	2	B96522	hypothetical prote	810	25	59.5	574	2	T47566	hypothetical prote
738	25	59.5	425	2	T46355	hypothetical prote	811	25	59.5	574	2	JC7327	cytochrome P450 en
739	25	59.5	428	2	C83806	histidyl-tRNA synt	812	25	59.5	576	2	A48765	G protein-coupled
740	25	59.5	430	2	A56209	transcription fact	813	25	59.5	577	1	D46328	hemagglutinin-neur
741	25	59.5	430	2	T37549	hypothetical prote	814	25	59.5	577	1	F46328	hemagglutinin-neur
742	25	59.5	432	1	JN0317	protein-tyrosine-p	815	25	59.5	577	1	HNNZNC	hemagglutinin-neur
743	25	59.5	432	2	T08944	hypothetical prote	816	25	59.5	577	2	T41727	F-box domain prote
744	25	59.5	433	2	B81940	probable adenosylm	817	25	59.5	578	2	S51379	probable phosphoes
745	25	59.5	433	2	D81164	adenosylmethionine	818	25	59.5	580	2	T36393	L-asparatate oxidas
746	25	59.5	433	2	T48320	hypothetical prote	819	25	59.5	581	2	S45114	hemagglutinin-neur
747	25	59.5	434	2	AC2410	hypothetical prote	820	25	59.5	581	2	B86318	protein F15H18.9 l
748	25	59.5	436	2	T46895	acyl-coA dehydroge	821	25	59.5	582	2	A70755	hypothetical prote
749	25	59.5	437	2	JC4929	transcription fact	822	25	59.5	584	2	T45944	laccase-like prote
750	25	59.5	439	2	B70629	hypothetical prote	823	25	59.5	586	2	JC6500	hnf-3/forhead tra
751	25	59.5	440	2	D95952	probable glycosylt	824	25	59.5	589	2	JG0196	G protein-coupled
752	25	59.5	441	2	T10815	ribulose-bisphosph	825	25	59.5	590	1	A54372	protein-coupled
753	25	59.5	445	2	T41416	probable tyrosine-	826	25	59.5	590	2	A48277	G protein-coupled
754	25	59.5	447	2	S25817	hypothetical prote	827	25	59.5	591	2	G96592	probable beta-fruc
755	25	59.5	447	2	G64640	hypothetical prote	828	25	59.5	593	2	B90144	hypothetical prote
756	25	59.5	451	1	S49016	protein-tyrosine k	829	25	59.5	593	2	T43323	cell division cycl
757	25	59.5	454	1	T45297	tyrosine phenol-ly	830	25	59.5	596	2	S46001	probable amino aci
758	25	59.5	464	2	E96836	hypothetical prote	831	25	59.5	597	1	S37849	DNA intrastrand cr
759	25	59.5	466	2	B45693	neuraminidase - in	832	25	59.5	600	2	T39873	hypothetical prote

833	25	59.5	600	2	B83875	two-component sens	906	25	59.5	811	2	S04085	ovarian tumor prot
834	25	59.5	601	2	G96558	probable protein k	907	25	59.5	812	2	C97105	glycogen phosphory
835	25	59.5	602	2	S36475	El protein - human	908	25	59.5	813	2	T40632	translacion elonga
836	25	59.5	608	2	S51790	centromere protein	909	25	59.5	814	2	D82101	oxidoreductase, ac
837	25	59.5	609	2	S36481	El protein - human	910	25	59.5	815	2	I76775	O9 mannan biosynth
838	25	59.5	610	2	F86453	granule-bound star	911	25	59.5	819	2	T45690	receptor-like prot
839	25	59.5	614	2	T39215	dna repair protein	912	25	59.5	825	2	B89944	hypothetical prote
840	25	59.5	614	2	B71551	probable s/c prote	913	25	59.5	833	2	S45041	genome polyprotein
841	25	59.5	615	2	S75808	modulation protein	914	25	59.5	838	2	B38656	vacuolar proton pu
842	25	59.5	615	2	S42797	rad 26 protein - f	915	25	59.5	846	2	AD0379	probable vitulence
843	25	59.5	616	1	A46328	hemagglutinin-neur	916	25	59.5	849	2	T41085	probable ubiquitin
844	25	59.5	616	1	B46328	hemagglutinin-neur	917	25	59.5	851	2	T38173	probable phosphat
845	25	59.5	616	1	C46328	hemagglutinin-neur	918	25	59.5	856	2	S46750	aminopeptidase AAP
846	25	59.5	616	1	HNNZOD	hemagglutinin-neur	919	25	59.5	859	2	F69159	protoporphyrin IX
847	25	59.5	616	1	HNNZUI	hemagglutinin-neur	920	25	59.5	862	2	B36786	hypothetical prote
848	25	59.5	620	2	B64379	hypothetical prote	921	25	59.5	865	2	S69044	hypothetical prote
849	25	59.5	620	2	A70635	probable fadd31 pr	922	25	59.5	866	2	F88481	protein C16A3.1 [i
850	25	59.5	623	2	C84694	probable protein x	923	25	59.5	874	2	S37557	endopeptidase clp
851	25	59.5	625	2	T06184	sucrose-fructan 6-	924	25	59.5	875	2	AE0401	alanine-tRNA ligas
852	25	59.5	625	2	T26047	hypothetical prote	925	25	59.5	887	2	DEECPV	pyruvate dehydrog
853	25	59.5	629	2	JG0195	protein kinase DYR	926	25	59.5	887	2	AG0521	pyruvate dehydrog
854	25	59.5	630	2	T41307	conserved hypochet	927	25	59.5	887	2	F85494	pyruvate dehydrog
855	25	59.5	632	2	AF1889	hypothetical prote	928	25	59.5	887	2	F90643	pyruvate dehydrog
856	25	59.5	645	2	H96011	asparagine synthas	929	25	59.5	891	2	T38195	probable alpha,alp
857	25	59.5	646	2	T17631	hypothetical prote	930	25	59.5	894	2	T27007	hypothetical prote
858	25	59.5	647	2	T28214	probable nucleosid	931	25	59.5	922	1	S31164	endopeptidase clp
859	25	59.5	649	2	S42894	metalloproteinase	932	25	59.5	923	1	B35905	endopeptidase clp
860	25	59.5	650	1	JC1450	fibroblast growth	933	25	59.5	928	2	T52292	endopeptidase clp
861	25	59.5	656	2	E29826	hypothetical 72.4k	934	25	59.5	929	2	A44048	genome polyprotein
862	25	59.5	657	2	G86250	protein F25C20.14	935	25	59.5	931	2	T39143	hypothetical prote
863	25	59.5	658	2	T24851	hypothetical prote	936	25	59.5	944	2	S56936	vacuolar protein-s
864	25	59.5	660	2	H64671	conserved hypochet	937	25	59.5	948	2	T24445	hypothetical prote
865	25	59.5	661	1	VCMVCB	env polyprotein -	938	25	59.5	950	2	T15915	hypothetical prote
866	25	59.5	663	2	T40493	hnf-3/forhead tra	939	25	59.5	951	2	G82965	conserved hypochet
867	25	59.5	664	2	G90059	hypothetical prote	940	25	59.5	952	1	A32609	alpha-glucosidase
868	25	59.5	667	1	VCLJGL	env polyprotein pr	941	25	59.5	952	2	A99823	probable tail leng
869	25	59.5	668	2	T34317	protein-tyrosine-p	942	25	59.5	965	2	C89260	exonuclease ABC c
870	25	59.5	670	2	I65967	d1sintegrin-like m	943	25	59.5	969	2	B85843	probable tail comp
871	25	59.5	673	2	AC0073	2,4-dienoyl-CoA re	944	25	59.5	972	2	T50400	origin recognition
872	25	59.5	675	2	T01234	probable anthranil	945	25	59.5	977	2	H84469	hypothetical prote
873	25	59.5	691	2	T41724	probable adenosine	946	25	59.5	980	2	B86589	CT590 hypothetical
874	25	59.5	703	2	E69769	hypothetical prote	947	25	59.5	982	2	E72035	conserved hypochet
875	25	59.5	713	2	S01999	phenylalanine ammo	948	25	59.5	997	2	S33754	glutamate receptor
876	25	59.5	722	2	A82617	glycyl-tRNA synthe	949	25	59.5	1006	2	T41439	putative sulfite r
877	25	59.5	725	2	S60712	band-6-protein - h	950	25	59.5	1026	2	C90854	probable tail leng
878	25	59.5	727	2	T18600	hypothetical prote	951	25	59.5	1026	2	G90876	probable tail leng
879	25	59.5	730	2	T16455	hypothetical prote	952	25	59.5	1026	2	F85692	probable tail comp
880	25	59.5	733	2	T49679	probable branching	953	25	59.5	1030	2	I39987	lanthibiotic subtitl
881	25	59.5	735	2	G02937	fertilin beta - cr	954	25	59.5	1045	2	G69167	cobalamin biosynth
882	25	59.5	742	1	VGBEHT	glycoprotein H pre	955	25	59.5	1045	2	T16275	hypothetical prote
883	25	59.5	743	1	VGBEHC	glycoprotein H pre	956	25	59.5	1057	2	T18171	hugl protein - hum
884	25	59.5	754	2	JC4898	Down-syndrome-crit	957	25	59.5	1058	2	T08935	COP1-interacting p
885	25	59.5	758	2	E84933	5-methyltetrahydro	958	25	59.5	1071	2	T43255	tricorn proteinase
886	25	59.5	759	2	G81841	ribonucleoside-dip	959	25	59.5	1080	2	H90908	probable tail leng
887	25	59.5	759	2	B81101	ribonucleoside-dip	960	25	59.5	1086	2	T40354	hypothetical prote
888	25	59.5	761	1	RDECIJ	ribonucleoside-dip	961	25	59.5	1095	2	AD0301	conserved hypochet
889	25	59.5	761	2	AC0791	ribonucleoside-dip	962	25	59.5	1113	2	T000271	hypothetical prote
890	25	59.5	761	2	G85862	hypothetical prote	963	25	59.5	1167	2	E96563	DNA polymerase III
891	25	59.5	761	2	E91018	hypothetical prote	964	25	59.5	1186	2	T19334	hypothetical prote
892	25	59.5	761	2	S32629	ribonucleoside-dip	965	25	59.5	1187	2	T35661	probable chromosom
893	25	59.5	761	2	E82223	ribonucleoside-dip	966	25	59.5	1187	2	AI2044	pyruvate flavodoxi
894	25	59.5	762	2	AI0148	ribonucleoside-dip	967	25	59.5	1202	2	T17197	adenylate cyclase
895	25	59.5	766	2	G71845	probable role in o	968	25	59.5	1229	2	S42391	SIR3 protein - yea
896	25	59.5	768	2	T18461	hypothetical prote	969	25	59.5	1245	2	T42920	hypothetical prote
897	25	59.5	781	2	B64135	ribonucleoside-dip	970	25	59.5	1257	2	T09493	period protein hom
898	25	59.5	781	2	A86205	hypothetical prote	971	25	59.5	1257	2	T13957	A-type inclusion p
899	25	59.5	787	2	T16901	hypothetical prote	972	25	59.5	1284	1	MMVZAI	cobalamin biosynth
900	25	59.5	791	2	H96839	hypothetical prote	973	25	59.5	1329	2	C69048	DNA-directed RNA p
901	25	59.5	793	2	S68238	trp-1 protein - hu	974	25	59.5	1481	2	S78373	phosphoinositide 3
902	25	59.5	799	2	S18209	fibroblast growth	975	25	59.5	1506	2	JC5385	AAA protein L4171.
903	25	59.5	802	1	TVHUP4	protein F2265.28 l	976	25	59.5	1541	2	T02831	protoporphyrin IX
904	25	59.5	808	2	G86208	TRPC1 protein - hu	977	25	59.5	1561	1	C69145	hypothetical prote
905	25	59.5	810	2	I38361		978	25	59.5	1626	2	T29093	

979 25 59.5 1628 2 T38055 hypotheoretical prote
980 25 59.5 1668 1 C69224 cobatamin biosynth
981 25 59.5 1701 2 T43213 EMBP protein - ba
982 25 59.5 1708 2 A05205 hypotheoretical prote
983 25 59.5 1778 2 J70382 apolipoprotein B -
984 25 59.5 1787 2 D69195 protoporphyrin IX
985 25 59.5 1865 2 G86152 T7123.15 protein -
986 25 59.5 1867 2 T38348 probable 1,3-beta-
987 25 59.5 2116 1 ZLVNSY genome polyprotein
988 25 59.5 2131 2 S01446 hypotheoretical prote
989 25 59.5 2207 2 T24629 glutamate synthase
990 25 59.5 2216 2 S78398 hypotheoretical prote
991 25 59.5 2241 2 T16064 hypotheoretical prote
992 25 59.5 2301 1 GNNYTN genome polyprotein
993 25 59.5 2303 1 GNNYTM genome polyprotein
994 25 59.5 2303 1 GNNYTP genome polyprotein
995 25 59.5 2303 2 S13544 genome polyprotein
996 25 59.5 2351 2 G71415 hypotheoretical prote
997 25 59.5 2531 2 T31070 notch homolog - se
998 25 59.5 2670 2 A46719 inositol 1,4,5-tri
999 25 59.5 2671 2 A49873 inositol 1,4,5-tri
1000 25 59.5 2731 1 VF1H0H genome polyprotein

ALIGNMENTS

RESULT 1
T40438
hypotheoretical protein SPC0409.11 - fission yeast (Schizosaccharomyces pombe)
C/Species: Schizosaccharomyces pombe
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C/Accession: T40438
R/Lyne, M.H.; Rajadream, M.A.; Barrell, B.G.; Chillingworth, T.; Churcher, C.M.
submitted to the EMBL Data Library, August 1999
A/Reference number: 221929
A/Accession: T40438
A/Status: preliminary; translated from GB/EMBL/DDBU
A/Molecule type: DNA
A/Residues: 1-553 <LTY>
A/Cross-references: UNIPROT:Q9UUB3; UNIPARC:UPI000012EE95; EMBL:AL109822; PIDN:CB52613.
A/Experimental source: strain 972h-; cosmid c409
C/Genetics:
A/Gene: SPBC409.11
A/Map position: 2

Query Match 90.5%; Score 38; DB 2; Length 553;
Best Local Similarity 87.5%; Pred. No. 3.5;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
DB 304 HKYLSRT 311

RESULT 2
PH1054
Ig light chain V region (clone 202.135) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C/Accession: PH1054
R/Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marlon, T.N.
J. Exp. Med. 176, 761-779, 1992
A/Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B
A/Reference number: PH0971; MUID:92381444; PMID:1512540
A/Accession: PH1054
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-103 <TL>
A/Cross-references: UNIPARC:UPI0000176AAE
A/Experimental source: B cell, strain [NZB x NZW] F1
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: immunoglobulin

F;16-96/Domain: immunoglobulin homology <IMM>

Query Match 83.3%; Score 35; DB 2; Length 103;
Best Local Similarity 87.5%; Pred. No. 2.6;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
DB 95 HOYLSRT 102

RESULT 3

C82627
hypotheoretical protein XFI883 [imported] - Xylella fastidiosa (strain 9a5c)
C/Species: Xylella fastidiosa
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C/Accession: C82627
R/anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequenc
Nature 406, 151-157, 2000
A/Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A/Reference number: A82515; MUID:20365717; PMID:10910347
A/Note: for a complete list of authors see reference number A59328 below
A/Accession: C82627
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-88 <SIM>
A/Cross-references: UNIPROT:Q9PC98; UNIPARC:UPI0000CC287D; GB:AE004008; GB:AE003849; NID:
A/Experimental source: strain 9a5c
R/Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A]
Briiones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carreir, H.
as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to Genbank, June 2000

A/Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohme
J.D.; Junqueira, M.L.; Kemper, E.L.; Kiteajima, J.P.; Krieger, J.E.; Kuramse, E.E.; Laigre
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Martino, C.L.; Marques, M.V.; Martins, E.
A/Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A/Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tsubako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A/Reference number: A59328
A/Contents: annotation
C/Genetics:
A/Gene: XFI883

Query Match 78.6%; Score 33; DB 2; Length 88;
Best Local Similarity 75.0%; Pred. No. 3.9;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
DB 15 HOYLSRT 22

RESULT 4

B82572
P-protein XF2325 [imported] - Xylella fastidiosa (strain 9a5c)
C/Species: Xylella fastidiosa
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 05-Oct-2004
C/Accession: B82572
R/anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequenc
Nature 406, 151-157, 2000
A/Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A/Reference number: A82515; MUID:20365717; PMID:10910347
A/Note: for a complete list of authors see reference number A59328 below
A/Accession: B82572
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-374 <SIM>
A/Cross-references: UNIPARC:UPI0000007CA1; GB:AE004043; GB:AE003849; NID:G9107486; PIDN:
A/Experimental source: strain 9a5c
R/Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A]
Briiones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carreir, H

as-Neto, E.; Docena, C.; El-Dorty, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Perro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; From
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitzjima, J.P.; Krieger, J.E.; Kurame, E.B.; Laig
Chado, J.; Madeira, A.M.B.N.; Madeira, H.M.F.; Martino, C.L.; Marques, M.V.; Martins, E
A.; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A.; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tsubako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A:Reference number: A59328
A:Contents: annotation
A:Genetics:
C:Superfamily: bifunctional chorismate mutase/prephenate dehydratase (P-protein); prephe

Query Match 78.6%; Score 33; DB 2; Length 374;
Best Local Similarity 75.0%; Pred. No. 27;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 HOYLSRT 8
Db 186 HOYLSRTS 193

RESULT 5

T32516
hypothetical protein C44B12.7 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T32516
R:Lin-Mollam, A.
submitted to the EMBL Data Library, December 1997
A:Description: The sequence of C. elegans cosmid C44B12.
A:Reference number: Z21183
A:Accession: T32516
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-389 <TN>
A:Cross-references: UNIPROT:Q44147; UNIPARC:UPI000007P0B; EMBL:AF036692; PDB:AA88330.
A:Experimental source: strain Bristol N2; clone C44B12
C:Genetics:
A:Gene: CESP:C44B12.7
A:Map position: 4
A:Insertions: 122/3
C:Superfamily: Caenorhabditis elegans ZK1236.4 protein

Query Match 78.6%; Score 33; DB 2; Length 389;
Best Local Similarity 75.0%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 HOYLSRT 8
Db 30 HDPLSRT 37

RESULT 6

S53074
hypothetical protein YMR252c - yeast (Saccharomyces cerevisiae)

N:Alternate names: hypothetical protein YMR252c.06c
C:Species: Saccharomyces cerevisiae
C>Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C:Accession: S53074
R:Hunt, S.; Bowman, S.
submitted to the EMBL Data Library, March 1995
A:Reference number: S53069
A:Accession: S53074
A:Molecule type: DNA
A:Residues: 1-134 <HUN>
A:Cross-references: UNIPROT:Q04814; UNIPARC:UPI000013B931; EMBL:Z46639; NID:G732924; PID
C:Genetics:
A:Gene: MIP5:YMR252C
A:Cross-references: SGD:S0004865

A:Map position: 13R
C:Superfamily: Saccharomyces cerevisiae hypothetical protein YMR252c

Query Match 76.2%; Score 32; DB 2; Length 134;
Best Local Similarity 75.0%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 HOYLSRT 8
Db 65 HOYPSRT 72

RESULT 7

Q01722
3b protein - canine coronavirus

C:Species: canine coronavirus
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: Q01722
R:Horsburgh, B.C.; Brierley, I.; Brown, T.D.K.
J. Gen. Virol. 73, 2849-2862, 1992
A:Title: Analysis of a 9.6 kb sequence from the 3' end of canine coronavirus genomic RNA
A:Reference number: PQ0481; MUID:93057357; PMID:1431811
A:Accession: Q01722
A:Molecule type: mRNA
A:Residues: 1-251 <HOR>
A:Cross-references: UNIPARC:UPI000017A864; DBJ:DJ3096
A:Experimental source: strain Inaevc-1

Query Match 76.2%; Score 32; DB 2; Length 251;
Best Local Similarity 62.5%; Pred. No. 129;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HOYLSRT 8
Db 40 HOVSART 47

RESULT 8

JS0198
genome polyprotein - foot-and-mouth disease virus SAT3 (strain Bec 1/65) (fragment)

N:Contents: coat protein VP1; coat protein VP2; coat protein VP3; coat protein VP4; core
C:Species: Aphthovirus SAT3 (foot-and-mouth disease virus SAT3)
A>Note: host Artiodactyla (cloven-footed mammals)
C>Date: 31-Mar-1990 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
C:Accession: JS0198
R:Brown, A.L.; Campbell, R.O.; Clarke, B.E.
Gene 75, 225-234, 1989
A:Title: The nucleotide sequence of the structural-protein-coding region of foot-and-mou
A:Reference number: JS0198; MUID:89232753; PMID:2541051
A:Accession: JS0198
A:Molecule type: genomic RNA
A:Residues: 1-757 <BRO>
A:Cross-references: UNIPROT:Q65106; UNIPARC:UPI00001784D4
A>Note: the authors translated the codon CAC for residue 216 as Ser and codon TCG for res
C:Superfamily: foot-and-mouth disease virus genome polyprotein
C:Keywords: blocked amino end; coat protein; core protein; lipoprotein; myristylation; nc
F:1/Product: nonstructural protein p20a (fragment) #status predicted <VP4>
F:2-86/Product: coat protein VP4 #status predicted <VP4>
F:87-304/Product: coat protein VP2 #status predicted <VP2>
F:305-524/Product: coat protein VP3 #status predicted <VP3>
F:525-741/Product: coat protein VP1 #status predicted <VP1>
F:742-757/Product: core protein p2A (fragment) #status predicted <ACP>
F:2/Modified site: myristylated amino end (dly) (in mature form) #status predicted

Query Match 76.2%; Score 32; DB 2; Length 757;
Best Local Similarity 62.5%; Pred. No. 94;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 HOYLSRT 8
Db 231 HOYINRT 238

```
RESULT 9
S26337
ig light chain V region - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 20-Jun-2000
C/Accession: S26337; S78449
R/Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A/Title: Antibodies that are specific for a single amino acid interchange in a protein
A/Reference number: S26309; MUID:91341421; PMID:1908510
A/Accession: S26337
A/Molecule type: mRNA
A/Residues: 1-101 <STA>
A/Cross-references: UNIPARC:UPI00001769B0; EMBL:X59193
R/Caton, A.J.
submitted to the EMBL Data Library, April 1991
A/Reference number: S78447
A/Accession: S78449
A/Molecule type: mRNA
A/Residues: 1-60, 'T', 62-91, 'S', 93-101 <CAT>
A/Cross-references: UNIPARC:UPI0000115F7F; EMBL:X59193; NID:952323; PIND:CAA41903.1; PID
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F:8-88/Domain: immunoglobulin homology <IMM>

Query Match          73.8%; Score 31; DB 2; Length 101;
Best Local Similarity 75.0%; Pred. No. 18;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSRST 8
| | | | |
| | | | |
Db 87 HOYLSRST 94

RESULT 10
S51125
genome polypeptide - human rhinovirus 58 (fragment)
N/Contains: coat protein VP2
C/Species: human rhinovirus 58
C/Date: 19-Mar-1997 #sequence_revision 30-Jan-1998 #text_change 09-Jul-2004
C/Accession: S51125
R/Hornell, C.; Hughes, P.J.; Gama, R.E.; Stanway, G.
submitted to the EMBL Data Library, January 1995
A/Description: Sequence analysis of 21 human rhinovirus serotypes reveals two distinct
A/Reference number: S51121
A/Accession: S51125
A/Molecule type: genomic RNA
A/Residues: 1-112 <HOR>
A/Cross-references: UNIPROT:Q82090; UNIPARC:UPI00000F9777; EMBL:Z47570; NID:9623227; PID
C/Superfamily: poliovirus genome polypeptide
C/Keywords: coat protein; polypeptide
F:1-112/Product: coat protein VP2 (fragment) #status predicted <VP2>

Query Match          73.8%; Score 31; DB 2; Length 112;
Best Local Similarity 62.5%; Pred. No. 20;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSRST 8
| | | | |
| | | | |
Db 95 HOYLSRST 102

RESULT 11
S51124
genome polypeptide - human rhinovirus 7 (fragment)
N/Contains: coat protein VP2
C/Species: human rhinovirus 7
C/Date: 19-Mar-1997 #sequence_revision 30-Jan-1998 #text_change 09-Jul-2004
C/Accession: S51124
R/Hornell, C.; Hughes, P.J.; Gama, R.E.; Stanway, G.
submitted to the EMBL Data Library, January 1995
A/Description: Sequence analysis of 21 human rhinovirus serotypes reveals two distinct
A/Reference number: S51121
```

```
A/Accession: S51124
A/Molecule type: genomic RNA
A/Residues: 1-112 <HOR>
A/Cross-references: UNIPROT:Q82095; UNIPARC:UPI0000055DEC; EMBL:Z47564; NID:9623233; PID
C/Superfamily: poliovirus genome polypeptide
C/Keywords: coat protein; polypeptide
F:1-112/Product: coat protein VP2 (fragment) #status predicted <VP2>

Query Match          73.8%; Score 31; DB 2; Length 112;
Best Local Similarity 62.5%; Pred. No. 20;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSRST 8
| | | | |
| | | | |
Db 95 HOYLSRST 102

RESULT 12
A84605
hypothetical protein At2g21780 [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C/Accession: A84605
R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Sheth, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
Nuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A/Reference number: A84420; MUID:20083487; PMID:10617197
A/Accession: A84605
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-112 <STO>
A/Cross-references: UNIPROT:Q9SUJ21; UNIPARC:UPI00000A83CD; GB:AE002093; NID:9417272; PII
C/Genetics:
A/Map position: 2

Query Match          73.8%; Score 31; DB 2; Length 112;
Best Local Similarity 71.4%; Pred. No. 20;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYLSRST 7
| | | | |
| | | | |
Db 60 HEYSSR 66

RESULT 13
S25459
ribosomal protein PRT123, mitochondrial - yeast (Saccharomyces cerevisiae)
N/Alternate names: protein O3557; protein YOR158w
C/Species: Saccharomyces cerevisiae
C/Date: 23-Apr-1993 #sequence_revision 23-Apr-1993 #text_change 09-Jul-2004
C/Accession: S25459; S67046
R/Haefliger, P.; McMillin, T.W.; Fox, T.D.
Genetics 125, 495-503, 1990
A/Title: A genetic link between an mRNA-specific translational activator and the translat
A/Reference number: S25459; MUID:90337293; PMID:1696234
A/Accession: S25459
A/Molecule type: DNA
A/Residues: 1-318 <HAF>
A/Cross-references: UNIPROT:P17558; UNIPARC:UPI0000053092; EMBL:X52362; NID:94130; PIND:
R/Bordone, R.; Camases, A.; Madania, A.; Martin, R.P.; Poch, O.; Tarasov, I.A.; Winsor
submitted to the Protein Sequence Database, July 1996
A/Reference number: S67032
A/Accession: S67046
A/Molecule type: DNA
A/Residues: 1-318 <BOR>
A/Cross-references: UNIPARC:UPI0000053092; EMBL:Z75066; NID:91420392; PID:e252376; PID:91
A/Experimental source: strain S288C
C/Genetics:
A/Gene: SGD:PRT123
A/Cross-references: SGD:S0005684; MIPS:YOR158w
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A;Map position: 15R
A;Genome: nuclear
C;Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 73.8%; Score 31; DB 2; Length 318;
Best Local Similarity 62.5%; Pred. No. 62;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
|:|:|
Db 122 HEYLOKRT 129

RESULT 14

S44259

sucrose operon regulatory protein scr - *Pediococcus pentosaceus*

C;Species: *Pediococcus pentosaceus*
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C;Accession: S44259

R;Leenhoude, K.K.J.; Bolhuis, A.A.; Kok, J.J.; Venema, G.G.

submitted to the EMBL Data Library, April 1994

A;Description: The sucrose and raffinose operons of *Pediococcus pentosaceus* PPE1.0.

A;Reference number: S44252

A;Accession: S44259

A;Molecule type: DNA

A;Residues: 1-326 <LEE>

A;Cross-references: UNIPROT:P43472; UNIPARC:UPI00001356A9; EMBL:Z32771; NID:g493728; PIR

C;Genetics:

A;Gene: scrR

C;Superfamily: lac repressor

C;Keywords: DNA binding; transcription regulation

Query Match 73.8%; Score 31; DB 1; Length 326;
Best Local Similarity 75.0%; Pred. No. 63;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
|:|:|
Db 26 HGYLSSQT 33

RESULT 15

H89717

protein C18B12.2 [imported] - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 31-Dec-2004

C;Accession: H89717

R;anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A;Title: Genome sequence of the nematode *C. elegans*: a platform for investigating biology

A;Reference number: A75000; MUID:99069613; PMID:9851916 and www.sanger.ac.uk/Projects/C_eleg

A;Note: see website genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_eleg

A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

A;Accession: H89717

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-377 <STO>

A;Cross-references: UNIPROT:Q9U3P6; UNIPARC:UPI000017CB9E; GB:chr_X; PTDN:CAA20927.1; PIR

C;Genetics:

A;Gene: C18B12.2

A;Map position: X

C;Superfamily: glucagon receptor

Query Match 73.8%; Score 31; DB 2; Length 377;
Best Local Similarity 71.4%; Pred. No. 74;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYLSRT 7
|:|:|
Db 181 HOYISSQ 187

RESULT 16

T43170
probable triacylglycerol lipase (EC 3.1.1.3) - fission yeast (*Schizosaccharomyces pombe*)

C;Species: *Schizosaccharomyces pombe*

C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004

C;Accession: T43170

R;Yoshioaka, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H.

DNA Res. 4, 363-369, 1997

A;Title: Identification of open reading frames in *Schizosaccharomyces pombe* cDNAs.

A;Reference number: Z17323; MUID:98162722; PMID:9501991

A;Accession: T43170

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-413 <YOS>

A;Cross-references: UNIPROT:P78898; UNIPARC:UPI000016911F; EMBL:D89249; NID:g1749705; PIR

A;Experimental source: strain PR745

C;Superfamily: triacylglycerol lipase, lingual

C;Keywords: carboxylic ester hydrolase

Query Match 73.8%; Score 31; DB 2; Length 413;
Best Local Similarity 62.5%; Pred. No. 81;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
|:|:|
Db 65 HYYISST 72

RESULT 17

T39540

triacylglyceride lipase-cholesterol esterase - fission yeast (*Schizosaccharomyces pombe*)

C;Species: *Schizosaccharomyces pombe*

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C;Accession: T39540

R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Beck, A.; Reinhardt, R.

submitted to the EMBL Data Library, February 1998

A;Reference number: Z21862

A;Accession: T39540

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-443 <WOO>

A;Cross-references: UNIPROT:P78898; UNIPARC:UPI000006C8CB; EMBL:AL021748; PTDN:CAA16863.1

A;Experimental source: strain 972h-; cosmid c16A3

C;Genetics:

A;Gene: SPDB:SPBC16A3.12c

A;Map position: 2

A;Insertions: 11/2; 152/3; 282/1; 398/3

C;Superfamily: triacylglycerol lipase, lingual

Query Match 73.8%; Score 31; DB 2; Length 443;
Best Local Similarity 62.5%; Pred. No. 88;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
|:|:|
Db 54 HYYISST 61

RESULT 18

T19380

hypothetical protein C18B12.2 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T19380

R;Iloyd, C.

submitted to the EMBL Data Library, September 1998

A;Reference number: Z19116

A;Accession: T19380

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-454 <WIL>

A;Cross-references: UNIPROT:Q9U3P6; UNIPARC:UPI00000804F7; EMBL:AL031620; PTDN:CAA20927.2

A;Experimental source: clone C18B12

C;Genetics:

A:Gene: CESP:C18B12.2
A:Map position: X
A:Intons: 26/2; 67/1; 106/3; 144/3; 191/3; 292/3; 321/2; 363/3; 395/2; 440/3
C:Superfamily: glucagon receptor

Query Match 73.8%; Score 31; DB 2; Length 454;
Best Local Similarity 71.4%; Pred. No. 90;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 HQYLSR 7
|||:|
Db 258 HQYISSQ 264

RESULT 19

A35905
endopeptidase Clp (EC 3.4.21.-) ATP-binding chain cd4A, chloroplast [similarity] - tomato
N:Alternate names: ATP-dependent Clp proteinase regulatory chain A; CD4A protein
C:Species: Lycopersicon esculentum (tomato)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004

C:Accession: A35905
R:Gottesman, S.; Squires, C.; Pichersky, E.; Carrington, M.; Hobbs, M.; Mattick, J.S.; D
Proc. Natl. Acad. Sci. U.S.A. 87, 3513-3517, 1990
A:Title: Conservation of the regulatory subunit for the Clp ATP-dependent protease in pr
A:Reference number: A35905; MUID:30239044; PMID:2185473
A:Accession: A35905
A:Molecule type: DNA
A:Residues: 1-926 <GOT>
A:Cross-references: UNIPROT:P31541; UNIPARC:UPI0000127A85; GB:M52603; NID:G170432; PIND;

C:Genetics:
A:Gene: cd4A
A:Map position: 3
C:Function: allows clp to hydrolyze polypeptides and proteins, probably by a chaperon
e activity; ATP hydrolysis is required for Clp hydrolysis of proteins but not of smaller
C:Superfamily: endopeptidase Clp ATP-binding chain

C:Keywords: ATP; chloroplast; hydrolase; molecular chaperone; nucleotide binding; P-loop
F:302-309/Region: nucleotide-binding motif A (P-loop)
F:367-371/Region: nucleotide-binding motif B
F:646-653/Region: nucleotide-binding motif A (P-loop)
F:711-715/Region: nucleotide-binding motif B

F:308/Binding site: ATP (Lys) #status predicted
F:652/Binding site: ATP (Lys) #status predicted
Query Match 73.8%; Score 31; DB 1; Length 926;
Best Local Similarity 71.4%; Pred. No. 1.9e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HQYLSR 7
|||:|
Db 473 HQYISDR 479

RESULT 20

T52456
endopeptidase Clp ATP-binding chain C [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 09-Jul-2004

C:Accession: T52456
R:Nakabayashi, K.; Ito, M.; Kiyosue, T.; Shinozaki, K.; Watanabe, A.
Plant Cell Physiol. 40, 504-514, 1999
A:Title: Identification of clp genes expressed in senescing Arabidopsis leaves.
A:Reference number: Z22128; MUID:99356780; PMID:10427773

A:Accession: T52456
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-952 <NNK>
A:Cross-references: UNIPROT:O9SXJ7; UNIPARC:UPI00000AA4E7; EMBL:AB022324; NID:G5360573;
C:Experimental source: strain Columbia
C:Genetics:
A:Gene: clpC
C:Superfamily: endopeptidase Clp ATP-binding chain

Query Match 73.8%; Score 31; DB 2; Length 952;
Best Local Similarity 71.4%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HQYLSR 7
|||:|
Db 494 HQYISDR 500

RESULT 21

T49283
AtCipC - Arabidopsis thaliana
N:Alternate names: protein T21J18.140
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004

C:Accession: T49283
R:Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Mewes, H.W.; Rudd, S.;
submitted to the Protein Sequence Database, April 2000
A:Reference number: Z25021
A:Accession: T49283
A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-952 <RIB>
A:Cross-references: UNIPROT:Q9M226; UNIPARC:UPI00000A4D54; EMBL:AL132963; GSPDB:GN00061;
C:Experimental source: cultivar Columbia; BAC clone T21J18
C:Genetics:
A:Gene: ATSP:T21J18.140
A:Map position: 3
A:Intons: 212/1; 250/3; 291/3; 353/3; 425/3; 498/2; 523/3; 553/3

C:Superfamily: endopeptidase Clp ATP-binding chain
C:Keywords: ATP; molecular chaperone; nucleotide binding; P-loop
F:323-330/Region: nucleotide-binding motif A (P-loop)
F:390-395/Region: nucleotide-binding motif B
F:666-673/Region: nucleotide-binding motif A (P-loop)
F:734-739/Region: nucleotide-binding motif B

F:739/Binding site: ATP (Lys) #status predicted
F:672/Binding site: ATP (Lys) #status predicted
Query Match 73.8%; Score 31; DB 2; Length 952;
Best Local Similarity 71.4%; Pred. No. 2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HQYLSR 7
|||:|
Db 494 HQYISDR 500

RESULT 22

T29021
hypochemical protein W03F11.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000

C:Accession: T29021
R:Magg1, L.
submitted to the EMBL Data Library, May 1997
A:Description: The sequence of C. elegans cosmid W03F11.
A:Reference number: Z20554
A:Accession: T29021

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1280 <MAG>
A:Cross-references: UNIPARC:UPI000017610C; EMBL:AF003135; PIND:AA854148.1; GSPDB:GN00019;
A:Experimental source: strain Bristol N2; clone W03F11
C:Genetics:
A:Gene: CESP:W03F11.2

A:Map position: 1
A:Intons: 6/3; 62/2; 92/3; 160/3; 208/2; 245/1; 329/1; 371/1; 410/3; 451/3; 608/2; 634/3;
C:Superfamily: membrane-bound guanylate cyclase; guanylate cyclase catalytic domain homo3

Query Match 73.8%; Score 31; DB 2; Length 1280;
Best Local Similarity 75.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
|:|:|:|:
Db 872 HOYLSRTS 879

RESULT 23

151018
cobra venom factor precursor - monocled cobra
C/Species: Naja naja kaouthia, Naja naja siamensis (monocled cobra)
C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 17-Mar-2000
C/Accession: 151018
R/Fitzinger, D.C.; Bredhorst, R.; Vogel, C.W.
Proc. Natl. Acad. Sci. U.S.A. 91, 12775-12779, 1994
A/Title: Molecular cloning and derived primary structure of cobra venom factor.
A/Reference number: 151018; MUID:95108041; PMID:7809120
A/Accession: 151018
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-1642 <FRI>
A/Cross-references: UNIPARC:UPI00000F8186; EMBL:U09369; NID:9881914; PIDN:AAA68989.1; PT
C/Superfamily: alpha-2-macroglobulin

Query Match 73.8%; Score 31; DB 2; Length 1642;
Best Local Similarity 71.4%; Pred. No. 3.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSRT 7
|:|:|:|:
Db 1561 HOYLSRT 1567

RESULT 24

GNMY89
genome polypeptide - human rhinovirus 89
N/Contains: coat protein VP1; coat protein VP2; coat protein VP3; coat protein VP4; core
RNA-directed RNA polymerase (EC 2.7.7.48)
C/Species: human rhinovirus 89
C/Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 16-Jul-1999
R/Decker, M.; Stern, T.; Sommerhuber, W.; Neubauer, C.; Gruendler, P.; Fogt, I.; Blas
Proc. Natl. Acad. Sci. U.S.A. 84, 2605-2609, 1987
A/Title: Evolutionary relationships within the human rhinovirus genus: comparison of ser
A/Reference number: A29862; MUID:87204179; PMID:3033653
A/Accession: A29862
A/Molecule type: genomic RNA
A/Residues: 1-2164 <DUB>
A/Cross-references: UNIPARC:UPI000002C612; GB:M16248; NID:9330039; PIDN:AAA45762.1; PID:
C/Superfamily: poliovirus genome polypeptide
C/Keywords: coat protein; core protein; genome-linked protein; nucleotidyltransferase; F
F:1-69/Product: coat protein VP4 #status predicted <VP4>
F:70-536/Product: coat protein VP2 #status predicted <VP2>
F:537-574/Product: coat protein VP3 #status predicted <VP3>
F:575-572/Product: coat protein VP1 #status predicted <VP1>
F:873-1008/Product: core protein P2-A #status predicted <P2A>
F:1009-1103/Product: core protein P2-B #status predicted <P2B>
F:1104-1424/Product: core protein P2-C #status predicted <P2C>
F:1425-1500/Product: core protein P3-A #status predicted <P3A>
F:1501-1521/Product: genome-linked protein VPg #status predicted <VPg>
F:1522-1704/Product: proteinase #status predicted <PTS>
F:1705-2164/Product: RNA-directed RNA polymerase #status predicted <PMS>
F:1503/Binding site: phosphoryl-RNA (Tyr) (covalent) #status predicted

Query Match 73.8%; Score 31; DB 1; Length 2164;
Best Local Similarity 62.5%; Pred. No. 4.7e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
|:|:|:|:
Db 258 HOYLSRT 265

RESULT 25

RRXPTV
genome polypeptide - Tacaribe virus
N/Contains: RNA-directed RNA polymerase (EC 2.7.7.48)
C/Species: Tacaribe virus
C/Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 31-Dec-2004
C/Accession: A31468
R/Iapalucci, S.; Lopez, R.; Rey, O.; Lopez, N.; Franze-Fernandez, M.T.; Cohen, G.N.; Luc
Virology 170, 40-47, 1989
A/Title: Tacaribe virus L gene encodes a protein of 2210 amino acid residues.
A/Reference number: A31468; MUID:89243206; PMID:2718387
A/Accession: A31468
A/Molecule type: genomic RNA
A/Residues: 1-2210 <IAP>
A/Cross-references: UNIPROT:P20430; UNIPARC:UPI0000134847; GB:J04340; GB:M33513; NID:9335
C/Genetics:
A/Map position: segment L
C/Superfamily: RNA-directed RNA polymerase, Arenaviridae type
C/Keywords: nucleotidyltransferase

Query Match 73.8%; Score 31; DB 1; Length 2210;
Best Local Similarity 71.4%; Pred. No. 4.8e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYLSRT 7
|:|:|:|:
Db 1357 HOYLSRT 1363

RESULT 26

GNMY4F
genome polypeptide - foot-and-mouth disease virus A (strain A12)
N/Contains: coat protein VP1; coat protein VP2; coat protein VP3; coat protein VP4; core
tein VPg2; genome-linked protein VPg3; nonstructural protein p20a; proteinase (EC 3.4.-
C/Species: Aphthovirus A (foot-and-mouth disease virus A)
C/Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 16-Jul-1999
R/Robertson, B.H.; Grubman, M.J.; Weddell, J.N.; Moore, D.M.; Welsh, J.D.; Fischer, T.; I
J. Virol. 54, 651-660, 1985
A/Title: Nucleotide and amino acid sequence coding for polypeptides of foot-and-mouth di
A/Reference number: A25794; MUID:85211015; PMID:287518
A/Accession: A25794
A/Molecule type: genomic RNA
A/Residues: 1-2332 <ROB>
A/Cross-references: UNIPARC:UPI000011E113; GB:M10975; NID:9210306; PIDN:AAA42593.1; PID:
C/Superfamily: foot-and-mouth disease virus genome polypeptide
C/Keywords: coat protein; core protein; genome-linked protein; hydrolase; nonstructural
F:1-216/Product: nonstructural protein p20a #status predicted <NP2A>
F:217-285/Product: coat protein VP4 #status predicted <VP4>
F:286-503/Product: coat protein VP2 #status predicted <VP2>
F:504-723/Product: coat protein VP3 #status predicted <VP3>
F:724-937/Product: coat protein VP1 #status predicted <VP1>
F:938-953/Product: core protein X #status predicted <CPX>
F:954-1107/Product: core protein p14 #status predicted <CP14>
F:1108-1425/Product: core protein p41 #status predicted <CP41>
F:1426-1578/Product: core protein p19 #status predicted <CP19>
F:1579-1601/Product: genome-linked protein VPg1 #status predicted <VPg1>
F:1602-1625/Product: genome-linked protein VPg2 #status predicted <VPg2>
F:1626-1649/Product: genome-linked protein VPg3 #status predicted <VPg3>
F:1650-1862/Product: proteinase #status predicted <PTS>
F:1863-2332/Product: RNA-directed RNA polymerase #status predicted <RPP>

Query Match 73.8%; Score 31; DB 1; Length 2332;
Best Local Similarity 62.5%; Pred. No. 5.1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
|:|:|:|:
Db 430 HOYLSRT 437

RESULT 27

GNMY2F
genome polypeptide - foot-and-mouth disease virus A (strain A[10]61)

N/Contains: coat protein VP1; coat protein VP2; coat protein VP3; coat protein VP4; core protein p20a; nonstructural protein p20b; RNA-directed RNA polymerase (EC 2.7.7.48)
C/Species: Apathovirus A (foot-and-mouth disease virus A)
C/Date: 17-Dec-1992 #sequence_revision 28-Aug-1985 #text_change 16-Jul-1999
A/Accession: A93508; A91491; S30753
R/Carroll, A.R.; Rowlands, D.J.; Clarke, B.E.
Nucleic Acids Res. 12, 2461-2472, 1984
A/Title: The complete nucleotide sequence of the RNA coding for the primary translation
A/Reference number: A93508; MUID:84169547; PMID:6324120
A/Accession: A93508
A/Molecule type: genomic RNA
A/Residues: 1-2333 <CAR>
A/Cross-references: UNIPARC:UPI0000131E11; GB:X00429
R/Boothroyd, J.C.; Harris, T.J.R.; Rowlands, D.J.; Lowe, P.A.
Gene 17, 153-161, 1982
A/Title: The nucleotide sequence of cDNA coding for the structural proteins of foot-and-
A/Reference number: A91491; MUID:82211814; PMID:6282711
A/Accession: A91491
A/Molecule type: genomic RNA
A/Residues: 115-395, 'C', 397-631, 'L', 633-1048 <BOO>
A/Cross-references: UNIPARC:UPI0000170FB2; GB:V01130; NID:961048; PIDN:CAA24361.1; PID:9
R/Sengar, D.V.; Newton, S.E.; Rowlands, D.J.; Clarke, B.E.
Nucleic Acids Res. 15, 3005-3315, 1987
A/Title: All foot and mouth disease virus serotypes initiate protein synthesis at two se
A/Reference number: S30753; MUID:87203363; PMID:3033601
A/Accession: S30753
A/Molecule type: genomic RNA
A/Residues: 1-32 <SAN>
A/Cross-references: UNIPARC:UPI00000614D3; EMBL:M31575; NID:9210486; PIDN:AAA2655.1; PI
C/Superfamily: foot-and-mouth disease virus genome polyprotein
C/Keywords: coat protein; core protein; genome-linked protein; nonstructural protein; nu
F/1-204/Product: nonstructural protein p20a #status predicted <NPA>
F/205-286/Product: coat protein VP4 #status predicted <VP4>
F/287-504/Product: coat protein VP3 #status predicted <VP3>
F/505-725/Product: coat protein VP2 #status predicted <VP2>
F/726-937/Product: coat protein VP1 #status predicted <VP1>
F/938-1578/Product: genome-linked protein VPg1 #status predicted <GL1>
F/1579-1601/Product: genome-linked protein VPg2 #status predicted <GL2>
F/1602-1623/Product: genome-linked protein VPg3 #status predicted <GL3>
F/1626-1649/Product: genome-linked protein VPg4 #status predicted <GL4>
F/1650-1863/Product: nonstructural protein p20b #status predicted <NPB>
F/1864-2333/Product: RNA-directed RNA polymerase #status predicted <RRP>
Query Match 73.8%; Score 31; DB 1; Length 2333;
Best Local Similarity 62.5%; Pred. No. 5.1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 HOYLSRT 8
Db 431 HQFISPT 438
RESULT 28
S37077
genome polyprotein - foot-and-mouth disease virus A (strain A22/550 Azerbaijan 65)
N/Contains: coat protein VP1; coat protein VP2; coat protein VP3; coat protein VP4; core
tein VPg2; genome-linked protein VPg3; nonstructural protein p20a; proteinase (EC 3.4.-.
C/Species: Apathovirus A (foot-and-mouth disease virus A)
C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C/Accession: S37077; JN0413
R/Sosnovtsev, S.V.; Onischenko, A.M.; Petrov, N.A.; Kalashnikova, T.I.; Mamaeva, N.V.; D
submitted to the EMBL Data Library, August 1993
A/Reference number: S37077
A/Accession: S37077
A/Molecule type: genomic RNA
A/Residues: 1-2336 <SOS>
A/Cross-references: UNIPROT:P49303; UNIPARC:UPI0000131E17; EMBL:X74812; NID:9397965; PI
R/Onischenko, A.M.; Petrov, N.A.; Blinov, V.M.; Vassilenko, S.K.; Sandakchiev, L.S.; B
Bioorg. Khim. 12, 416-419, 1986
A/Title: The DNA-copy primary structure for the gene of the FMDV A22 serotype VP1-prot
A/Reference number: JN0413; MUID:86186952; PMID:2421736
A/Accession: JN0413
A/Molecule type: genomic RNA

A/Residues: 702-955 <ONI>
A/Cross-references: UNIPARC:UPI000005949; GB:M38362; NID:9210514; PIDN:AAA42664.1; PID:9
C/Superfamily: foot-and-mouth disease virus genome polyprotein
C/Keywords: coat protein; core protein; genome-linked protein; hydrolase; nonstructural I
F/1-211/Product: nonstructural protein p20a #status predicted <NPA>
F/218-286/Product: coat protein VP4 #status predicted <VP4>
F/287-504/Product: coat protein VP3 #status predicted <VP3>
F/505-724/Product: coat protein VP2 #status predicted <VP2>
F/725-938/Product: coat protein VP1 #status predicted <VP1>
F/939-954/Product: core protein X #status predicted <CPX>
F/955-1108/Product: core protein p14 #status predicted <C14>
F/1109-1426/Product: core protein p11 #status predicted <C11>
F/1427-1579/Product: core protein p19 #status predicted <C19>
F/1580-1602/Product: genome-linked protein VPg1 #status predicted <VG1>
F/1603-1626/Product: genome-linked protein VPg2 #status predicted <VG2>
F/1627-1650/Product: genome-linked protein VPg3 #status predicted <VG3>
F/1651-1863/Product: proteinase #status predicted <PRS>
F/1864-2333/Product: RNA-directed RNA polymerase #status predicted <RRP>
Query Match 73.8%; Score 31; DB 2; Length 2336;
Best Local Similarity 62.5%; Pred. No. 5.1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 HOYLSRT 8
Db 431 HQFISPT 438
RESULT 29
AE2014
hypothetical protein asr1667 [imported] - Nobtloc sp. (strain PCC 7120)
C/Species: Nobtloc sp. strain PCC 7120
A/Note: Nobtloc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C/Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C/Accession: AE2014
R/Kanezo, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takezawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A/Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anat
A/Reference number: AB1807; MUID:21595285; PMID:11759840
A/Accession: AE2014
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-79 <KUR>
A/Cross-references: UNIPROT:Q8YWE6; UNIPARC:UPI00000CE17F; GB:BA000019; PIDN:BA878033.1;
C/Genetics:
A/Experimental source: strain PCC 7120
A/Gene: asr1667
Query Match 71.4%; Score 30; DB 2; Length 79;
Best Local Similarity 75.0%; Pred. No. 23;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 HOYLSRT 8
Db 60 NSYLSRT 67
RESULT 30
S24203
protein 1 - Neisseria gonorrhoeae (fragment)
C/Species: Neisseria gonorrhoeae
C/Date: 22-Nov-1993 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
C/Accession: S24203
R/Jyga, A.M.; Huguenel, E.D.
submitted to the EMBL Data Library, February 1991
A/Description: Nucleotide and deduced amino acid sequence of protein I from P1A and P1B
A/Reference number: S24202
A/Accession: S24203
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-328 <LYG>
A/Cross-references: UNIPROT:Q51012; UNIPARC:UPI00000B5FAE; EMBL:X58074; NID:944922; PIDN:

C:Superfamily: outer membrane protein class 1

Query Match 71.4%; Score 30; DB 2; Length 328;
Best Local Similarity 71.4%; Pred. No. 1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 HOYLSR 7
|:|:|:|:
127 HRYLSAR 133

RESULT 31

G70628

probable ackA protein - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis

C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 05-Oct-2004

C/Accession: G70628

R/Collection: S.T.; Broesch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.

R/Conor, R.; Davies, R.; Devlin, K.; Fellwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A/Authors: Sgarbes, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A/Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A/Reference number: A70500; MUID:98295987; PMID:9634230

A/Accession: G70628

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-385 <COL>

A/Cross-references: UNIPROT:P96255; UNIPARC:UPI0000125297; GB:Z84724; GB:AL123456; NID:9

A/Experimental source: strain H37RV

C/Genetics:

A/Gene: ackA

C/Superfamily: acetate/propionate kinase

Query Match 71.4%; Score 30; DB 2; Length 385;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 HOYLSR 7
|:|:|:|:
168 HOYVSR 174

RESULT 32

S57689

hypothetical protein YGR225w - yeast (Saccharomyces cerevisiae)

N/Alternate names: hypothetical protein G8541

C/Species: Saccharomyces cerevisiae

C>Date: 19-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004

C/Accession: S57689; S64549; S63905

R/van der Aart, O.J.M.; Kleene, K.; Steensma, H.Y.

submitted to the EMBL Data Library, June 1995

A/Description: Sequence analysis of the 43 KB CRM1-YLM9-PET54-SM11-PH081-YHB4-PFK1 region

A/Reference number: S57680

A/Accession: S57689

A/Molecule type: DNA

A/Residues: 1-409 <VAM>

A/Cross-references: UNIPROT:P50082; UNIPARC:UPI000013AFAB; EMBL:X87941; NID:9886908; PII

R/van der Aart, O.J.M.; Steensma, H.Y.

submitted to the Protein Sequence Database, May 1996

A/Reference number: S64541

A/Accession: S64549

A/Molecule type: DNA

A/Residues: 1-409 <VAM>

A/Cross-references: UNIPARC:UPI000013AFAB; EMBL:Z73010; NID:G1333405; PIDN:CAA97253.1; F

A/Experimental source: strain S288C

R/van der Aart, O.J.M.; Kleene, K.; Steensma, H.Y.

Yeast 12, 385-390, 1996

A/Title: Sequence analysis of the 43 kb CRM1-YLM9-PET54-DIE2-SM11-PH081-YHB4-PFK1 region

A/Reference number: S63905; MUID:96267763; PMID:8701610

A/Accession: S63905

A/Status: nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-409 <VAF>

A/Cross-references: UNIPARC:UPI000013AFAB; EMBL:X87941; NID:9886908; PIDN:CAA61174.1; PII

A/Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1995

C/Genetics:

A/Gene: SGD:AMAI

A/Cross-references: SGD:S0003457

A/Map position: 7R

A/Note: YGR225W

Query Match 71.4%; Score 30; DB 2; Length 409;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 HOYLSR 7
|:|:|:|:
266 HOYLSR 272

RESULT 33

S77350

hypothetical protein sll1717 - Synechocystis sp. (strain PCC 6803)

C/Species: Synechocystis sp.

A/Variety: PCC 6803

C/Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

C/Accession: S77350

R/Kanehisa, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.

O, K.; Okumura, S.; Shimp, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda,

DNA Res. 3, 109-136, 1996

A/Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis

A/Reference number: S74322; MUID:97061201; PMID:8905231

A/Accession: S77350

A/Status: nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-511 <KAN>

A/Cross-references: UNIPROT:P73433; UNIPARC:UPI00000C0CF6; EMBL:D90906; GB:AB001339; NID

A/Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 71.4%; Score 30; DB 2; Length 511;
Best Local Similarity 71.4%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 HOYLSR 7
|:|:|:|:
62 HOYLSR 68

RESULT 34

T02466

probable ATP-dependent RNA helicase [imported] - Arabidopsis thaliana

N/Alternate names: hypothetical protein F4118.21

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 09-Jul-2004

C/Accession: T02466; B84895

R/Rounsley, S.D.; Lin, X.; Kechum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul,

submitted to the EMBL Data Library, August 1998

A/Description: Arabidopsis thaliana chromosome II BAC F4118 genomic sequence.

A/Reference number: Z14674

A/Accession: T02466

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-528 <ROU>

A/Cross-references: UNIPROT:O80838; UNIPARC:UPI000009D455; EMBL:AC004665; NID:G3386593; I

A/Experimental source: cultivar Columbia

R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.L.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A/Reference number: A84420; MUID:20083487; PMID:10617157

A/Accession: B84895

A/Status: preliminary

A:Molecule type: DNA
A:Residues: 1-528 <STO>
A:Cross-references: UNIPARC:UPI000009D455; GB:AE002093; NID:g3386613; P1DN:AAC28543.1; C
C:Genetics:
A:Gene: At2g45810; F4118.2
A:Map position: 2
C:Insertions: 126/2; 146/3; 225/1; 304/3; 388/3; 449/1; 478/3; 503/2
C:Superfamily: ATP-dependent RNA helicase DHH1
C:Keywords: ATP; nucleotide binding; P-loop
F:158-205/Region: nucleotide-binding motif A (P-loop)
F:299-304/Region: nucleotide-binding motif B
F:303-306/Region: DEAD motif

Query Match 71.4%; Score 30; DB 2; Length 528;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 QYLSRT 8
|||
38 QYLSRT 44

RESULT 35
E96722
hypothetical protein F20P5.27 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: E96722
R:Theologas, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huzar, L.
Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: E96722
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-574 <STO>
A:Cross-references: UNIPROT:O04545; UNIPARC:UPI00000AB863; GB:AE005173; NID:g2194138; P1
C:Genetics:
A:Gene: F20P5.27
A:Map position: 1

Query Match 71.4%; Score 30; DB 2; Length 574;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 HOYLSS 6
|||
397 HOYLSS 402

RESULT 36
AF0835
probable type I secretion protein, ATP-binding protein STY2877 [imported] - Salmonella
C:Species: Salmonella enterica subsp. enterica serovar Typh
A>Note: this species has also been called Salmonella typhi
C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 05-Oct-2004
C:Accession: AF0835
R:Parikh, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Churcher,
th, T.; Compton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001

A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AF0835
A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-718 <PAR>
A:Cross-references: UNIPARC:UPI000005A2EB; GB:AL513382; P1DN:CAD05869.1; PID:g16503844; C
C:Genetics:
A:Gene: STY2877
C:Superfamily: ATP dependent ABC transporter

Query Match 71.4%; Score 30; DB 2; Length 718;
Best Local Similarity 62.5%; Pred. No. 2.4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 HOYLSSRT 8
|||
665 HOYLSSRT 672

RESULT 37
E98121
hypothetical protein clpC-truncation [imported] - Streptococcus pneumoniae (strain R6)
C:Species: Streptococcus pneumoniae
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C:Accession: E98121
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; Dehoff, B.S.; E
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001

A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: E98121
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-762 <KUR>
A:Cross-references: UNIPROT:Q8DN00; UNIPARC:UPI00000E3764; GB:AE007317; P1DN:ALU00802.1;
C:Genetics:
A:Gene: clpC-truncation
C:Superfamily: endopeptidase Clp ATP-binding chain

Query Match 71.4%; Score 30; DB 2; Length 762;
Best Local Similarity 71.4%; Pred. No. 2.5e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 HOYLSSR 7
|||
406 HOYLSSR 412

RESULT 38
S13410
chloride channel protein - marbled electric ray
C:Species: Torpedo marmorata (marbled electric ray)
C>Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S13410
R:Jentsch, T.J.; Steinmeyer, K.; Schwarz, G.
Nature 348, 510-514, 1990

A:Title: Primary structure of Torpedo marmorata chloride channel isolated by expression
A:Reference number: S13410; MUID:91061906; PMID:2174129
A:Accession: S13410
A:Molecule type: mRNA
A:Residues: 1-805 <JEN>
A:Cross-references: UNIPROT:P21564; UNIPARC:UPI0000127992; EMBL:X55758; NID:g64424; P1DN
A:Experimental source: electric organ
C:Complex: dimer
C:Function:
A:Description: chloride channel
A>Note: voltage-gated channel
C:Keywords: channel-forming protein; chloride channel; transmembrane protein
F:52-72/Domain: transmembrane #status predicted <TM01>
F:93-116/Domain: transmembrane #status predicted <TM02>
F:140-161/Domain: transmembrane #status predicted <TM03>
F:169-188/Domain: transmembrane #status predicted <TM04>
F:201-225/Domain: transmembrane #status predicted <TM05>
F:240-257/Domain: transmembrane #status predicted <TM06>

F;285-304/Domain: transmembrane #status predicted <TM07>
 F;326-349/Domain: transmembrane #status predicted <TM08>
 F;390-411/Domain: transmembrane #status predicted <TM09>
 F;415-437/Domain: transmembrane #status predicted <TM10>
 F;459-480/Domain: transmembrane #status predicted <TM11>
 F;487-507/Domain: transmembrane #status predicted <TM12>
 F;722-769/Domain: CBS homology <CBS>
 F;747-768/Domain: transmembrane #status predicted <TM13>

Query Match 71.4%; Score 30; DB 2; Length 805;
 Best Local Similarity 62.5%; Pred. No. 2.7e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSSRT 8
 Db 138 HEYLTLRT 145

RESULT 39

D95256

ATP-dependent Clp protease, ATP-binding chain [imported] - Streptococcus pneumoniae (S

C/Species: Streptococcus pneumoniae
 C/Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004

C/Accession: D95256

R;Title: H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
 on, J.D.; Umeyam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfel,
 nson, T.D.; Hickey, E.K.; Holt, I.E.
 Science 293, 498-506, 2001

A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
 A;Title: Complete genome sequence of a virulent isolate of Streptococcus pneumoniae.
 A;Reference number: A95000; MUID:21357209; PMID:11463916

A/Accession: D95256

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-810 <KUR>

A/Cross-references: UNIPROT:Q97N72; UNIPARC:UPI0000051B6B; GB:AE005672; PIDD:AAK76245.1;

A/Experimental source: strain TIGR4

C/Genetics:

A/Gene: SP2194

C;Superfamily: endopeptidase clp ATP-binding chain

Query Match 71.4%; Score 30; DB 2; Length 810;
 Best Local Similarity 71.4%; Pred. No. 2.7e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYLSSRT 7
 Db 406 HRYLTSR 412

RESULT 40

S19725

voltage-gated chloride channel protein - Pacific electric ray

C/Species: Torpedo californica (Pacific electric ray)

C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C/Accession: S19725; S16859

R;O'Neill, G.P.; Grygorczyk, R.; Adam, M.; Ford-Hutchinson, A.W.
 Biochim. Biophys. Acta 1129, 131-134, 1991

A;Title: The nucleotide sequence of a voltage-gated chloride channel from the electric c

A/Reference number: S19725; MUID:92096455; PMID:11721838

A/Accession: S19725

A/Molecule type: mRNA

A/Residues: 1-810 <ONE>

A/Cross-references: UNIPROT:P35522; UNIPARC:UPI00001714BD; EMBL:X60433; NID:G64405; PIDD:

C/Keywords: transmembrane protein

F;52-72/Domain: transmembrane #status predicted <TM1>

F;93-116/Domain: transmembrane #status predicted <TM2>

F;140-161/Domain: transmembrane #status predicted <TM3>

F;169-188/Domain: transmembrane #status predicted <TM4>

F;201-225/Domain: transmembrane #status predicted <TM5>

F;240-257/Domain: transmembrane #status predicted <TM6>

F;285-304/Domain: transmembrane #status predicted <TM7>

F;390-411/Domain: transmembrane #status predicted <TM9>
 F;415-437/Domain: transmembrane #status predicted <TM10>
 F;459-480/Domain: transmembrane #status predicted <TM11>
 F;487-507/Domain: transmembrane #status predicted <TM12>
 F;727-774/Domain: CBS homology <CBS>
 F;752-773/Domain: transmembrane #status predicted <TM13>

Query Match 71.4%; Score 30; DB 2; Length 810;
 Best Local Similarity 62.5%; Pred. No. 2.7e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSSRT 8
 Db 138 HEYLTLRT 145

RESULT 41

B89472

protein ZC53.4 [imported] - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C/Accession: B89472

R;Anonymous, The C. elegans Sequencing Consortium.
 Science 282, 2012-2018, 1998

A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology

A;Reference number: A75000; MUID:99069613; PMID:9851916

A;Note: see websties genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C_eleg

A;Note: published extra appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

A/Accession: B89472

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-855 <STO>

A/Cross-references: UNIPROT:Q23371; UNIPARC:UPI000017CB78; GB:chr_X; PIDD:AA52621.1; PIR

C/Genetics:

A/Gene: ZC53.4

A/Map position: X

Query Match 71.4%; Score 30; DB 2; Length 855;
 Best Local Similarity 71.4%; Pred. No. 2.9e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYLSSRT 7
 Db 690 HOYLAQ 696

RESULT 42

T16204

hypothetical protein F28F5.3 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 04-Mar-2000

C/Accession: T16204

R;Pauley, A.
 submitted to the EMBL Data Library, April 1994

A;Description: The sequence of C. elegans cosmid F28F5.

A/Reference number: Z18477

A/Accession: T16204

A/Status: preliminary; translated from GB/EMBL/DDBU

A/Molecule type: DNA

A/Residues: 1-899 <PAU>

A/Cross-references: UNIPARC:UPI0000173B3; EMBL:U00045; NID:G470353; PID:G470357; PIDD:AV

C;Superfamily: Caenorhabditis elegans hypothetical protein F28F5.3

Query Match 71.4%; Score 30; DB 2; Length 899;
 Best Local Similarity 83.3%; Pred. No. 3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYLSS 6
 |||:|

Db 219 HOYMSS 224

RESULT 43

T18197

Reverse transcriptase-like protein - silkworm

C/Species: Bombyx mori (silkworm)

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C/Accession: T18197

R/Burke, W.D.; Calalang, C.C.; Eickbush, T.H.

Mol. Cell. Biol. 7, 2221-2230, 1987

A/Title: The site-specific ribosomal insertion element type II of Bombyx mori (R2Bm) con

A/Reference number: Z18810; MUID:87257937; PMID:2439905

A/Accession: T18197

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-1114 <BUR>

A/Cross-references: UNIPARC:UPI000011DE36; EMBL:M16558; NID:g156011; PID:g903695; PIDN:A

Query Match 71.4%; Score 30; DB 2; Length 1114;

Best Local Similarity 62.5%; Pred. No. 3.6e+02;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HOYLSRT 8

Db 677 HHYLTXT 684

RESULT 44

T30283

polyketide synthase - Streptomyces sp. (strain MA6548)

C/Species: Streptomyces sp.

A/Variety: strain MA6548

C/Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-May-2004

C/Accession: T30283

R/McMeadl, H.; Cai, S.J.; Shafiee, S.J.; Elliston, K.O.

Eur. J. Biochem. 244, 74-80, 1997

A/Title: Structural organization of a multifunctional polyketide synthase involved in th

A/Reference number: Z20806; MUID:97217427; PMID:9063448

A/Accession: T30283

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-6420 <NOT>

A/Cross-references: UNIPARC:UPI000011020C; EMBL:Y10438; NID:el014806; PID:e290681; PIDN:

C/Genetics:

A/Note: EkDa

C/Keywords: carrier protein

F:51-433/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS1>

F:1930-2325/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS2>

F:3391-3462/Domain: acyl carrier protein homology <ACP1>

F:3505-3900/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS3>

F:3583-4254/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT1>

F:5307-5376/Domain: acyl carrier protein homology <ACP2>

F:5431-5831/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS4>

F:5932-6206/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT2>

F:6293-6364/Domain: acyl carrier protein homology <ACP3>

Query Match 71.4%; Score 30; DB 2; Length 6420;

Best Local Similarity 75.0%; Pred. No. 2.4e+03;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HOYLSRT 8

Db 3160 HTYLSRT 3167

RESULT 45

T10351

hypothetical protein 82 - Orgyia pseudotsugata nuclear polyhedrosis virus

C/Species: Orgyia pseudotsugata nuclear polyhedrosis virus, OPMNV

C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000

C/Accession: T10351

R/Ahrens, C.A.; Russell, R.R.; Funk, C.J.; Evans, J.; Harwood, S.; Rohrmann, G.F.

Virology 229, 381-399, 1997

A/Title: The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhedrosis

A/Reference number: Z17011; MUID:97271300; PMID:9126251

A/Accession: T10351

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-104 <NR>

A/Cross-references: UNIPARC:UPI000006183E; EMBL:U75930; NID:g2934903; PIDN:AAC59081.1; P1

C/Superfamily: hypothetical protein 312

Query Match 69.0%; Score 29; DB 2; Length 104;

Best Local Similarity 83.3%; Pred. No. 50;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HOYLS 6

Db 94 HOYLSA 99

RESULT 46

T44160

hypothetical protein U13 [imported] - human herpesvirus 6 (strain Z29)

C/Species: human herpesvirus 6

A/Variety: strain Z29

C/Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 02-Jun-2000

C/Accession: T44160

R/Dominguez, G.; Dambaugh, T.R.; Stamey, F.R.; Dewhurst, S.; Inoue, N.; Pellett, P.E.

J. Virol. 73, 8040-8052, 1999

A/Title: Human herpesvirus 6B genome sequence: coding content and comparison with human 1

A/Reference number: Z22734; MUID:99412318; PMID:10482553

A/Accession: T44160

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-107 <DOM>

A/Cross-references: UNIPARC:UPI00000F998B; EMBL:A157706; PIDN:AA049628.1

A/Experimental source: strain Z29; variant B

C/Genetics:

A/Note: U13

Query Match 69.0%; Score 29; DB 2; Length 107;

Best Local Similarity 50.0%; Pred. No. 52;

Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HOYLSRT 8

Db 43 HDYIASRT 50

RESULT 47

T09305

EBF1 protein - human herpesvirus 6 (strain U1102)

C/Species: human herpesvirus 6

C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C/Accession: T09305

R/Nicholas, J.; Martin, M.

J. Virol. 68, 597-610, 1994

A/Title: Nucleotide sequence analysis of a 38.5-kilobase-pair region of the genome of hun

A/Reference number: Z16644; MUID:94118404; PMID:8289364

A/Accession: T09305

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-107 <NIC>

A/Cross-references: UNIPROT:Q69036; UNIPARC:UPI00000EC340; EMBL:L25528; NID:g451932; PIDN

C/Genetics:

A/Gene: EBF1

Query Match 69.0%; Score 29; DB 2; Length 107;

Best Local Similarity 50.0%; Pred. No. 52;

Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HOYLSRT 8

Db 44 HDYIASRT 51

RESULT 48

T43973

hypothetical protein U13 [imported] - human herpesvirus 6 (strain HST)

C/Species: human herpesvirus 6

A/Variety: strain HST

C/Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004

C/Accession: T43973

R/Hatch, Y.; Makai, T.; Nakano, K.; Kagawa, M.; Chen, J.; Mori, Y.; Sunagawa, T.; Kawa

J.; Virol. 73, 8053-8063, 1999

A/Title: Comparison of the complete DNA sequences of human herpesvirus 6 variants A and

A/Reference number: 222732; MUID:99412319; PMID:10482554

A/Accession: T43973

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-107 <HSE>

A/Cross-references: UNIPROT:Q9WT51; UNIPARC:UPI000000F647D; EMBL:AB021506; NID:g4995977;

A/Experimental source: strain HST; pop. variant B

C/Genetics:

A/Note: U13

Query Match

Best Local Similarity 69.0%; Score 29; DB 2; Length 107;

Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 HOYLSRT 8

Db 43 HRHLSRT 50

RESULT 49

A35881

histone H2A.2 - human

C/Species: Homo sapiens (man)

C/Date: 23-Oct-1990 #sequence_revision 23-Oct-1990 #text_change 31-Dec-2004

C/Accession: A35881; S03643

R/Hatch, C.L.; Bonner, W.M.

J. Biol. Chem. 265, 15211-15218, 1990

A/Title: The human histone H2A.2 gene. Sequence and regulation.

A/Reference number: A35881; MUID:90368704; PMID:1697587

A/Accession: A35881

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-128 <HRT1>

A/Cross-references: UNIPROT:P17317; UNIPARC:UPI0000000F6F; GB:M33917

R/Hatch, C.L.; Bonner, W.M.

Nucleic Acids Res. 16, 1113-1124, 1988

A/Title: Sequence of cDNAs for mammalian H2A.2, an evolutionarily diverged but highly co

A/Reference number: S03642; MUID:88143983; PMID:3344202

A/Accession: S03643

A/Molecule type: mRNA

A/Residues: 1-128 <HRT2>

A/Cross-references: UNIPARC:UPI0000000F6F; EMBL:X52317; NID:g31974; PIDN:CA36553.1; PII

A/Map position: 4q24-4q24

C/Superfamily: histone H1

C/Keywords: DNA binding; nucleus

Query Match

Best Local Similarity 69.0%; Score 29; DB 2; Length 128;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 HOYLSRT 8

Db 34 HRHLSRT 41

RESULT 50

S03642

histone H2A.2 - bovine

C/Species: Bos primigenius taurus (cattle)

C/Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 31-Dec-2004

C/Accession: S03642

R/Hatch, C.L.; Bonner, W.M.

Nucleic Acids Res. 16, 1113-1124, 1988

A/Title: Sequence of cDNAs for mammalian H2A.2, an evolutionarily diverged but highly co

A/Reference number: S03642; MUID:88143983; PMID:3344202

A/Accession: S03642

A/Molecule type: mRNA

A/Residues: 1-128 <HRT>

A/Cross-references: UNIPROT:P17317; UNIPARC:UPI0000000F6F; EMBL:X52318; NID:g409; PIDN:CA

A/Note: the authors translated the codon GAC for residue 9 as Ala and CAG for residue 22

C/Superfamily: histone H1

C/Keywords: DNA binding; nucleus

Query Match

Best Local Similarity 69.0%; Score 29; DB 2; Length 128;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 HOYLSRT 8

Db 34 HRHLSRT 41

Search completed: May 4, 2006, 13:08:02

Job time : 51.4286 secs

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GenCore version 5.1.7
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OM-protein - protein search, using sw model

Run on: May 4, 2006, 12:46:39 ; Search time 74.9206 Seconds
(without alignments)
75.336 Million cell updates/sec

Title: US-10-700-632-6

Perfect score: 42

Sequence: 1.HOYLSSRT 8

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

1: uniprot_05.80.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	90.5	553	1 MEU18_SCHPO	Q9ub3 schizosacch
2	37	88.1	155	1 IL21_HUMAN	Q9hba4 homo sapien
3	35	83.3	277	2 08RTX2_LACP	08RTX2 lactobacill
4	34	81.0	270	2 02TX2_LEPIC	02TX2 leptospira
5	34	81.0	270	2 08F192_LEPIN	08F192 leptospira
6	34	81.0	270	2 054X5_DICDI	054X5 dictyostell
7	33	78.6	88	2 09PC98_XYLPA	09PC98 xylella fas
8	33	78.6	340	2 068648_PSEPU	068648 pseudomonas
9	33	78.6	374	2 087BUI_XYLPA	087BUI xylella fas
10	33	78.6	374	2 09PB20_XYLPA	09PB20 xylella fas
11	33	78.6	389	2 044147_CAEEL	044147 caenorhabdi
12	33	78.6	447	2 06PX52_DROMA	06PX52 drosophila
13	33	78.6	447	2 06PX53_DROMA	06PX53 drosophila
14	33	78.6	547	2 05SMC9_CRYNE	05SMC9 cryptococcu
15	33	78.6	547	2 05K864_CRYNE	05K864 cryptococcu
16	33	78.6	617	2 05ARR9_EMENT	05ARR9 aspergillus
17	33	78.6	734	2 06F028_CANCA	06F028 candida gla
18	33	78.6	1035	2 06COM5_KLJUA	06COM5 kluyveriomy
19	33	78.6	2024	2 07NDY7_CHRYO	07NDY7 chromobacte
20	33	78.6	2210	2 05PY79_JUNIN	05PY79 junin arena
21	33	78.6	2210	2 0642U5_JUNIN	0642U5 junin arena
22	33	78.6	2210	2 06IVU4_JUNIN	06IVU4 junin arena
23	33	78.6	2210	2 06UY74_JUNIN	06UY74 junin arena
24	32	76.2	99	2 09Q0B0_NPVAG	09Q0B0 antiscaria
25	32	76.2	99	2 06VTR5_NPVCD	06VTR5 choristoneu
26	32	76.2	134	1 YM86_YEAST	004814 saccharomye
27	32	76.2	136	2 08LCK9_ARATH	08LCK9 arabidopsis
28	32	76.2	136	2 09FKW8_ARATH	09FKW8 arabidopsis
29	32	76.2	172	2 04VOT7_BACCA	04VOT7 bacillus ce
30	32	76.2	178	2 09QEV7_GCOKO	09QEV7 porcine res
31	32	76.2	195	2 04HY01_GIBZE	04HY01 gibberella

32	32	76.2	212	2 09F3M7_STRCO	09F3M7 streptomyc
33	32	76.2	225	2 08ODJ1_9HIV1	08ODJ1 human immun
34	32	76.2	229	2 09QEV6_GCOKO	09QEV6 porcine res
35	32	76.2	250	1 VNS3_CTCAR	03685 canine ente
36	32	76.2	270	2 082G95_STRAM	082G95 streptomyc
37	32	76.2	271	2 09FCG3_STRCO	09FCG3 streptomyc
38	32	76.2	296	2 08ED48_SHEON	08ED48 shewanella
39	32	76.2	299	2 05P9T3_ANAMM	05P9T3 anaplasma m
40	32	76.2	312	2 07N1J4_GLOVI	07N1J4 gloeobacter
41	32	76.2	444	2 04PPI1_USTMA	04PPI1 ustilago ma
42	32	76.2	453	2 05BGP9_EMENT	05BGP9 aspergillus
43	32	76.2	466	2 073V57_MYCPA	073V57 mycobacteri
44	32	76.2	493	2 04JBW9_SULAC	04JBW9 sulfolobus
45	32	76.2	711	2 06NVJ4_BRARE	06NVJ4 brachydanio
46	32	76.2	758	2 065106_9PICO	065106 foot-and-mo
47	32	76.2	850	2 054Z08_DICDI	054Z08 dictyostell
48	32	76.2	861	2 080G12_9ENTM	080G12 human enter
49	32	76.2	1353	2 04PH70_USTMA	04PH70 ustilago ma
50	32	76.2	1401	2 05KTM2_BOMMO	05KTM2 bombyx mori
51	32	76.2	2335	2 06PMT3_9PICO	06PMT3 foot-and-mo
52	32	76.2	2340	2 06PMU2_9PICO	06PMU2 foot-and-mo
53	31	73.8	75	2 08RIN6_BACFT	08RIN6 bacillus st
54	31	73.8	103	2 06XQ15_9VIRU	06XQ15 sabia virus
55	31	73.8	108	2 08LDT7_ARATH	08LDT7 arabidopsis
56	31	73.8	112	2 09S3J21_ARATH	09S3J21 arabidopsis
57	31	73.8	112	2 082090_9PICO	082090 human rhino
58	31	73.8	112	2 082095_9PICO	082095 human rhino
59	31	73.8	113	2 06XQH1_TACY	06XQH1 tacaribe vi
60	31	73.8	124	2 08RWS0_ARATH	08RWS0 arabidopsis
61	31	73.8	133	2 082PT2_STRAM	082PT2 streptomyc
62	31	73.8	135	2 07R5E4_GIALA	07R5E4 giardia lam
63	31	73.8	154	2 042192_ARATH	042192 arabidopsis
64	31	73.8	192	2 0596U4_9HIV1	0596U4 human immun
65	31	73.8	192	2 05EBT6_9HIV1	05EBT6 human immun
66	31	73.8	192	2 06PR13_9HIV1	06PR13 human immun
67	31	73.8	192	2 04JG94_9HIV1	04JG94 human immun
68	31	73.8	192	2 04JGK4_9HIV1	04JGK4 human immun
69	31	73.8	206	2 073CWO_BACCI	073CWO bacillus ce
70	31	73.8	217	2 091URS_9HIV1	091URS human immun
71	31	73.8	218	2 0650J5_9PICO	0650J5 foot-and-mo
72	31	73.8	252	1 TPIS_BUCBP	059462 buchnera ap
73	31	73.8	260	2 09YWP8_9RBDV	09YWP8 kadipiro vi
74	31	73.8	290	2 05RMZ4_BRARE	05RMZ4 brachydanio
75	31	73.8	318	1 RTPT_YEAST	017558 saccharomye
76	31	73.8	326	1 SCRR_PBDPE	043472 pediococcus
77	31	73.8	326	2 082V7_LACP	082V7 lactobacill
78	31	73.8	340	2 05DYW6_VIBF1	05DYW6 vibrio fisc
79	31	73.8	342	2 07NSN7_PHOIL	07NSN7 photorhabdu
80	31	73.8	346	2 05S827_CRYNE	05S827 cryptococcu
81	31	73.8	346	2 05KGH9_CRYNE	05KGH9 cryptococcu
82	31	73.8	350	2 0914H8_9VIRU	0914H8 sulfolobus
83	31	73.8	361	2 09BHE1_DROME	09BHE1 drosophila
84	31	73.8	375	1 DPO3B_SYNEP	052023 synecchococ
85	31	73.8	390	2 05N1Y4_SYNEP	05N1Y4 synecchococ
86	31	73.8	398	1 ACKRA_CORER	08fmb7 corynebacte
87	31	73.8	400	2 087954_XANCA	087954 xanthomonas
88	31	73.8	401	1 ACKA_HEHP	07y413 helicobacte
89	31	73.8	402	2 05H080_XANOR	05H080 xanthomonas
90	31	73.8	402	2 08PLY6_XANAC	08PLY6 xanthomonas
91	31	73.8	406	2 04UTD0_XANCP	04UTD0 xanthomonas
92	31	73.8	406	2 08PA96_XANCP	08PA96 xanthomonas
93	31	73.8	443	2 078898_SCHPO	078898 schizosacch
94	31	73.8	444	2 04W913_ASPFU	04W913 aspergillus
95	31	73.8	446	2 04WKC6_ASPFU	04WKC6 aspergillus
96	31	73.8	454	2 09U3P6_CAEEL	09U3P6 caenorhabdi
97	31	73.8	479	2 04SY54_TERNG	04SY54 tetraodon n
98	31	73.8	524	2 04SCS5_TERNG	04SCS5 tetraodon n
99	31	73.8	554	2 09U916_9DIPT	09U916 chrysops sp
100	31	73.8	558	2 09JZM4_ARATH	09JZM4 arabidopsis
101	31	73.8	569	2 073VL3_MYCPA	073VL3 mycobacteri
102	31	73.8	612	2 04RHG9_TERNG	04RHG9 tetraodon n
103	31	73.8	652	2 09Q2N8_9PICO	09Q2N8 foot-and-mo
104	31	73.8	690	2 07TOY4_XENTIA	07TOY4 xenopus lae

105	31	73.8	720	2	Q02568_9PICO	Q02568	foot-and-mo	178	30	71.4	179	2	Q5G219_NEIGO	Q5G219	neisseria g
106	31	73.8	724	2	Q91YK2_MOUSE	Q91YK2	mus musculu	179	30	71.4	179	2	Q5G2J1_NEIGO	Q5G2J1	neisseria g
107	31	73.8	737	2	Q91LY1_9PICO	Q91LY1	foot-and-mo	180	30	71.4	179	2	Q5G2J4_NEIGD	Q5G2J4	neisseria g
108	31	73.8	788	2	Q5SQM2_CRYNE	Q5SQM2	cryptococcu	181	30	71.4	179	2	Q5G2J5_NEIGO	Q5G2J5	neisseria g
109	31	73.8	788	2	Q5KEU3_CRYNE	Q5KEU3	cryptococcu	182	30	71.4	179	2	Q5G2K2_NEIGO	Q5G2K2	neisseria g
110	31	73.8	823	2	Q75JEB3_DICDI	Q75JEB3	dictyosteli	183	30	71.4	179	2	Q5G2K4_NEIGO	Q5G2K4	neisseria g
111	31	73.8	853	2	Q5SAK9_DICDI	Q5SAK9	dictyosteli	184	30	71.4	179	2	Q5G2K6_NEIGO	Q5G2K6	neisseria g
112	31	73.8	926	1	CLAA_LYCES	P1541	lycoperisico	185	30	71.4	179	2	Q5G2K8_NEIGO	Q5G2K8	neisseria g
113	31	73.8	952	2	Q9M2Z6_ARATH	Q9M2Z6	arabidopsis	186	30	71.4	179	2	Q5G2L5_NEIGO	Q5G2L5	neisseria g
114	31	73.8	952	2	Q9SXJ7_ARATH	Q9SXJ7	arabidopsis	187	30	71.4	179	2	Q5G2M1_NEIGO	Q5G2M1	neisseria g
115	31	73.8	969	2	Q9Q2N6_9PICO	Q9Q2N6	foot-and-mo	188	30	71.4	179	2	Q5G2M4_NEIGO	Q5G2M4	neisseria g
116	31	73.8	1024	2	Q8C0B3_MOUSE	Q8C0B3	mus musculu	189	30	71.4	179	2	Q5G2M6_NEIGO	Q5G2M6	neisseria g
117	31	73.8	1146	2	Q01779_CAEEL	Q01779	caenorhabdi	190	30	71.4	179	2	Q5G2N0_NEIGD	Q5G2N0	neisseria g
118	31	73.8	1297	2	Q4Q7E8_LEIMA	Q4Q7E8	leishmania	191	30	71.4	179	2	Q5G2N2_NEIGD	Q5G2N2	neisseria g
119	31	73.8	1372	2	Q4I8P4_GIBBEZ	Q4I8P4	gibberella	192	30	71.4	179	2	Q5G2N3_NEIGD	Q5G2N3	neisseria g
120	31	73.8	1642	1	CO3_NAUTKA	Q91132	naja kaouth	193	30	71.4	179	2	Q5G2N4_NEIGD	Q5G2N4	neisseria g
121	31	73.8	2163	1	POLG_HRVB9	P07210	h genome po	194	30	71.4	179	2	Q5G2N4_NEIGD	Q5G2N4	neisseria g
122	31	73.8	2210	1	RRPO_TACV	P20430	taccaribe vi	195	30	71.4	180	2	Q5G2I0_NEIGO	Q5G2I0	neisseria g
123	31	73.8	2212	2	Q6UY61_9VIRU	Q6UY61	sabia virus	196	30	71.4	181	2	Q5G2I7_NEIGO	Q5G2I7	neisseria g
124	31	73.8	2305	2	Q6PMZ9_9PICO	Q6PMZ9	foot-and-mo	197	30	71.4	182	2	Q6PQZ9_9HIV1	Q6PQZ9	human immun
125	31	73.8	2331	2	Q6PNZ6_9PICO	Q6PNZ6	foot-and-mo	198	30	71.4	192	2	Q6S7X7_9HIV1	Q6S7X7	human immun
126	31	73.8	2332	1	POLG_FMDV1	P03306	f genome po	199	30	71.4	192	2	Q6UR01_9HIV1	Q6UR01	human immun
127	31	73.8	2332	1	FOLG_FMDVA	P03308	f genome po	200	30	71.4	192	2	Q994Q2_9HIV1	Q994Q2	human immun
128	31	73.8	2332	2	Q6PMZ4_9PICO	Q6PMZ4	foot-and-mo	201	30	71.4	192	2	Q995B6_9HIV1	Q995B6	human immun
129	31	73.8	2332	2	Q6PMZ7_9PICO	Q6PMZ7	foot-and-mo	202	30	71.4	192	2	Q9YKQ3_9HIV1	Q9YKQ3	human immun
130	31	73.8	2332	2	Q6PN05_9PICO	Q6PN05	foot-and-mo	203	30	71.4	192	2	Q9YKQ7_9HIV1	Q9YKQ7	human immun
131	31	73.8	2332	2	Q6PN06_9PICO	Q6PN06	foot-and-mo	204	30	71.4	195	2	Q6S841_9HIV1	Q6S841	human immun
132	31	73.8	2332	2	Q6PN07_9PICO	Q6PN07	foot-and-mo	205	30	71.4	231	2	Q4YUT9_PLABE	Q4YUT9	plasmodius
133	31	73.8	2332	2	Q6PN08_9PICO	Q6PN08	foot-and-mo	206	30	71.4	231	2	Q4YU71_ACRGR	Q4YU71	acrodordus
134	31	73.8	2332	2	Q6PN09_9PICO	Q6PN09	foot-and-mo	207	30	71.4	255	2	Q4IYW9_GSPHN	Q4IYW9	erythrobact
135	31	73.8	2332	2	Q6PN12_9PICO	Q6PN12	foot-and-mo	208	30	71.4	261	2	Q9ALL3_ECOLI	Q9ALL3	escherichia
136	31	73.8	2332	2	Q6PN15_9PICO	Q6PN15	foot-and-mo	209	30	71.4	289	1	SPER_PHOL	Q7B82	photorhabd
137	31	73.8	2332	2	Q6PN17_9PICO	Q6PN17	foot-and-mo	210	30	71.4	317	2	Q9R4I5_NEIGO	Q9R4I5	neisseria g
138	31	73.8	2332	2	Q6PN19_9PICO	Q6PN19	foot-and-mo	211	30	71.4	317	2	Q9RFR0_NEIGO	Q9RFR0	neisseria g
139	31	73.8	2332	2	Q6PN27_9PICO	Q6PN27	foot-and-mo	212	30	71.4	317	2	Q9RFR1_NEIGO	Q9RFR1	neisseria g
140	31	73.8	2332	2	Q6PN32_9PICO	Q6PN32	foot-and-mo	213	30	71.4	319	2	Q9R3G2_NEIGO	Q9R3G2	neisseria g
141	31	73.8	2332	2	Q6PN35_9PICO	Q6PN35	foot-and-mo	214	30	71.4	319	2	Q9R421_NEIGO	Q9R421	neisseria g
142	31	73.8	2332	2	Q6PMY4_9PICO	Q6PMY4	foot-and-mo	215	30	71.4	319	2	Q9R3S7_NEIGO	Q9R3S7	neisseria g
143	31	73.8	2332	2	Q6PMZ3_9PICO	Q6PMZ3	foot-and-mo	216	30	71.4	319	2	Q9RFS6_NEIGO	Q9RFS6	neisseria g
144	31	73.8	2332	2	Q6PMZ5_9PICO	Q6PMZ5	foot-and-mo	217	30	71.4	319	2	Q9RFR6_NEIGO	Q9RFR6	neisseria g
145	31	73.8	2332	2	Q6PMZ6_9PICO	Q6PMZ6	foot-and-mo	218	30	71.4	319	2	Q9RFR7_NEIGO	Q9RFR7	neisseria g
146	31	73.8	2332	2	Q6PMZ8_9PICO	Q6PMZ8	foot-and-mo	219	30	71.4	333	2	Q6BFT8_ACIAD	Q6BFT8	acinetobact
147	31	73.8	2332	2	Q6PN00_9PICO	Q6PN00	foot-and-mo	220	30	71.4	335	2	Q9EZ36_NEIGO	Q9EZ36	neisseria g
148	31	73.8	2332	2	Q6PN01_9PICO	Q6PN01	foot-and-mo	221	30	71.4	335	2	Q9EZ37_NEIGO	Q9EZ37	neisseria g
149	31	73.8	2332	2	Q6PN02_9PICO	Q6PN02	foot-and-mo	222	30	71.4	335	2	Q9EZ42_NEIGO	Q9EZ42	neisseria g
150	31	73.8	2332	2	Q6PN11_9PICO	Q6PN11	foot-and-mo	223	30	71.4	335	2	Q9EZ43_NEIGO	Q9EZ43	neisseria g
151	31	73.8	2332	2	Q6PN14_9PICO	Q6PN14	foot-and-mo	224	30	71.4	335	2	Q9EZ44_NEIGO	Q9EZ44	neisseria g
152	31	73.8	2332	2	Q6PN16_9PICO	Q6PN16	foot-and-mo	225	30	71.4	335	2	Q9EZ45_NEIGO	Q9EZ45	neisseria g
153	31	73.8	2332	2	Q6PN18_9PICO	Q6PN18	foot-and-mo	226	30	71.4	335	2	Q9EZ46_NEIGO	Q9EZ46	neisseria g
154	31	73.8	2332	2	Q6PN20_9PICO	Q6PN20	foot-and-mo	227	30	71.4	337	2	Q7MZD2_PHOLL	Q7MZD2	photorhabd
155	31	73.8	2332	2	Q6PN21_9PICO	Q6PN21	foot-and-mo	228	30	71.4	338	2	Q5I012_NEIGO	Q5I012	neisseria g
156	31	73.8	2332	2	Q6PN28_9PICO	Q6PN28	foot-and-mo	229	30	71.4	339	2	Q5O935_NEIGO	Q5O935	neisseria g
157	31	73.8	2332	2	Q6PN29_9PICO	Q6PN29	foot-and-mo	230	30	71.4	332	2	Q5XKW8_NEIGO	Q5XKW8	neisseria g
158	31	73.8	2332	2	Q6PN30_9PICO	Q6PN30	foot-and-mo	231	30	71.4	333	2	Q4I9B3_GIBBEZ	Q4I9B3	gibberella
159	31	73.8	2332	2	Q6PN33_9PICO	Q6PN33	foot-and-mo	232	30	71.4	340	2	Q5N0G6_SYNP6	Q5N0G6	synthococc
160	31	73.8	2332	2	Q6PN34_9PICO	Q6PN34	foot-and-mo	233	30	71.4	342	2	Q7V4A8_PROMM	Q7V4A8	prochlorococ
161	31	73.8	2334	2	Q6PN25_9PICO	Q6PN25	foot-and-mo	234	30	71.4	344	2	Q6DJR5_XENTR	Q6DJR5	xenopus tro
162	31	73.8	2334	2	Q6PN25_9PICO	Q6PN25	foot-and-mo	235	30	71.4	345	2	Q5XKX2_NEIGO	Q5XKX2	neisseria g
163	31	73.8	2336	1	POLG_FMDVZ	P03303	f genome po	236	30	71.4	346	2	Q52699_NEIGO	Q52699	neisseria g
164	31	73.8	2336	2	Q6PMY3_9PICO	Q6PMY3	foot-and-mo	237	30	71.4	347	2	Q5I943_NEIGO	Q5I943	neisseria g
165	31	73.8	2336	2	Q6PN23_9PICO	Q6PN23	foot-and-mo	238	30	71.4	347	2	Q5N3W6_SYNP6	Q5N3W6	synthococc
166	31	73.8	2350	2	Q6PN10_9PICO	Q6PN10	foot-and-mo	239	30	71.4	348	2	Q52694_NEIGO	Q52694	neisseria g
167	31	73.8	2521	2	Q672R3_9PICO	Q672R3	duck picorn	240	30	71.4	348	2	Q52695_NEIGO	Q52695	neisseria g
168	31	73.8	2646	2	Q6XHA6_DICDI	Q6XHA6	dictyosteli	241	30	71.4	348	2	Q52696_NEIGO	Q52696	neisseria g
169	30	71.4	79	2	Q8YWE6_ANASP	Q8YWE6	anabena sp	242	30	71.4	348	2	Q52700_NEIGO	Q52700	neisseria g
170	30	71.4	82	2	Q87NA6_VIBPA	Q87NA6	vibrio para	243	30	71.4	348	2	P95344_NEIGO	P95344	neisseria g
171	30	71.4	141	2	Q6PU03_9HIV1	Q6PU03	human immun	244	30	71.4	348	2	P95345_NEIGO	P95345	neisseria g
172	30	71.4	151	2	Q4TFR8_TETNG	Q4TFR8	tetradon n	245	30	71.4	348	2	P95346_NEIGO	P95346	neisseria g
173	30	71.4	179	2	Q5G2G5_NEIGO	Q5G2G5	neisseria g	246	30	71.4	348	2	P95347_NEIGO	P95347	neisseria g
174	30	71.4	179	2	Q5G2H4_NEIGO	Q5G2H4	neisseria g	247	30	71.4	348	2	P95348_NEIGO	P95348	neisseria g
175	30	71.4	179	2	Q5G2H8_NEIGO	Q5G2H8	neisseria g	248	30	71.4	348	2	P95349_NEIGO	P95349	neisseria g
176	30	71.4	179	2	Q5G2I3_NEIGO	Q5G2I3	neisseria g	249	30	71.4	348	2	P95350_NEIGO	P95350	neisseria g
177	30	71.4	179	2	Q5G2I5_NEIGO	Q5G2I5	neisseria g	250	30	71.4	348	2	P95352_NEIGO	P95352	neisseria g

251	30	71.4	348	2	Q5XKX0_NEICO	Q5xkx0_neisseria g	324	30	71.4	850	2	Q5BF08_EMENI	Q5bf08_aspergillus
252	30	71.4	348	2	Q5XKX4_NEICO	Q5xkx4_neisseria g	325	30	71.4	902	2	Q9UW4_PLESA	Q9uw4_pleurotus s
253	30	71.4	348	2	Q7WMS5_NEICO	Q7wms5_neisseria g	326	30	71.4	970	2	Q99Q01_SHIFL	Q99q01_shigella fl
254	30	71.4	348	2	Q9R973_NEICO	Q9r973_neisseria g	327	30	71.4	970	2	Q8VSB7_SHIFL	Q8vSB7_shigella fl
255	30	71.4	348	2	Q9RON8_NEICO	Q9rON8_neisseria g	328	30	71.4	1114	2	Q5K671_BOMMO	Q5k671_bombxq mori
256	30	71.4	348	2	Q9S364_NEICO	Q9s364_neisseria g	329	30	71.4	1114	2	Q8MY64_BOMMO	Q8my64_bombxq mori
257	30	71.4	348	2	Q9S365_NEICO	Q9s365_neisseria g	330	30	71.4	1183	2	Q5QW08_ORYSA	Q5qw08_oryza sativ
258	30	71.4	348	2	Q4PR65_NEICO	Q4pr65_neisseria g	331	30	71.4	1195	2	Q9PMU2_XENIA	Q9pmu2_xenopus lae
259	30	71.4	348	2	Q4PR64_NEICO	Q4pr64_neisseria g	332	30	71.4	1251	2	Q583S9_STRYP	Q583s9_trypanosoma
260	30	71.4	378	2	Q988P2_RHIL0	Q988p2_rhizobium l	333	30	71.4	1410	2	Q23371_CAREL	Q23371_caenorhabdi
261	30	71.4	385	1	ACKA_MYCBO	Pe33410_mycobacteri	334	30	71.4	1563	2	Q5SS52_MOUSE	Q5ss52_mus musculu
262	30	71.4	385	1	ACKA_MYCTU	Pe3409_mycobacteri	335	30	71.4	1575	2	Q4SA48_TETNG	Q4sa48_tetradon n
263	30	71.4	401	2	Q9ADZ2_9RH1Z	Q9adZ2_agrobacteri	336	30	71.4	1604	1	UBP32_HUMAN	UBp32_homo sapien
264	30	71.4	402	2	Q5N855_ORYSA	Q5n855_oryza sativ	337	30	71.4	1709	2	Q86L43_DICD1	Q86l43_dicystosteli
265	30	71.4	415	2	Q8DGH7_SYNTL	Q8dgh7_synecococc	338	30	71.4	1713	2	Q54B29_DICD1	Q54b29_dicystosteli
266	30	71.4	421	2	Q82AH2_STRAM	Q82ah2_streptomyce	339	30	71.4	2144	2	Q9ULU2_HUMAN	Q9ulu2_homo sapien
267	30	71.4	435	2	Q97A10_THERO	Q97a10_thermoplasma	340	30	71.4	2339	2	Q6PMU0_9PICO	Q6pmu0_foot-and-mo
268	30	71.4	439	2	Q8S0U6_ORYSA	Q8s0u6_oryza sativ	341	30	71.4	2339	2	Q6PMU1_9PICO	Q6pmu1_foot-and-mo
269	30	71.4	442	2	Q8E0P3_STRAS	Q8e0p3_streptococc	342	30	71.4	2339	2	Q6PMU3_9PICO	Q6pmu3_foot-and-mo
270	30	71.4	445	2	Q4TB39_TETNG	Q4tb39_tetradon n	343	30	71.4	2339	2	Q6PMU4_9PICO	Q6pmu4_foot-and-mo
271	30	71.4	476	2	Q8TZS4_PYRPU	Q8tzs4_pyrococcus	344	30	71.4	2339	2	Q6PMU5_9PICO	Q6pmu5_foot-and-mo
272	30	71.4	481	2	Q8EB67_STRAS	Q8eb67_streptococc	345	30	71.4	2339	2	Q6PMU6_9PICO	Q6pmu6_foot-and-mo
273	30	71.4	482	2	Q8EWG6_MYCPE	Q8ewg6_mycoplasma	346	30	71.4	2339	2	Q6PMU7_9PICO	Q6pmu7_foot-and-mo
274	30	71.4	492	2	Q8JC02_9H1V1	Q8jc02_human immun	347	30	71.4	2339	2	Q6PMU8_9PICO	Q6pmu8_foot-and-mo
275	30	71.4	503	2	Q7RD10_PLAYO	Q7rd10_plasmodiun	348	30	71.4	2420	2	Q9SMI18_CYNVO	Q9smi18_cynoecephalu
276	30	71.4	507	2	Q59WD1_CANAL	Q59wd1_candida alb	349	30	71.4	2764	2	Q9WTS5_MOUSE	Q9wts5_mus musculu
277	30	71.4	511	2	P73413_SYNY3	P73413_synecocyst	350	30	71.4	2764	2	Q5NEM8_MOUSE	Q5nem8_mus musculu
278	30	71.4	513	2	Q6DE92_XENIA	Q6de92_xenopus lae	351	30	71.4	2765	2	Q5NEM7_MOUSE	Q5nem7_mus musculu
279	30	71.4	524	2	Q8D861_VIBVU	Q8d861_vibrio vuln	352	30	71.4	2765	2	Q9RLK2_RAT	Q9rlk2_rattus norv
280	30	71.4	528	2	Q80838_ARATH	Q80838_arabidopsiis	353	30	71.4	3151	2	Q4QPB4_LEITMA	Q4qpb4_leishmania
281	30	71.4	528	2	Q94BV4_ARATH	Q94bv4_arabidopsiis	354	30	71.4	3351	2	Q9KIE1_STRHY	Q9kie1_streptomyce
282	30	71.4	532	1	ALO_ASHGO	Q752Y3_ashbya goss	355	30	71.4	6336	2	Q9KID7_STRHY	Q9kid7_streptomyce
283	30	71.4	534	2	Q4ITZ3_GIBZE	Q4itZ3_gibberella	356	30	71.4	6420	2	P95814_STRSO	P95814_streptomyce
284	30	71.4	539	2	Q5E078_VIBF1	Q5e078_vibrio fisc	357	30	71.4	7525	2	Q9KIE0_STRHY	Q9kie0_streptomyce
285	30	71.4	554	2	Q7MMB3_VIBVY	Q7mmB3_vibrio vuln	358	29	69.0	64	2	Q84Y69_AOUTA	Q84y69_aquilegia c
286	30	71.4	554	2	Q4TB64_TETNG	Q4tb64_tetradon n	359	29	69.0	81	2	Q72V84_LEPIC	Q72v84_leptospira l
287	30	71.4	560	2	Q88BM5_PSESM	Q88bm5_pseudomonas	360	29	69.0	101	2	Q6CHRO_YARJ1	Q6chro_yarrowia li
288	30	71.4	560	2	Q87YZ1_PSESM	Q87yz1_pseudomonas	361	29	69.0	102	2	Q6XQ18_VVIRU	Q6xq18_bear canyon
289	30	71.4	561	2	Q4ZVP2_PSESY	Q4zvp2_pseudomonas	362	29	69.0	104	1	Y079_NPVOF	Y0793_oryza pseu
290	30	71.4	562	2	Q60PS4_CABER	Q60ps4_caenorhabdi	363	29	69.0	106	2	Q69548_9BETA	Q69548_human herpe
291	30	71.4	574	2	Q04545_ARATH	Q04545_arabidopsiis	364	29	69.0	107	2	Q9QJ50_9BETA	Q9qj50_human herpe
292	30	71.4	583	2	Q4RSH6_TETNG	Q4rsh6_tetradon n	365	29	69.0	107	2	Q9MT51_9BETA	Q9mt51_human herpe
293	30	71.4	593	1	AMAI_YEAST	P50082_saccharomyc	366	29	69.0	107	2	Q69036_9BETA	Q69036_human herpe
294	30	71.4	602	2	Q4V901_BRARE	Q4v901_brachydanio	367	29	69.0	117	2	Q4PMA9_IXOSC	Q4pma9_ixodes scap
295	30	71.4	607	2	Q6FLI1_PLAF7	Q6fli1_plasmodiun	368	29	69.0	119	2	Q89U64_BRAJA	Q89u64_bradryhizob
296	30	71.4	619	2	Q4V8Y0_BRARE	Q4v8y0_brachydanio	369	29	69.0	121	2	Q51153_GVIRU	Q51153_microplitis
297	30	71.4	625	2	Q5RIG1_BRARE	Q5rig1_brachydanio	370	29	69.0	126	1	GVPJ_PSEAN	G9ak3_pseudanabae
298	30	71.4	626	2	Q5U3C7_BRARE	Q5u3c7_brachydanio	371	29	69.0	127	1	H2A2_HUMAN	P17317_homo sapien
299	30	71.4	628	2	Q6PGU4_BRARE	Q6pgu4_brachydanio	372	29	69.0	127	1	H2A2_ONCMY	P22647_oncorhynch
300	30	71.4	630	2	Q5ASV3_CANAL	Q5asv3_candida alb	373	29	69.0	128	2	Q619U0_HUMAN	Q619u0_homo sapien
301	30	71.4	635	1	SC5A6_HUMAN	Q9Y289_homo sapien	374	29	69.0	128	2	Q5RC42_PONFY	Q5rc42_pongo pygma
302	30	71.4	635	2	Q969Y5_HUMAN	Q969y5_homo sapien	375	29	69.0	128	2	Q6YNC8_SHEEP	Q6ync8_ovis aries
303	30	71.4	636	1	SC5A6_RABIT	Q9x177_cyctoclagus	376	29	69.0	128	2	Q68F02_MOUSE	Q68f02_m_h2a histo
304	30	71.4	663	2	Q5AR12_EMENI	Q5ar12_aspergillus ce	377	29	69.0	128	2	Q5U5H6_RAT	Q5u5h6_rattus norv
305	30	71.4	674	2	Q5AR12_EMENI	Q5ar12_aspergillus	378	29	69.0	128	2	Q5ZMD6_CHICK	Q5zmd6_gallus gall
306	30	71.4	691	2	Q6S0S9_MANSN	Q6s0s9_mammbelint	379	29	69.0	131	2	Q4VZT8_ANOBT	Q4vzt8_anopheles s
307	30	71.4	694	2	Q7VZS2_BORPE	Q7vzs2_bordetella	380	29	69.0	132	2	Q62229_CAEHL	Q62229_caenorhabdi
308	30	71.4	694	2	Q7WCR9_BORER	Q7wcr9_bordetella	381	29	69.0	133	2	Q5UM02_FRAAN	Q5um02_fragaria an
309	30	71.4	696	2	Q7W589_BORPA	Q7w589_bordetella	382	29	69.0	134	2	Q4VZT5_ANOBT	Q4vzt5_anopheles s
310	30	71.4	716	2	Q5A9X1_CANAL	Q5a9x1_candida alb	383	29	69.0	134	2	Q4VZT6_ANOBT	Q4vzt6_anopheles s
311	30	71.4	718	2	Q824H9_SALTI	Q824h9_salmonella	384	29	69.0	134	2	Q4VZT7_ANOBT	Q4vzt7_anopheles s
312	30	71.4	726	2	Q57L12_SALCH	Q57l12_salmonella	385	29	69.0	135	2	Q4PHE4_USITMA	Q4phe4_usutillago ma
313	30	71.4	726	2	Q5PPH8_SALCP	Q5pph8_salmonella	386	29	69.0	140	1	H2AV_DHOME	P08985_drosophila
314	30	71.4	726	2	Q8ZMW8_SALTY	Q8zwm8_salmonella	387	29	69.0	141	2	Q540X2_DROME	Q540x2_drosophila
315	30	71.4	746	2	Q90754_9PICO	Q90754_foot-and-mo	388	29	69.0	149	2	Q5B5Z2_EMENI	Q5b5z2_aspergillus
316	30	71.4	746	2	Q8V0G8_9PICO	Q8v0g8_foot-and-mo	389	29	69.0	151	2	Q9Z8M6_CHLEPN	Q9z8m6_chlamydia p
317	30	71.4	762	2	Q8DN00_STRR6	Q8dn00_streptococc	390	29	69.0	156	2	Q8NSX9_CONGL	Q8nsx9_corynebacte
318	30	71.4	775	2	Q4PB18_USITMA	Q4pb18_usutillago ma	391	29	69.0	169	2	Q6DFL2_XENIA	Q6df12_xenopus lae
319	30	71.4	795	2	Q4L3Y3_STANT	Q4l3y3_staphylococ	392	29	69.0	174	2	Q6MTL2_CONGL	Q6mtl2_corynebacte
320	30	71.4	796	2	Q80319_BRARE	Q80319_brachydanio	393	29	69.0	176	2	Q84ANI_VITSI	Q84ani_vitreoscilli
321	30	71.4	805	1	CICH_TORMA	P21564_torpedo mar	394	29	69.0	178	2	Q70B12_SYNPX	Q70b12_synecococc
322	30	71.4	809	1	CICH_TORCA	P35522_torpedo cal	395	29	69.0	185	2	Q84Y73_AOUAL	Q84y73_aquilegia a
323	30	71.4	810	2	Q97N72_STRBN	Q97n72_streptococc	396	29	69.0	189	2	Q4WBF5_ASPEU	Q4wbf5_aspergillus

397	29	69.0	192	2	0672U8_9H1V1	0672u8 human immun	470	29	69.0	363	2	0690S3_9H1V1	0690s3 human immun
398	29	69.0	192	2	08U006_9H1V1	08U006 human immun	471	29	69.0	367	1	Y273_CHIMU	09p135 chlamydia m
399	29	69.0	198	2	075UP0_PATYE	075up0 patinopsecte	472	29	69.0	376	2	06DA42_ERMCT	06da42 erwania car
400	29	69.0	198	2	081UK4_BACAN	081uk4 bacillus an	473	29	69.0	377	2	081W82_HUMAN	081w82 homo sapien
401	29	69.0	198	2	063FD8_BACAZ	063fd8 bacillus ce	474	29	69.0	378	2	0812F0_MOUSE	0812f0 mus musculi
402	29	69.0	199	2	07V7D9_PROWM	07v7d9 prochloroco	475	29	69.0	379	2	05CDY3_CRYHO	05cdy3 crypsospori
403	29	69.0	201	2	08BIN5_MOUSE	08bin5 mus musculi	476	29	69.0	383	2	04UNW4_XANCP	04unw4 xanthomonas
404	29	69.0	208	2	0649J4_EUCGR	0649j4 eucalyptus	477	29	69.0	387	2	04P8Y3_USYMA	04p8y3 ussiliago ma
405	29	69.0	209	2	0668H7_YERPS	0668h7 yerstinia ps	478	29	69.0	387	2	04P8Y3_USYMA	04p8y3 ussiliago ma
406	29	69.0	209	2	08ZCF0_YERPE	08zcf0 yerstinia ps	479	29	69.0	388	2	05M091_STRT1	05m091 streptococ
407	29	69.0	211	2	05G0F7_9MAGN	05g0f7 thalicttrum	480	29	69.0	390	1	SOX_MOUSE	05m091 streptococ
408	29	69.0	212	2	08AKS2_9H1V1	08aks2 human immun	481	29	69.0	394	2	05STP2_MOUSE	05stp2 mus musculi
409	29	69.0	214	2	05G0F6_9MAGN	05g0f6 thalicttrum	482	29	69.0	394	2	04HRR2_CAMUP	04hrr2 camylobact
410	29	69.0	215	2	04T9I5_TETNG	04t9i5 tetradodon n	483	29	69.0	398	2	093SB4_IACPE	093sb4 iacobacilli
411	29	69.0	219	2	091UV5_9H1V1	091uv5 human immun	484	29	69.0	398	2	088BK4_IACPL	088bk4 iacobacilli
412	29	69.0	220	2	08DOX7_YERPE	08dox7 yerstinia pe	485	29	69.0	401	2	06C779_YARLI	06c779 yarrowia li
413	29	69.0	220	2	093P01_HELHP	093p01 helicobacte	486	29	69.0	402	1	ACKA_DESVH	072666 desulfocibr
414	29	69.0	226	2	05HD47_STAAC	05hd47 staphylococ	487	29	69.0	402	1	09NFI4_CAEBL	09nfi4 caenorhabdi
415	29	69.0	226	2	06G6G9_STAAS	06g6g9 staphylococ	488	29	69.0	405	1	ACKA_ANASP	08y100 anabaena sp
416	29	69.0	226	2	06GDU1_STTAR	06gdu1 staphylococ	489	29	69.0	406	2	0237I9_ARATH	0237i9 arabidopsis
417	29	69.0	226	2	07A001_STTAM	07a001 staphylococ	490	29	69.0	408	2	05AST8_EMENI	05ast8 aspergillus
418	29	69.0	226	2	07A3J3_STANM	07a3j3 staphylococ	491	29	69.0	417	2	08H035_ORYSA	08h035 oryza sattiv
419	29	69.0	226	2	099RC8_STAMM	099rc8 staphylococ	492	29	69.0	428	2	0856H0_9CUD	0856h0 mycobacteri
420	29	69.0	227	2	07OKH6_ANOGA	07okh6 anopheles g	493	29	69.0	431	2	07WVS1_PORGI	07wvs1 porphyromon
421	29	69.0	227	2	05OX97_IDILO	05ox97 idiomarina	494	29	69.0	431	2	07N9P0_PHOLI	07n9p0 photorhabdu
422	29	69.0	229	2	065124_9MAGN	065124 dicentra ex	495	29	69.0	432	2	0590Z5_SYNP6	0590z5 candida alb
423	29	69.0	229	2	070QA0_9H1V1	070qa0 human immun	496	29	69.0	435	2	098SK5_9PERC	098sk5 amodrytes m
424	29	69.0	235	2	05SQM6_HUMAN	05sqm6 homo sapien	497	29	69.0	439	2	08ZNA2_YERPE	08zna2 yerstinia ps
425	29	69.0	239	2	087SP8_VIBPA	087sp8 vibrio para	498	29	69.0	442	2	066G66_YERPS	066g66 yerstinia ps
426	29	69.0	241	2	04G134_HUMAN	04g134 homo sapien	499	29	69.0	442	2	05TRV1_ANOGA	05trv1 anopheles g
427	29	69.0	244	2	097B03_THEVO	097b03 thermoplasma	500	29	69.0	443	2	04UC34_THEAN	04uc34 thelleria a
428	29	69.0	245	2	052AG7_MAGGR	052ag7 magnetotherm	501	29	69.0	446	2	061P50_CABER	061p50 caenorhabdi
429	29	69.0	250	2	05RC55_ROMPY	05rc55 pongo pygma	502	29	69.0	457	2	076633_CABEL	076633 caenorhabdi
430	29	69.0	250	2	05RC55_ROMPY	05rc55 pongo pygma	503	29	69.0	458	2	0827I8_LUPLU	0827i8 lupinus lut
431	29	69.0	257	1	THIM1_OCEIH	08es22 oceanobacil	504	29	69.0	459	2	0827I8_LUPLU	0827i8 lupinus lut
432	29	69.0	259	2	05EAS2_BRARE	05eas2 brachydanio	505	29	69.0	463	2	06GQ81_XENIA	06gq81 xenopus lae
433	29	69.0	261	2	08YW10_ANASP	08yw10 anabaena sp	506	29	69.0	464	2	08BKX8_MOUSE	08bkx8 mus musculi
434	29	69.0	263	2	05A221_CANAL	05a221 candida alb	507	29	69.0	476	2	061PV6_HUMAN	061pv6 homo sapien
435	29	69.0	263	2	09MYX2_PIG	09myx2 sus scrofa	508	29	69.0	479	2	089VD9_BRALJA	089vd9 bradyrhizob
436	29	69.0	267	2	04V008_XANCP	04v008 xanthomonas	509	29	69.0	487	2	06Q2M3_9H1V1	06q2m3 human immun
437	29	69.0	267	2	08PDK6_XANCP	08pdk6 xanthomonas	510	29	69.0	487	2	06Q2M3_9H1V1	06q2m3 human immun
438	29	69.0	268	2	08RI70_FUSNN	08ri70 fusobacteri	511	29	69.0	488	2	09VHZ9_DROME	09vhz9 drosophila
439	29	69.0	272	2	04ZMW4_PSESY	04zwm4 pseudomonas	512	29	69.0	488	2	04TQH1_9SPHN	04tqh1 erythrobact
440	29	69.0	273	2	04HBL7_9DBIO	04hbl7 deinoococcus	513	29	69.0	488	2	09A489_CAUCR	09a489 caulobacter
441	29	69.0	279	2	04J433_AZOVIT	04j433 azotobacter	514	29	69.0	497	2	088HM3_PSEPK	088hm3 pseudomonas
442	29	69.0	281	2	05FPB8_GLUOX	05fpb8 gluconobact	515	29	69.0	497	2	05UEV7_9H1V1	05uev7 human immun
443	29	69.0	282	1	P5D_COXBU	083aq4 coxiella bu	516	29	69.0	499	2	06YRW7_9H1V1	06yrw7 human immun
444	29	69.0	287	2	06F0S1_CANGA	06f0s1 candida gla	517	29	69.0	500	2	09TW43_CAEBL	09tw43 caenorhabdi
445	29	69.0	288	2	08ASW6_BACTN	08asw6 bacteroides	518	29	69.0	511	2	08SDU8_BPPPA	08sdu8 bacterioph
446	29	69.0	289	2	05WSQ1_LEGPI	05wsq1 legionella	519	29	69.0	511	2	04ZDV9_9VIRU	04zdv9 stabphylloc
447	29	69.0	289	2	05XOM9_LEGPA	05xom9 legionella	520	29	69.0	512	2	0931Y5_STAMM	0931y5 stabphylloc
448	29	69.0	289	2	05ZRH4_LEGPH	05zrh4 legionella	521	29	69.0	512	2	04ZDP4_9VIRU	04zdp4 bacterioph
449	29	69.0	299	2	07NMU4_CHRVA	07nmw4 chromobacte	522	29	69.0	516	2	04URS6_THRAP	04urs6 thelleria a
450	29	69.0	300	2	04P097_USTMA	04p097 ussiliago ma	523	29	69.0	525	2	054H02_DICD1	054h02 dictyostell
451	29	69.0	300	2	05E4Z2_VIBFI	05e4z2 vibrio fisc	524	29	69.0	526	2	08S8N5_ARATH	08s8n5 arabidopsis
452	29	69.0	301	2	006485_BACSU	006485 bacillus su	525	29	69.0	532	2	05SVN7_CRYNE	05svn7 cryptococc
453	29	69.0	305	2	08LIT6_9CAID	08lit6 lactococcus	526	29	69.0	532	2	05KKK1_CRYNE	05kkk1 cryptococc
454	29	69.0	308	2	06ZJG4_CRYSA	06zjg4 cryza sattiv	527	29	69.0	537	2	08P3E2_XANCP	08p3e2 xanthomonas
455	29	69.0	309	2	080U06_IARAR	080u06 iarus argen	528	29	69.0	543	2	053GES_HUMAN	053ges homo sapien
456	29	69.0	309	2	0804A6_IARAR	0804a6 iarus argen	529	29	69.0	543	2	09Y2S1_HUMAN	09y2s1 homo sapien
457	29	69.0	323	2	07PTI30_ANOGA	07pti30 anopheles g	530	29	69.0	545	2	09ULJ3_HUMAN	09ulj3 homo sapien
458	29	69.0	325	2	08E8X6_SHEON	08e8x6 shevmanella	531	29	69.0	548	2	04ANJ4_THRPA	04anj4 thelleria p
459	29	69.0	327	2	04OGS3_LEIMA	04ogs3 leishmania	532	29	69.0	563	2	05SZC8_CRYNE	05szc8 cryptococc
460	29	69.0	328	2	08IJU0_PLAF7	08ijj0 plasmodium	533	29	69.0	563	2	05KNP4_CRYNE	05knp4 cryptococc
461	29	69.0	334	2	069M12_ORYSA	069m12 oryza sattiv	534	29	69.0	567	2	06E3C6_9PELO	06e3c6 caenorhabdi
462	29	69.0	337	2	08DMW0_SYNEL	08dmw0 synechococc	535	29	69.0	567	2	0934W3_SALTI	0934w3 salmonella
463	29	69.0	339	1	ARGC_THEMEA	09x2a2 thermotoga	536	29	69.0	569	2	0616J0_CAEBR	0616j0 caenorhabdi
464	29	69.0	342	2	08G7G4_BIPLO	08g7g4 bifidobacte	537	29	69.0	569	2	05ZXL2_CHICK	05zxl2 gallus gall
465	29	69.0	346	2	06ZMG4_HUMAN	06zmg4 homo sapien	538	29	69.0	571	2	07NKS8_GLOVI	07nks8 gloobacter
466	29	69.0	349	2	08ADZ2_SHIVI	08adz2 human immun	539	29	69.0	580	2	09SYK0_ARATH	09syk0 arabidopsis
467	29	69.0	350	2	04MW74_ASPFU	04mw74 aspergillus	540	29	69.0	601	2	05URB8_MIMIV	05urb8 mimivirus
468	29	69.0	352	1	NUDI3_HUMAN	08ex67 homo sapien	541	29	69.0	605	2	05TSAB_ANOGA	05tsab anopheles g
469	29	69.0	352	2	06WIDI_BPKV4	06widi bacterioph	542	29	69.0	608	2	P92973_ARATH	p92973 arabidopsis

543	29	69.0	613	2	Q8WU2_HUMAN	Q8WU2_homo sapien	616	29	69.0	881	2	Q4LI19_9PICO	Q4LI19 equine rhin
544	29	69.0	624	2	Q8N825_HUMAN	Q8N825_homo sapien	617	29	69.0	886	2	Q9LY18_ARATH	Q9LY18 arabidopsis
545	29	69.0	632	1	ACDA2_METKA	Q8Xt5 methanopyru	618	29	69.0	901	1	POLG_ENMG3	P32540 mengo encp
546	29	69.0	640	2	Q5MB45_9MAGN	Q5mb45 onychopetal	619	29	69.0	901	2	Q707U5_EMCV	Q707U5 encephalomy
547	29	69.0	641	2	Q5FMQ1_XENLA	Q5fmq1 xenopus lae	620	29	69.0	901	2	Q707U6_EMCV	Q707U6 encephalomy
548	29	69.0	648	2	Q8LKU6_SORBI	Q8lku6 sorghum bic	621	29	69.0	901	2	Q707U7_EMCV	Q707U7 encephalomy
549	29	69.0	661	1	YDBU_SCHPO	Q10369 schizosacch	622	29	69.0	901	2	Q707U8_EMCV	Q707U8 encephalomy
550	29	69.0	672	2	Q8BEG3_SHEON	Q8eeg3 shewanella	623	29	69.0	901	2	Q707U9_EMCV	Q707U9 encephalomy
551	29	69.0	672	2	Q4SD83_TETNG	Q4sd83 tetraodon n	624	29	69.0	901	2	Q707V0_EMCV	Q707V0 encephalomy
552	29	69.0	677	2	Q5MB40_9MAGN	Q5mb40 unonopsis s	625	29	69.0	901	2	Q707V1_EMCV	Q707V1 encephalomy
553	29	69.0	687	2	Q86CZ4_TETUR	Q86cz4 tetraonchus	626	29	69.0	905	2	Q919R5_XENLA	Q919R5 xenopus lae
554	29	69.0	691	2	Q524K7_MAGGR	Q524k7 magnaportoc	627	29	69.0	907	2	Q8AWX1_XENTR	Q8awx1 xenopus tto
555	29	69.0	692	2	Q6EMT8_THADA	Q6emt8 chaunatotoc	628	29	69.0	917	2	Q7SYB9_BRAHE	Q7syb9 brachydanio
556	29	69.0	698	2	Q8T420_DROME	Q8t420 drosophila	629	29	69.0	975	2	Q7SHB0_NEUR	Q7shb0 neurospora
557	29	69.0	700	2	Q615R1_CAEBR	Q615r1 caenorhabdi	630	29	69.0	983	2	Q8BIS0_MOUSE	Q8bis0 mus musculu
558	29	69.0	705	2	Q7RSU9_GIALA	Q7rsu9 giardia lam	631	29	69.0	987	2	Q6Z921_ORYSA	Q6z921 oryza sativ
559	29	69.0	720	2	Q9XGV4_XENLA	Q9xgv4 xenopus lae	632	29	69.0	995	2	Q8L2D9_PROUV	Q8l2d9 proteus vul
560	29	69.0	721	1	GLGX_MTCBO	P044Y5 mycobacteri	633	29	69.0	1002	2	Q8CTN9_CRTIV	Q8ctn9 cryptospori
561	29	69.0	721	1	GLGX_MYCTU	P044Y4 mycobacteri	634	29	69.0	1002	2	Q5CP45_CRYHO	Q5cp45 cryospori
562	29	69.0	746	2	Q8JVE7_9PICO	Q8jve7 foot-and-mo	635	29	69.0	1025	2	Q7XFD0_ORYSA	Q7xf00 oryza sativ
563	29	69.0	760	2	Q925T8_RAT	Q925t8 rattus norv	636	29	69.0	1046	2	Q8A5M8_BACTN	Q8a5m8 bacteroides
564	29	69.0	760	2	Q8C1C9_MOUSE	Q8c1c9 mus musculu	637	29	69.0	1078	1	SC24A_HUMAN	Q9VOR8_drosophila
565	29	69.0	760	2	Q920D3_MOUSE	Q920d3 m bump/reclin	638	29	69.0	1123	2	Q5TQ68_ANOGA	Q5tq68 anopheles g
566	29	69.0	761	2	Q60477_HUMAN	Q60477 homo sapien	639	29	69.0	1127	2	Q56UN3_HUMAN	Q56un3 homo sapien
567	29	69.0	761	2	Q6PIA0_HUMAN	Q6pia0 homo sapien	640	29	69.0	1171	2	Q7XWK9_ORYSA	Q7xwk9 oryza sativ
568	29	69.0	761	2	Q5E912_BOVIN	Q5e912 bos taurus	641	29	69.0	1182	1	PHOB1_YEAST	Q8MRFB_DROME
569	29	69.0	761	2	Q9OXLO_MOUSE	Q9oxl0 mus musculu	642	29	69.0	1182	2	Q8MRFB_DROME	P17442 saccharomyc
570	29	69.0	761	2	Q7ZXR3_CHICK	Q7zxr3 gallus gall	643	29	69.0	1182	2	Q9VOR8_DROME	Q9vcr8 drosophila
571	29	69.0	768	2	Q8BZ10_MOUSE	Q8bz10 mus musculu	644	29	69.0	1182	2	Q7Q495_ANOGA	Q7q495 anopheles g
572	29	69.0	772	2	Q95UG9_PIG	Q95jg9 sus scrofa	645	29	69.0	1215	2	Q56UN4_HUMAN	Q56un4 homo sapien
573	29	69.0	772	2	Q4SDZ3_TETNG	Q4sdz3 tetraodon n	646	29	69.0	1251	2	Q6AVG0_ORYSA	Q6avg0 oryza sativ
574	29	69.0	782	2	Q9SSB4_ARATH	Q9ssb4 arabidopsis	647	29	69.0	1260	2	Q4ANG21_9MICC	Q4ang21 arthrobacte
575	29	69.0	792	2	Q8TED9_HUMAN	Q8ted9 homo sapien	648	29	69.0	1328	2	Q56UN5_HUMAN	Q56un5 homo sapien
576	29	69.0	793	2	Q7UKD3_RHOBA	Q7ukd3 rhodospirell	649	29	69.0	1360	1	GLI1_XENLA	Q91690 xenopus lae
577	29	69.0	794	2	Q5LEW7_CHLAE	Q5lew7 chlamydomphi	650	29	69.0	1380	2	Q54066_DICDI	Q54g66 dictyosteli
578	29	69.0	795	1	PALB_YARLI	Q9lic8 yarrowia 11	651	29	69.0	1393	2	Q7XGB2_ORYSA	Q7xgb2 oryza sativ
579	29	69.0	795	1	Q9APN1_MYCAV	Q9apn1 mycobacteri	652	29	69.0	1393	2	Q8SB13_ORYSA	Q8sb13 oryza sativ
580	29	69.0	797	2	Q5HMH9_STAEQ	Q5hmr9 staphylococ	653	29	69.0	1421	1	Q6NRI6_XENLA	Q6nri6 xenopus lae
581	29	69.0	800	2	Q6GBK7_STAAS	Q6gbk7 staphylococ	654	29	69.0	1470	1	YRMB_CAEEL	Q09417 caenorhabdi
582	29	69.0	800	2	Q6GJ47_STAAR	Q6gj47 staphylococ	655	29	69.0	1494	2	Q61ZP2_CAEBR	Q61z22 caenorhabdi
583	29	69.0	800	2	Q5H145_STAAC	Q5h145 staphylococ	656	29	69.0	1494	2	Q4Q1I9_LEIMA	Q4q1i9 leishmania
584	29	69.0	800	2	Q8NXT2_STAMW	Q8nxt2 staphylococ	657	29	69.0	1605	2	Q89ZN3_BACTN	Q89zn3 bacteroides
585	29	69.0	800	2	Q932F5_STAMW	Q932f5 staphylococ	658	29	69.0	1626	2	Q6FS05_CANGA	Q6fs05 candida gla
586	29	69.0	802	2	Q99VZ2_STAMW	Q99vz2 staphylococ	659	29	69.0	1632	2	Q4SID3_TETNG	Q4sid3 tetraodon n
587	29	69.0	802	2	Q6FS91_CANGA	Q6fs91 candida gla	660	29	69.0	1681	2	Q5ME83_ORYSA	Q5me83 oryza sativ
588	29	69.0	812	2	Q7YVC9_9TRYR	Q7yvc9 crypanosoma	661	29	69.0	1845	2	Q9W1Z8_HCMV	Q9w1z8 human cytom
589	29	69.0	812	2	Q7R118_GIALA	Q7r118 giardia lam	662	29	69.0	1865	2	Q4Q0I1_LEIMA	Q4q0i1 leishmania
590	29	69.0	817	2	Q4FY62_LEIMA	Q4fy62 leishmania	663	29	69.0	2057	2	Q4UDY1_THEAN	Q4udy1 thelletia a
591	29	69.0	825	2	Q5GJ77_BOVIN	Q5gj77 bos taurus	664	29	69.0	2192	2	Q804R1_BRAHE	Q804r1 brachydanio
592	29	69.0	827	1	PLSB_MOUSE	Q61586 mus musculu	665	29	69.0	2241	2	UL48_HCMVA	P16785 human cytom
593	29	69.0	827	1	Q8VCT2_MOUSE	Q8vct2 mus musculu	666	29	69.0	2241	2	Q6SWB4_HCMV	Q6swb4 human cytom
594	29	69.0	828	1	PLSB_HUMAN	Q9hc12 homo sapien	667	29	69.0	2242	2	Q6RXH0_HCMV	Q6rxh0 human cytom
595	29	69.0	828	1	PLSB_RAT	P97564 rattus norv	668	29	69.0	2280	1	POLG_EMCV	P03304 e genome po
596	29	69.0	828	1	Q6ZMF6_HUMAN	Q6zmf6 homo sapien	669	29	69.0	2282	1	POLG_EMCVB	P17593 e genome po
597	29	69.0	828	2	Q86T70_HUMAN	Q86t70 homo sapien	670	29	69.0	2292	1	POLG_EMCVD	P17594 e genome po
598	29	69.0	828	2	Q86T73_HUMAN	Q86t73 homo sapien	671	29	69.0	2292	1	Q7TE87_EMCV	Q7te87 encephalomy
599	29	69.0	828	2	Q8NIG6_HUMAN	Q8nig6 homo sapien	672	29	69.0	2292	2	Q8QV04_EMCV	Q8qv04 encephalomy
600	29	69.0	834	1	POLG_ENMGO	P12826 mengo encp	673	29	69.0	2292	2	Q89Z72_EMCV	Q89z72 encephalomy
601	29	69.0	837	2	Q7Q6Q4_ANOGA	Q7q6q4 anopheles g	674	29	69.0	2282	2	Q66763_EMCV	Q66763 encephalomy
602	29	69.0	848	2	Q69ZG4_MOUSE	Q69z94 mus musculu	675	29	69.0	2282	2	Q66765_EMCV	Q66765 encephalomy
603	29	69.0	854	1	CLPB_MEIRU	Q7x268 melothermus	676	29	69.0	2292	2	Q66850_EMCV	Q66850 encephalomy
604	29	69.0	861	2	Q7X7H5_ORYSA	Q7x7h5 oryza sativ	677	29	69.0	2293	2	Q83422_ENMGO	Q83422 mengo encp
605	29	69.0	861	2	Q7XP80_ORYSA	Q7xp80 oryza sativ	678	29	69.0	2319	2	Q4RT87_TETNG	Q4rt87 tetraodon n
606	29	69.0	864	2	Q5TRG5_ANOGA	Q5trg5 anopheles g	679	29	69.0	2429	2	Q8B552_9PICO	Q8b552 simian pico
607	29	69.0	866	2	Q4LI17_9PICO	Q4li17 equine rhin	680	29	69.0	2583	2	Q91LX8_9PICO	Q91lx8 equine rhin
608	29	69.0	875	2	Q744X4_MYCPA	Q744x4 mycobacteri	681	29	69.0	2589	2	Q66776_9PICO	Q66776 equine rhin
609	29	69.0	875	2	Q4LI11_9PICO	Q4li11 equine rhin	682	29	69.0	2705	2	Q9W6V6_CHICK	Q9w6v6 gallus gall
610	29	69.0	879	2	Q4LI13_9PICO	Q4li13 equine rhin	683	29	69.0	2725	2	Q9UKZ4_HUMAN	Q9ukz4 homo sapien
611	29	69.0	880	2	Q8S9K4_ARATH	Q8s9k4 arabidopsis	684	29	69.0	2725	2	Q5JZ17_HUMAN	Q5jz17 homo sapien
612	29	69.0	880	2	Q4LI12_9PICO	Q4li12 equine rhin	685	29	69.0	2731	2	Q9WTS4_MOUSE	Q9wts4 mus musculu
613	29	69.0	880	2	Q4LI15_9PICO	Q4li15 equine rhin	686	29	69.0	2771	2	Q9WTS7_MOUSE	Q9wts7 mus musculu
614	29	69.0	880	2	Q4LI16_9PICO	Q4li16 equine rhin	687	29	69.0	2802	2	Q7CWD9_AGRIS	Q7cwd9 agrobacteri
615	29	69.0	880	2	Q4LIJ1_9PICO	Q4li1j equine rhin	688	29	69.0	2802	2	Q9DBR5_CHICK	Q9db5 gallus gall

689	29	69.0	2822	2	05ATL1_EMENI	05atl1 aspergillus	762	28	66.7	112	2	P88574_9H1V1	P88574 human immun
690	29	69.0	2824	2	09W7R3_BRAE	09w7r3 brachydanio	763	28	66.7	112	2	P88575_9H1V1	P88575 human immun
691	29	69.0	2825	2	070465_MOUSE	070465 mus musculus	764	28	66.7	112	2	P88576_9H1V1	P88576 human immun
692	29	69.0	2831	2	08UBX0_AGR75	08ubx0 agrobacteri	765	28	66.7	112	2	P88577_9H1V1	P88577 human immun
693	29	69.0	2832	2	093N05_9RH1Z	093n05 agrobacteri	766	28	66.7	112	2	P88578_9H1V1	P88578 human immun
694	29	69.0	3193	2	07RLJ8_PLA0F	07rlj8 plasmodium	767	28	66.7	112	2	P88581_9H1V1	P88581 human immun
695	29	69.0	3597	2	08ILU5_PLAF7	08ilu5 plasmodium	768	28	66.7	116	2	05Z984_ORYSA	05z984 oryza sativ
696	29	69.0	10287	2	06LEZ3_PLAF7	06lez3 plasmodium	769	28	66.7	116	2	09WBJ0_9H1V1	09wbj0 human immun
697	28.5	67.9	651	2	075HM0_ORYSA	075hm0 oryza sativ	770	28	66.7	116	2	09WBJ3_9H1V1	09wbj3 human immun
698	28.5	67.9	1106	2	080M49_MOUSE	080m49 mus musculu	771	28	66.7	118	2	09JGH4_BACSB	09jgh4 bacillus su
699	28	66.7	47	2	05T017_MOUSE	05t017 mus musculu	772	28	66.7	118	2	09WB18_9H1V1	09wb18 human immun
700	28	66.7	55	2	07RY69_NEUCK	07ry69 neurospora	773	28	66.7	119	2	072889_9H1V1	072889 human immun
701	28	66.7	57	2	069KU2_ORYSA	069ku2 oryza sativ	774	28	66.7	119	2	072891_9H1V1	072891 human immun
702	28	66.7	57	2	053MD5_ORYSA	053md5 oryza sativ	775	28	66.7	119	2	072892_9H1V1	072892 human immun
703	28	66.7	58	1	03N6B_BRAOL	P68357 brassica ol	776	28	66.7	119	2	072894_9H1V1	072894 human immun
704	28	66.7	59	2	05ZAT6_ORYSA	05zat6 oryza sativ	777	28	66.7	119	2	09J676_9H1V1	09j676 human immun
705	28	66.7	62	2	05T07_RABIT	05t07 oryctolagus	778	28	66.7	119	2	09J6A3_9H1V1	09j6a3 human immun
706	28	66.7	63	2	089695_9CORO	089695 porcine res	779	28	66.7	119	2	09J6A4_9H1V1	09j6a4 human immun
707	28	66.7	65	2	07MGU8_VIBVY	07mgu8 vibrio vuln	780	28	66.7	120	1	STR16_ARATH	039129 arabidopsis
708	28	66.7	66	1	CSN6A_BRAOL	P68356 brassica ol	781	28	66.7	120	2	08Q412_9H1V1	08q412 human immun
709	28	66.7	74	2	09DKU2_9PAPI	09dku2 human papil	782	28	66.7	120	2	09WB15_9H1V1	09wb15 human immun
710	28	66.7	74	2	09DKU7_9PAPI	09dku7 human papil	783	28	66.7	121	2	0667G4_YERPS	0667g4 yerania ps
711	28	66.7	75	2	067TW1_ORYSA	067tw1 oryza sativ	784	28	66.7	121	2	077MW0_9H1V1	077mw0 human immun
712	28	66.7	75	2	0691Y0_ORYSA	0691y0 oryza sativ	785	28	66.7	121	2	09W9T7_9H1V1	09w9t7 human immun
713	28	66.7	75	2	06Z5B1_ORYSA	06z5b1 oryza sativ	786	28	66.7	121	2	09WB16_9H1V1	09wb16 human immun
714	28	66.7	82	2	070A37_9H1V1	070a37 human immun	787	28	66.7	121	2	09WB17_9H1V1	09wb17 human immun
715	28	66.7	88	2	070A13_9H1V1	070a13 human immun	788	28	66.7	121	2	09WB19_9H1V1	09wb19 human immun
716	28	66.7	89	2	0709V6_9H1V1	0709v6 human immun	789	28	66.7	121	2	09WB21_9H1V1	09wb21 human immun
717	28	66.7	89	2	070A68_9H1V1	070a68 human immun	790	28	66.7	121	2	09WB22_9H1V1	09wb22 human immun
718	28	66.7	90	2	07E242_ORYSA	07e242 oryza sativ	791	28	66.7	122	2	077WV5_9H1V1	077wv5 human immun
719	28	66.7	90	2	0709Y5_9H1V1	0709y5 human immun	792	28	66.7	122	2	08Q3V4_9H1V1	08q3v4 human immun
720	28	66.7	90	2	070A05_9H1V1	070a05 human immun	793	28	66.7	122	2	09W870_9H1V1	09w870 human immun
721	28	66.7	90	2	070A51_9H1V1	070a51 human immun	794	28	66.7	122	2	09WBK7_9H1V1	09wbk7 human immun
722	28	66.7	90	2	070A54_9H1V1	070a54 human immun	795	28	66.7	123	2	077WV6_9H1V1	077wv6 human immun
723	28	66.7	91	2	070A76_9H1V1	070a76 human immun	796	28	66.7	123	2	08URE7_9H1V1	08ure7 human immun
724	28	66.7	93	2	0709U6_9H1V1	0709u6 human immun	797	28	66.7	123	2	08URE8_9H1V1	08ure8 human immun
725	28	66.7	93	2	0709V2_9H1V1	0709v2 human immun	798	28	66.7	123	2	0995S6_9H1V1	0995s6 human immun
726	28	66.7	93	2	0709W7_9H1V1	0709w7 human immun	799	28	66.7	123	2	09W8T8_9H1V1	09w8t8 human immun
727	28	66.7	93	2	0709W7_9H1V1	0709w7 human immun	800	28	66.7	124	2	05FZV5_9H1V1	05fzv5 human immun
728	28	66.7	93	2	0709Y2_9H1V1	0709y2 human immun	801	28	66.7	124	2	08UR16_9H1V1	08ur16 human immun
729	28	66.7	93	2	0709Y3_9H1V1	0709y3 human immun	802	28	66.7	124	2	09WBK2_9H1V1	09wbk2 human immun
730	28	66.7	93	2	0709Y4_9H1V1	0709y4 human immun	803	28	66.7	125	2	077WV3_9H1V1	077wv3 human immun
731	28	66.7	93	2	070A70_9H1V1	070a70 human immun	804	28	66.7	125	2	077WV7_9H1V1	077wv7 human immun
732	28	66.7	93	2	070AA2_9H1V1	070aa2 human immun	805	28	66.7	125	2	077WV9_9H1V1	077wv9 human immun
733	28	66.7	94	2	0709V3_9H1V1	0709v3 human immun	806	28	66.7	125	2	077WV9_9H1V1	077wv9 human immun
734	28	66.7	94	2	0709V4_9H1V1	0709v4 human immun	807	28	66.7	125	2	08Q3W7_9H1V1	08q3w7 human immun
735	28	66.7	94	2	0709X4_9H1V1	0709x4 human immun	808	28	66.7	125	2	09WBK3_9H1V1	09wbk3 human immun
736	28	66.7	95	2	05Z7D3_ORYSA	05z7d3 oryza sativ	809	28	66.7	125	2	09WB29_9H1V1	09wb29 human immun
737	28	66.7	95	2	0709W8_9H1V1	0709w8 human immun	810	28	66.7	125	2	09W9U2_9H1V1	09w9u2 human immun
738	28	66.7	95	2	08URK8_9H1V1	08urk8 human immun	811	28	66.7	125	2	09WBJ4_9H1V1	09wbj4 human immun
739	28	66.7	96	2	072ER2_DESYH	072er2 desulfovibx	812	28	66.7	125	2	09WBJ5_9H1V1	09wbj5 human immun
740	28	66.7	96	2	0709X3_9H1V1	0709x3 human immun	813	28	66.7	125	2	09WBJ6_9H1V1	09wbj6 human immun
741	28	66.7	96	2	070A48_9H1V1	070a48 human immun	814	28	66.7	126	2	084M34_ORYSA	084m34 oryza sativ
742	28	66.7	101	2	091G12_NPVER	091g12 epiphyas po	815	28	66.7	126	2	077WV4_9H1V1	077wv4 human immun
743	28	66.7	103	2	039133_9H1V1	039133 human immun	816	28	66.7	126	2	0995S1_9H1V1	0995s1 human immun
744	28	66.7	103	2	039134_9H1V1	039134 human immun	817	28	66.7	127	2	09W9S9_9H1V1	09w9s9 human immun
745	28	66.7	103	2	039135_9H1V1	039135 human immun	818	28	66.7	127	2	077209_9H1V1	077209 human immun
746	28	66.7	103	2	039137_9H1V1	039137 human immun	819	28	66.7	127	2	0995R4_9H1V1	0995r4 human immun
747	28	66.7	103	2	P88761_9H1V1	P88761 human immun	820	28	66.7	128	2	06ZUT4_HUMAN	06zut4 homo sapien
748	28	66.7	103	2	P88762_9H1V1	P88762 human immun	821	28	66.7	128	2	075987_9H1V1	075987 human immun
749	28	66.7	103	2	P88763_9H1V1	P88763 human immun	822	28	66.7	128	2	08Q3X8_9H1V1	08q3x8 human immun
750	28	66.7	103	2	071238_9H1V1	071238 human immun	823	28	66.7	128	2	08Q3Z6_9H1V1	08q3z6 human immun
751	28	66.7	103	2	077R10_9H1V1	077r10 human immun	824	28	66.7	128	2	091KR8_9H1V1	091kr8 human immun
752	28	66.7	103	2	09W904_9H1V1	09w904 human immun	825	28	66.7	128	2	09IM18_9H1V1	09im18 human immun
753	28	66.7	103	2	09WFW0_9H1V1	09wfw0 human immun	826	28	66.7	128	2	09QFM2_9H1V1	09qfm2 human immun
754	28	66.7	103	2	09WFW2_9H1V1	09wfw2 human immun	827	28	66.7	128	2	09WBK9_9H1V1	09wbk9 human immun
755	28	66.7	103	2	09WFW5_9H1V1	09wfw5 human immun	828	28	66.7	129	2	036843_9H1V1	036843 human immun
756	28	66.7	105	2	08KEJ0_CHLFE	08kej0 chlorobium	829	28	66.7	129	2	036857_9H1V1	036857 human immun
757	28	66.7	106	2	06XOH5_9VIRU	06xoh5 tamiwacex	830	28	66.7	129	2	036862_9H1V1	036862 human immun
758	28	66.7	107	2	06XOH6_9VIRU	06xoh6 tamiwacex	831	28	66.7	129	2	036868_9H1V1	036868 human immun
759	28	66.7	109	2	075SR3_9H1V1	075sr3 human immun	832	28	66.7	129	2	036869_9H1V1	036869 human immun
760	28	66.7	112	2	09SLV7_TOBAC	09slv7 nicotiana t	833	28	66.7	129	2	036873_9H1V1	036873 human immun
761	28	66.7	112	2	P88573_9H1V1	P88573 human immun	834	28	66.7	129	2	036874_9H1V1	036874 human immun

835	28	66.7	129	2	036880	human	immun	908	28	66.7	130	2	076817	9H1V1	076817	human	immun
836	28	66.7	129	2	036894	human	immun	909	28	66.7	130	2	076818	9H1V1	076818	human	immun
837	28	66.7	129	2	036895	human	immun	910	28	66.7	130	2	076819	9H1V1	076819	human	immun
838	28	66.7	129	2	036901	human	immun	911	28	66.7	130	2	076830	9H1V1	076830	human	immun
839	28	66.7	129	2	036920	human	immun	912	28	66.7	130	2	076831	9H1V1	076831	human	immun
840	28	66.7	129	2	036923	human	immun	913	28	66.7	130	2	076832	9H1V1	076832	human	immun
841	28	66.7	129	2	036934	human	immun	914	28	66.7	130	2	076833	9H1V1	076833	human	immun
842	28	66.7	129	2	036935	human	immun	915	28	66.7	130	2	076834	9H1V1	076834	human	immun
843	28	66.7	129	2	036936	human	immun	916	28	66.7	130	2	076835	9H1V1	076835	human	immun
844	28	66.7	129	2	036941	human	immun	917	28	66.7	130	2	076836	9H1V1	076836	human	immun
845	28	66.7	129	2	036955	human	immun	918	28	66.7	130	2	076837	9H1V1	076837	human	immun
846	28	66.7	129	2	076826	human	immun	919	28	66.7	130	2	076838	9H1V1	076838	human	immun
847	28	66.7	129	2	0803Y0	human	immun	920	28	66.7	130	2	076839	9H1V1	076839	human	immun
848	28	66.7	129	2	0803Y1	human	immun	921	28	66.7	130	2	076850	9H1V1	076850	human	immun
849	28	66.7	129	2	0803Z8	human	immun	922	28	66.7	130	2	076852	9H1V1	076852	human	immun
850	28	66.7	129	2	080401	9H1V1	human	923	28	66.7	130	2	076853	9H1V1	076853	human	immun
851	28	66.7	129	2	080422	9H1V1	human	924	28	66.7	130	2	076854	9H1V1	076854	human	immun
852	28	66.7	129	2	080R18	human	immun	925	28	66.7	130	2	076855	9H1V1	076855	human	immun
853	28	66.7	129	2	090F06	human	immun	926	28	66.7	130	2	076856	9H1V1	076856	human	immun
854	28	66.7	129	2	090F08	human	immun	927	28	66.7	130	2	076857	9H1V1	076857	human	immun
855	28	66.7	130	2	036768	human	immun	928	28	66.7	130	2	076858	9H1V1	076858	human	immun
856	28	66.7	130	2	036780	9H1V1	human	929	28	66.7	130	2	076860	9H1V1	076860	human	immun
857	28	66.7	130	2	036781	9H1V1	human	930	28	66.7	130	2	077174	9H1V1	077174	human	immun
858	28	66.7	130	2	036795	human	immun	931	28	66.7	130	2	077175	9H1V1	077175	human	immun
859	28	66.7	130	2	036814	human	immun	932	28	66.7	130	2	077176	9H1V1	077176	human	immun
860	28	66.7	130	2	036818	human	immun	933	28	66.7	130	2	077177	9H1V1	077177	human	immun
861	28	66.7	130	2	036819	9H1V1	human	934	28	66.7	130	2	077178	9H1V1	077178	human	immun
862	28	66.7	130	2	036828	human	immun	935	28	66.7	130	2	077179	9H1V1	077179	human	immun
863	28	66.7	130	2	036832	human	immun	936	28	66.7	130	2	077180	9H1V1	077180	human	immun
864	28	66.7	130	2	036852	human	immun	937	28	66.7	130	2	077181	9H1V1	077181	human	immun
865	28	66.7	130	2	036953	human	immun	938	28	66.7	130	2	077182	9H1V1	077182	human	immun
866	28	66.7	130	2	036958	9H1V1	human	939	28	66.7	130	2	077202	9H1V1	077202	human	immun
867	28	66.7	130	2	071007	9H1V1	human	940	28	66.7	130	2	077203	9H1V1	077203	human	immun
868	28	66.7	130	2	071008	9H1V1	human	941	28	66.7	130	2	077204	9H1V1	077204	human	immun
869	28	66.7	130	2	071009	human	immun	942	28	66.7	130	2	077205	9H1V1	077205	human	immun
870	28	66.7	130	2	075853	human	immun	943	28	66.7	130	2	077206	9H1V1	077206	human	immun
871	28	66.7	130	2	075905	9H1V1	human	944	28	66.7	130	2	077207	9H1V1	077207	human	immun
872	28	66.7	130	2	075906	human	immun	945	28	66.7	130	2	077208	9H1V1	077208	human	immun
873	28	66.7	130	2	075907	9H1V1	human	946	28	66.7	130	2	077210	9H1V1	077210	human	immun
874	28	66.7	130	2	075908	9H1V1	human	947	28	66.7	130	2	077220	9H1V1	077220	human	immun
875	28	66.7	130	2	075909	9H1V1	human	948	28	66.7	130	2	077221	9H1V1	077221	human	immun
876	28	66.7	130	2	075910	human	immun	949	28	66.7	130	2	077222	9H1V1	077222	human	immun
877	28	66.7	130	2	075911	human	immun	950	28	66.7	130	2	077223	9H1V1	077223	human	immun
878	28	66.7	130	2	075912	9H1V1	human	951	28	66.7	130	2	077224	9H1V1	077224	human	immun
879	28	66.7	130	2	075913	human	immun	952	28	66.7	130	2	077225	9H1V1	077225	human	immun
880	28	66.7	130	2	075914	9H1V1	human	953	28	66.7	130	2	077226	9H1V1	077226	human	immun
881	28	66.7	130	2	075925	human	immun	954	28	66.7	130	2	077227	9H1V1	077227	human	immun
882	28	66.7	130	2	075926	9H1V1	human	955	28	66.7	130	2	077230	9H1V1	077230	human	immun
883	28	66.7	130	2	075927	human	immun	956	28	66.7	130	2	077233	9H1V1	077233	human	immun
884	28	66.7	130	2	075928	9H1V1	human	957	28	66.7	130	2	077240	9H1V1	077240	human	immun
885	28	66.7	130	2	075929	human	immun	958	28	66.7	130	2	077241	9H1V1	077241	human	immun
886	28	66.7	130	2	075930	9H1V1	human	959	28	66.7	130	2	077242	9H1V1	077242	human	immun
887	28	66.7	130	2	075931	human	immun	960	28	66.7	130	2	077244	9H1V1	077244	human	immun
888	28	66.7	130	2	075932	9H1V1	human	961	28	66.7	130	2	077245	9H1V1	077245	human	immun
889	28	66.7	130	2	075933	human	immun	962	28	66.7	130	2	077246	9H1V1	077246	human	immun
890	28	66.7	130	2	075934	9H1V1	human	963	28	66.7	130	2	077247	9H1V1	077247	human	immun
891	28	66.7	130	2	076790	9H1V1	human	964	28	66.7	130	2	0776R2	9H1V1	0776R2	human	immun
892	28	66.7	130	2	076791	9H1V1	human	965	28	66.7	130	2	078614	9H1V1	078614	human	immun
893	28	66.7	130	2	076792	9H1V1	human	966	28	66.7	130	2	078615	9H1V1	078615	human	immun
894	28	66.7	130	2	076793	human	immun	967	28	66.7	130	2	078616	9H1V1	078616	human	immun
895	28	66.7	130	2	076794	9H1V1	human	968	28	66.7	130	2	078617	9H1V1	078617	human	immun
896	28	66.7	130	2	076795	9H1V1	human	969	28	66.7	130	2	078618	9H1V1	078618	human	immun
897	28	66.7	130	2	076796	9H1V1	human	970	28	66.7	130	2	078619	9H1V1	078619	human	immun
898	28	66.7	130	2	076797	9H1V1	human	971	28	66.7	130	2	078620	9H1V1	078620	human	immun
899	28	66.7	130	2	076798	9H1V1	human	972	28	66.7	130	2	078621	9H1V1	078621	human	immun
900	28	66.7	130	2	076799	9H1V1	human	973	28	66.7	130	2	078622	9H1V1	078622	human	immun
901	28	66.7	130	2	076810	9H1V1	human	974	28	66.7	130	2	078623	9H1V1	078623	human	immun
902	28	66.7	130	2	076811	9H1V1	human	975	28	66.7	130	2	078624	9H1V1	078624	human	immun
903	28	66.7	130	2	076812	9H1V1	human	976	28	66.7	130	2	078625	9H1V1	078625	human	immun
904	28	66.7	130	2	076813	9H1V1	human	977	28	66.7	130	2	078627	9H1V1	078627	human	immun
905	28	66.7	130	2	076814	9H1V1	human	978	28	66.7	130	2	078628	9H1V1	078628	human	immun
906	28	66.7	130	2	076815	human	immun	979	28	66.7	130	2	078629	9H1V1	078629	human	immun
907	28	66.7	130	2	076816	9H1V1	human	980	28	66.7	130	2	078630	9H1V1	078630	human	immun

Accession	Length	Score	DB	Length	Score	DB	Length	Score	DB
981	28	66.7	130	2	078631	9HIV1	078631	human	immun
982	28	66.7	130	2	078633	9HIV1	078633	human	immun
983	28	66.7	130	2	078634	9HIV1	078634	human	immun
984	28	66.7	130	2	078635	9HIV1	078635	human	immun
985	28	66.7	130	2	078636	9HIV1	078636	human	immun
986	28	66.7	130	2	078637	9HIV1	078637	human	immun
987	28	66.7	130	2	080676	9HIV1	080676	human	immun
988	28	66.7	130	2	080679	9HIV1	080679	human	immun
989	28	66.7	130	2	0803X1	9HIV1	0803X1	human	immun
990	28	66.7	130	2	09QFK0	9HIV1	09QFK0	human	immun
991	28	66.7	130	2	09QFK1	9HIV1	09QFK1	human	immun
992	28	66.7	130	2	09QFK2	9HIV1	09QFK2	human	immun
993	28	66.7	130	2	09QFK3	9HIV1	09QFK3	human	immun
994	28	66.7	130	2	09QFK4	9HIV1	09QFK4	human	immun
995	28	66.7	130	2	09QFK5	9HIV1	09QFK5	human	immun
996	28	66.7	130	2	09QFK6	9HIV1	09QFK6	human	immun
997	28	66.7	130	2	09QFK7	9HIV1	09QFK7	human	immun
998	28	66.7	130	2	09QFK8	9HIV1	09QFK8	human	immun
999	28	66.7	130	2	09QFK9	9HIV1	09QFK9	human	immun
1000	28	66.7	130	2	09QFK10	9HIV1	09QFK10	human	immun

ALIGNMENTS

RESULT 1
MEU18_SCHPO STANDARD; PRT; 553 AA.

AC Q9UB83; Q96W94;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Meiotic expression up-regulated protein 18.
GN Name=meu18; ORFNames=SPBC409.11;
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
NCBI_Taxid=4996;

NCBI_Taxid=4996;

NCBI_Taxid=4996;

NCBI_Taxid=4996;

NCBI_Taxid=4996;

NCBI_Taxid=4996;

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NCBI_Taxid=4996;

NCBI_Taxid=4996;

NCBI_Taxid=4996;

RA Matanabe T., Miyashita K., Saito T.T., Yoneki T., Kakinara Y.,
RA Nishishima K., Kishi Y.A., Shimoda C., Nishijima H.;
RT "Comprehensive isolation of meiosis-specific genes identifies novel
RT proteins and unusual non-coding transcripts in Schizosaccharomyces
RT pombe.";
RL Nucleic Acids Res. 29:2327-2337(2001).
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL, ensuring
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AL09822; CAB52613.1; -; Genomic_DNA.
DR EMBL; AB054302; BAB60871.1; -; mRNA.
DR PIR; T40438; T40438.
DR GeneDB_Spombe; SPBC409.11; -.
KW Complete proteome; Meiosis.
SQ SEQUENCE 553 AA; 64794 MW; 44930879C96E45FC CRC64;

Query Match 90.5%; Score 38; DB 1; Length 553;
Best Local Similarity 87.5%; Pred. No. 23;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HOYLSRT 8
Db 304 HXYLSRT 311

RESULT 2
IL21_HUMAN STANDARD; PRT; 155 AA.

AC Q9HBE4;
DT 01-FEB-2005 (Rel. 46, Last sequence update)
DT 01-FEB-2005 (Rel. 46, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Interleukin-21 precursor (IL-21) (Za11).
GN Name=IL21;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
NCBI_Taxid=9606;

NCBI_Taxid=9606;

NCBI_Taxid=9606;

NCBI_Taxid=9606;

NCBI_Taxid=9606;

NCBI_Taxid=9606;

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NCBI_Taxid=9606;

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NCBI_Taxid=9606;

NCBI_Taxid=9606;

NCBI_Taxid=9606;

NCBI_Taxid=9606;

NCBI_Taxid=9606;

NCBI_Taxid=9606;

NCBI_Taxid=9606;

NCBI_Taxid=9606;

RA Stapleton M., Saares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedon T.B., Toshiyuki S., Carrincci P., Prange C.,
 RA Raha S.S., Loguallano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McKean P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shvchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Schermer A., Schein J.E., Jones S.J.M., Matra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RL [4]
 RP FUNCTION.
 RX PubMed=15178704; DOI=10.1189/jlb.1003488;
 RA Strengell M., Julkunen I., Matikainen S.,
 RT "IFN- α 1 α regulates IL-21 and IL-21R expression in human NK and T
 RT cells.";
 RL J. Leukoc. Biol. 76:416-422(2004).
 RN [5]
 RP REVIEW.
 RX PubMed=15147560; DOI=10.1111/j.1365-2567.2004.01886.x;
 RA Sivakumar P.V., Foster D.C., Clegg C.H.,
 RT "Interleukin-21 is a T-helper cytokine that regulates humoral immunity
 RT and cell-mediated anti-tumour responses.";
 RL Immunology 112:177-182(2004).
 CC -1- FUNCTION: Cytokine with immunoregulatory activity. May promote the
 CC transition between innate and adaptive immunity. Induces the
 CC production of Igg(1) and Igg(3) in B-cells (By similarity). May
 CC play a role in proliferation and maturation of natural killer (NK)
 CC cells in synergy with IL15. May regulate proliferation of mature
 CC B- and T-cells in response to activating stimuli. In synergy with
 CC IL15 and IL18 stimulates interferon gamma production in T-cells
 CC and NK cells. During T-cell mediated immune response may inhibit
 CC dendritic cells (DC) activation and maturation.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed in activated CD4-positive T-cells
 CC but not in CD8-positive T-cells, B-cells, or monocytes.
 CC -1- SIMILARITY: Belongs to the IL-21 family.
 CC
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use as long as its content is in no way modified and this statement is not
 CC removed.

Query Match 88.1%; Score 37; DB 1; Length 155;
 Best Local Similarity 87.5%; Pred. No. 9.7;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 HOYLSRT 8
 Db 142 HOYLSRT 149
 RESULT 3
 Q88TX2_LACPL
 ID Q88TX2_LACPL PRELIMINARY; PRT; 477 AA.
 AC Q88TX2;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Hydrolase, HAD superfamily, Cof family.
 GN OrderedLocustNames=lp_2787;
 OS Lactobacillus plantarum.
 CC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 CC Lactobacillus.
 CC NCBI_TaxID=1590;
 CX [1]
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=NCIMB 8826 / WCFS1;
 RX MEDLINE=22480296; PubMed=12565566; DOI=10.1073/pnas.0337704100;
 RA Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,
 RA Kuipers O.P., Leer R., Tarchini R., Peters S.A., Sandbrink H.M.,
 RA Fiers M.W.E.J., Stiekema W., Klein Lankhorst R.M., Bron P.A.,
 RA De Vos W.M., Stierop Groot M.N., Kerkhoven R., De Vries M., Ursing B.,
 RT "Complete genome sequence of Lactobacillus plantarum WCFS1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995(2003).
 CC EMBL; AL335260; CAP65014.1; -, genomic DNA.
 CC GO; GO:0016787; F:hydrolase activity; IEA.
 CC DR; GO:0008152; P:metabolism; IEA.
 CC DR; InterPro; IPR005834; Dehal like hydro.
 CC DR; InterPro; IPR006379; HAD SF 11B.
 CC DR; InterPro; IPR000150; Hypochet_cof.
 CC DR; Pfam; PF00702; Hydrolase; 1.
 CC DR; TIGRFAMs; TIGR00099; Cof-subfamily; 1.
 CC DR; TIGRFAMs; TIGR01484; HAD-SF-11B; 1.
 CC DR; PROSITE; PS01228; COF_1; UNKNOWN_1.
 CC DR; PROSITE; PS01229; COF_2; UNKNOWN_1.
 CC KW Complete proteome; Hydrolase.
 SQ SEQUENCE 277 AA; 30997 MW; 7A40B0619F75A170 CRC64;
 Query Match 83.3%; Score 35; DB 2; Length 277;
 Best Local Similarity 75.0%; Pred. No. 49;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 HOYLSRT 8
 Db 18 HOYLSRT 25
 RESULT 4
 Q72TX2_LEPIC
 ID Q72TX2_LEPIC PRELIMINARY; PRT; 270 AA.
 AC Q72TX2;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Biopolymer transport exbB-like protein.
 GN OrderedLocustNames=LIC10892;
 OS Leptospira interrogans (serogroup Icterohaemorrhagiae / serovar
 OS Copenhagen1).
 CC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
 CC NCBI_TaxID=44275;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RP STRAIN=Floccruz LI-130;

RA PubMed=15028702; DOI=10.1128/JB.186.7.2164-2172.2004;
RA Nascimento A.L.T.O., Ko A.I., Martins E.A.L., Monteiro-Vitorello C.B.,
RA Ho P.U., Haake D.A., Verjovsky-Almeida S., Hartskeert R.A.,
RA Marques M.V., Oliveira W.C., Menck C.F.M., Leite L.C.C., Carrer H.,
RA Coutinho L.L., Degraeve W.M., Dellagostin O.A., El-Dorri H.,
RA Perro E.S., Perro M.I.T., Furlan L.R., Gambellini M., Gigliotti E.A.,
RA Gees-Neto S.M., Goldman G.H., Goldman M.H.S., Harakava R.,
RA Jeronimo S.M.B., Junqueira-de-Azevedo I.L.M., Kimura E.T.,
RA Karamae E.E., Lemos E.G.M., Lemos M.V.P., Marino C.L., Nunes L.R.,
RA de Oliveira R.C., Pereira G.G., Reis W.S., Schriener A.,
RA Siqueira W.J., Sommer P., Tsai S.M., Simpson A.J.G., Perro J.A.,
RA Camargo L.E.A., Kitchajina J.P., Setubal J.C., Van Sluys M.A.;
RT "Comparative genomics of two Leptospira interrogans serovars reveals
RT novel insights into physiology and pathogenesis.",
RL J. Bacteriol. 186:2164-2172(2004).
DR EMBL; AE017290; AAS69506.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008565; F:protein transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002898; MOTA_ExDB.
DR Pfam; PF01618; MOTA_ExDB; 1.
DR Complete proteome; Transmembrane; Transport.
KW SEQUENCE 270 AA; 29261 MW; 20D1PA4B953B9529 CRC64;
QY Query Match 81.0%; Score 34; DB 2; Length 270;
Db Best Local Similarity 85.7%; Pred. No. 78;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
1 HOYLSSR 7
237 HOYLSSR 243
RESULT 5
ID Q8F192_LEPIN PRELIMINARY; PRT; 270 AA.
AC Q8F192;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Biopolymer transport protein, putative.
GN OrderedLocustNames=LA3244;
OS Leptospira interrogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX NCBI_TaxID=113;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar Ia1;
RX MEDLINE=22598143; PubMed=12712204; DOI=10.1038/nature01597;
RA Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,
RA Zhang J.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-O., Jia J., Tu Y.-F.,
RA Jiang Y., Zhu G.-F., Wan W., Huang H.-L., Qian Z., Wang S.-I., Ma W.,
RA Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,
RA Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,
RA Xu J.-G., Zhao G.-P.;
RT "Unique physiological and pathogenic features of Leptospira
RT interrogans revealed by whole-genome sequencing.",
RL Nature 422:888-893(2003).
DR EMBL; AE011485; AAN50442.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008565; F:protein transporter activity; IEA.
DR InterPro; IPR002898; MOTA_ExDB.
DR Pfam; PF01618; MOTA_ExDB; 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 270 AA; 29231 MW; 34C5FA5F813B9529 CRC64;
QY Query Match 81.0%; Score 34; DB 2; Length 270;
Db Best Local Similarity 85.7%; Pred. No. 78;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
1 HOYLSSR 7

Db 237 HOYLSSR 243
||||:||||
237 HOYLSSR 243
RESULT 6
ID Q54XX5_DICD1 PRELIMINARY; PRT; 848 AA.
AC Q54XX5;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Ankyrin repeat-containing protein.
GN Name=DD80229849; ORFNames=DD80229849;
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Eukaryota; Dictyosteliales; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RA Eichinger L., Pachbat J.A., Gloeckner G., Rajandream M.-A.,
RA Sugeng R., Berriman M., Song J., Olsen R., Szafrański K., Xu Q.,
RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
RA Bankier A.T., Lehmann R., Hamlin N., Davies K., Gaudet P., Fey P.,
RA Plücker K., Chen G., Saunders D., Sodergren E., Davis P.,
RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
RA Farbrother P., Desany B., Just E., Morio T., Roest R., Churcher C.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Muzny D., Moutier T., Pain A., Lu M., Harper D., Lindsay R.,
RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchieser C.,
RA Waidropfer A., Felder M., Thangavelu M., Johnson D., Knights A.,
RA Loulèsseg H., Mungall K., Oliver K., Price C., Quail M.A.,
RA Urushihara H., Hernandez J., Rabinowitsch E., Steffen D., Sanders M.,
RA Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
RA Sugano S., White B., Walker D., Woodward J., Winkler T., Tanaka Y.,
RA Shaulsky G., Schleicher M., Weinstock G., Rosenthal A., Cox E.C.,
RA Williams R.L., Gibbs R., Loomis W.F., Platzer M., Kay R.R.,
RA Williams J., Dear P.H., Noegel A.A., Barrell B., Kupa A.;
RT "The genome of the social amoeba Dictyostelium discoideum";
RL Nature 0:0-0(2005).
CC CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAF101000052; EML68440.1; -; Genomic_DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001660; SAM.
DR InterPro; IPR008271; Ser_thr_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00023; ANK; 5.
DR Pfam; PF00536; SAM_1; 1.
DR PRINTS; PR01415; ANKYRIN.
DR ProDom; PD0000001; Prot_kinase; 1.
DR SMART; SM00248; ANK; 5.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00454; SAM; 1.
DR SMART; SM00219; TYKc; 1.
DR PROSITE; PS50297; ANK_REPEAT_1.
DR PROSITE; PS50088; ANK_REPEAT_3.
DR PROSITE; PS50107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50105; SAM_DOMAIN; 1.
SQ SEQUENCE 848 AA; 94576 MW; 93B08846C85ED4A CRC64;
QY Query Match 81.0%; Score 34; DB 2; Length 848;
Db Best Local Similarity 62.5%; Pred. No. 2.7e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HOYLSRT 8
 Db 796 HOYLSRT 803

RESULT 7

Q9PC98.XYLFA PRELIMINARY; PRT; 88 AA.
 ID 09PC98
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
 DE Hypothetical protein.
 GN OrderedlocusNames=Xf1883;
 OS Xylella fastidiosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 OC Xanthomonadaceae; Xylella.
 NCBI_TaxID=3371;
 [1]
 NUCLEOTIDE SEQUENCE.

RC MEDLINE=20365717; PubMed=10910347; DOI=10.1038/35018003;
 RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Agencio M.,
 RA Alvares R., Alves L.M.C., Araya J.E., Bala G.S., Baptista C.S.,
 RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Brites M.R.S.,
 RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carier H.,
 RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
 RA Faciniani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
 RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
 RA Garner M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
 RA Ho P.L., Hobeisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
 RA Krieger J.E., Kuramae E.E., Laigret S.A., Lopes C.R., Machado J.A.,
 RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
 RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Martino C.L.,
 RA Marques M.V., Martins E.A.L., Martins B.M.F., Matsukuma A.Y.,
 RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
 RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
 RA Nham A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
 RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
 RA Paixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
 RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
 RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
 RA da Silva A.C.R., da Silva A.M., da Silva W.J., Silva W.A. Jr.,
 RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
 RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
 RA Zago M.A., Zatz M., Zeldanis J., Zetubal J.C.,
 RT "The genome sequence of the plant pathogen Xylella fastidiosa.",
 RL Nature 406:151-159(2000).
 DR EMBL: AE004008; AAF84689.1; -; Genomic_DNA.
 DR PIR: C82627; C82627.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 88 AA; 9913 MW; 3EEBA9A47B58C9A CRC64;

Query Match 78.6%; Score 33; DB 2; Length 88;
 Best Local Similarity 75.0%; Pred. No. 39;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HOYLSRT 8
 Db 15 HOYLSRT 22

RESULT 8
 O68648.PSEPU PRELIMINARY; PRT; 340 AA.
 ID 068648
 DT 01-AUG-1998 (Tremblrel. 07, Created)
 DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
 DE Transposase.
 GN Name=tnpA;

OS Pseudomonas putida.
 OG Plasmid pPGH1.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 NCBI_TaxID=303;
 [1]
 NUCLEOTIDE SEQUENCE.

RC STRAIN=H;
 RA Lauf U., Mueller C., Herrmann H.;
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 [2]
 NUCLEOTIDE SEQUENCE.
 RC STRAIN=H;
 RA Rost R., Lauf U., Mueller C., Burchardt G., Herrmann H.;
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF052750; AAC98742.1; -; Genomic_DNA.
 DR GO: GO:0003677; F:DNA binding; IEA.
 DR GO: GO:0004803; F:transposase activity; IEA.
 DR GO: GO:0006313; P:DNA transposition; IEA.
 DR Interpro: IPR001584; Rve.
 DR Interpro: IPR001598; Transposase_1S30.
 DR Pfam: PF00665; rve; 1.
 DR PROSITE: PS01043; TRANSPOSASE_1S30; 1.
 KW Plasmid.
 SQ SEQUENCE 340 AA; 38491 MW; 3279B3AC8551047C CRC64;

Query Match 78.6%; Score 33; DB 2; Length 340;
 Best Local Similarity 87.5%; Pred. No. 16+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HOYLSRT 8
 Db 250 HOYLSRT 257

RESULT 9

Q087BU1.XYLFT PRELIMINARY; PRT; 374 AA.
 ID 087BU1
 DT 01-JUN-2003 (Tremblrel. 24, Created)
 DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
 DE P-protein.
 GN Name=pheA; OrderedlocusNames=PDJ357;
 OS Xylella fastidiosa (strain Temecual / ATCC 700964).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 OC Xanthomonadaceae; Xylella.
 NCBI_TaxID=183190;
 [1]
 NUCLEOTIDE SEQUENCE.

RP MEDLINE=22421331; PubMed=12533478;
 RX DOI=10.1128/JB.185.3.1018-1026.2003;
 RA Van Slyke M.A., de Oliveira M.C., Monteiro-Vitorello C.B.,
 RA Miyaki C.Y., Furlan L.R., Camargo L.E.A., da Silva A.C.R., Moon D.H.,
 RA Takita M.A., Lemos E.G.M., Machado M.A., Ferro J.A., da Silva F.R.,
 RA Goldman M.H.S., Goldman G.H., Lemos M.V.F., El-Dorry H., Tsai S.M.,
 RA Carrier H., Carraro D.M., de Oliveira R.C., Nunes L.R., Siqueira W.J.,
 RA Coutinho L.L., Kimura E.T., Ferro R.S., Harakava R., Kuramae E.E.,
 RA Martino C.L., Gigliotti E., Abreu I.L., Alves L.M.C., do Amaral A.M.,
 RA Baia G.S., Blanco S.R., Brito M.S., Cathavan F.S., Celestino A.V.,
 RA da Cunha A.F., Fenille R.C., Ferro J.A., Formighieri E.F., Kishi L.T.,
 RA Leoni S.G., Oliveira A.R., Rosa V.E. Jr., Sasaki F.T., Sena J.A.D.,
 RA de Souza A.A., Truffi D., Tsukumo F., Yanai G.M., Zatz L.G.,
 RA Civerolo E.L., Simpson A.J.G., Almeida N.F. Jr., Zetubal J.C.,
 RA Kitajima J.P.,
 RT "Comparative analyses of the complete genome sequences of Pierce's
 RT disease and citrus variegated chlorosis strains of Xylella
 RT fastidiosa.",
 RL J. Bacteriol. 185:1018-1026(2003).
 DR EMBL: AE012558; AAO29204.1; -; Genomic_DNA.
 DR GO: GO:0005737; C:Cytoplasm; IEA.
 DR GO: GO:0016597; F:amino acid binding; IEA.
 DR GO: GO:0004106; F:chorismate mutase activity; IEA.

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DR GO: GO:0004664; F:prephenate dehydratase activity; IEA.
DR GO: GO:0009054; P:L-phenylalanine biosynthesis; IEA.
DR GO: GO:0008152; P:metabolism; IEA.
DR InterPro: IPR002912; ACT.
DR InterPro: IPR002701; Chorismate mut.
DR InterPro: IPR008242; Chor mut_pdt_Ppr.
DR InterPro: IPR010957; CM_P2.
DR InterPro: IPR01086; Preph_dehydratase.
DR Pfam: PF01842; ACT; 1.
DR Pfam: PF01817; CM_2; 1.
DR Pfam: PF00800; PDT; 1.
DR PIRSF: PIRSF01500; Chor mut_pdt_Ppr; 1.
DR TIGRFAMs: TIGR01807; CM_P2; 1.
DR Complete proteome.
SQ SEQUENCE 374 AA; 41764 MW; 080938B3DF974945 CRC64;

Query Match 78.6%; Score 33; DB 2; Length 374;
Best Local Similarity 75.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
DB 186 HOYLSRS 193

RESULT 10
Q9PB20_XYLFA PRELIMINARY; PRT; 374 AA.
ID Q9PB20_XYLFA
AC Q9PB20;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE P-protein.
GN OrderedLocustNames=Xf2325;
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xylella.
ON NCBI_TaxID=2371;
RX NUCLEOTIDE SEQUENCE.
RC STRAIN=945C;
RX MEDLINE=20369717; PubMed=10910347; DOI=10.1038/35018003;
RA Simpson A.J.G., Rehnach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvaraga R., Alves L.M.C., Araya J.E., Baia J.E., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Brites M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carter H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
RA Facinani A., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohne M., Furlan L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hohsels J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Martino C.L.,
RA Marches M.V., Martins E.A.L., Martins E.M.F., Matukuma A.Y.,
RA Menck C.F.M., Miraca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nhani A., Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmeri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A., Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E., Jr., de Sa R.G., Santelli R.V., Sawasaki H.B.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A., Jr.,
RA da Silva J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tshako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidants J., Setubal J.C.;
RT "the genome sequence of the plant pathogen Xylella fastidiosa.";
RL Nature 406:151-159(2000).
DR EMBL; AE004043; AAF5124.1; -; Genomic_DNA.
DR PIR; B82572; B82572.
DR GO; GO:0005737; C:cytoplasm; IEA.

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DR GO: GO:0016597; F:amino acid binding; IEA.
DR GO: GO:0004106; F:chorismate mutase activity; IEA.
DR GO: GO:0004664; F:prephenate dehydratase activity; IEA.
DR GO: GO:0009094; P:L-phenylalanine biosynthesis; IEA.
DR GO: GO:0008152; P:metabolism; IEA.
DR InterPro: IPR002912; ACT.
DR InterPro: IPR002701; Chorismate mut.
DR InterPro: IPR010957; CM_P2.
DR InterPro: IPR01086; Preph_dehydratase.
DR Pfam: PF01842; ACT; 1.
DR Pfam: PF01817; CM_2; 1.
DR Pfam: PF00800; PDT; 1.
DR TIGRFAMs: TIGR01807; CM_P2; 1.
DR Complete proteome.
SQ SEQUENCE 374 AA; 41764 MW; 080938B3DF974945 CRC64;

Query Match 78.6%; Score 33; DB 2; Length 374;
Best Local Similarity 75.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
DB 186 HOYLSRS 193

RESULT 11
O44147_CABEL PRELIMINARY; PRT; 389 AA.
ID O44147_CABEL
AC O44147;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN ORFNames=C44B12.7;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
ON NCBI_TaxID=6239;
RX NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916; DOI=10.1126/science.282.5396.2012;
RT "The C. elegans sequencing consortium";
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL science 282:2012-2018(1998).
CC -!- SIMILARITY: Contains 1 reverse transcriptase domain.
DR EMBL; AF036692; AAB8330.1; -; Genomic_DNA.
DR PIR; T32516; T32516.
DR Ensemble; C44B12.7; Caenorhabditis elegans.
DR WormBase; WBGene00016640; C44B12.7.
DR WormPep; C44B12.7; CB16923.
DR GO: GO:0003723; F:RNA binding; IEA.
DR GO: GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR GO: GO:0006278; P:RNA-dependent DNA replication; IEA.
DR InterPro: IPR003285; Cc yltase.
DR InterPro: IPR00477; RVTase.
DR Pfam: PF00078; RVT_1; 1.
DR PRINTS; PR01345; CERVTRCPHASE.
DR PROSITE; PS50878; RT_POL; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 389 AA; 44006 MW; B047B696969FE7AC CRC64;

Query Match 78.6%; Score 33; DB 2; Length 389;
Best Local Similarity 75.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
DB 30 HDPLSRT 37

RESULT 12

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Q6PX52_DROMA
ID Q6PX52_DROMA PRELIMINARY; PRT; 447 AA.
AC Q6PX52;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Monkey-king.
GN Name=mkq;
OS Drosophila mauritiana (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7226;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15064762; DOI=10.1038/ng1338;
RA Wang W., Yu H., Long M.;
RT "Duplication-degeneration as a mechanism of gene fission and the
origin of new genes in Drosophila species.";
RL Nat. Genet. 36:523-527(2004).
DR EMBL: AY572496; AAS8935.1; -; Genomic_DNA.
DR EMBL: AY562984; AAS72424.1; -; mRNA.
DR GO: GO:0003676; F:nucleic acid binding; IEA.
DR GO: GO:0016779; F:nucleotidyltransferase activity; IEA.
DR GO: GO:0016740; F:transferase activity; IEA.
DR InterPro: IPR002934; DNA_pol_beta.
DR InterPro: IPR007087; PAP_25A_core.
DR Pfam: PF01909; NTP_transf_2; 1.
DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_1.
SQ SEQUENCE 447 AA; 50196 MW; E58E062BE8C238 CRC64;
Query Match 78.6%; Score 33; DB 2; Length 447;
Best Local Similarity 75.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 HOYLSRT 8
Db 154 HOYLYNRT 161

RESULT 13
Q6PX53_DROMA
ID Q6PX53_DROMA PRELIMINARY; PRT; 447 AA.
AC Q6PX53;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Monkey-king.
GN Name=mkq;
OS Drosophila mauritiana (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7226;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15064762; DOI=10.1038/ng1338;
RA Wang W., Yu H., Long M.;
RT "Duplication-degeneration as a mechanism of gene fission and the
origin of new genes in Drosophila species.";
RL Nat. Genet. 36:523-527(2004).
DR EMBL: AY572495; AAS8934.1; -; Genomic_DNA.
DR EMBL: AY562980; AAS72420.1; -; mRNA.
DR GO: GO:0003676; F:nucleic acid binding; IEA.
DR GO: GO:0016779; F:nucleotidyltransferase activity; IEA.
DR GO: GO:0016740; F:transferase activity; IEA.
DR InterPro: IPR002934; DNA_pol_beta.
DR InterPro: IPR001201; PAP_25A_core.
DR InterPro: IPR007087; Znf_C2H2.
DR Pfam: PF01909; NTP_transf_2; 1.
DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_1.
SQ SEQUENCE 447 AA; 50248 MW; 67A9A7660A8BCAIF CRC64;

Query Match 78.6%; Score 33; DB 2; Length 447;
Best Local Similarity 75.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 HOYLSRT 8
Db 154 HOYLYNRT 161

RESULT 14
Q55MC9_CRYNE
ID Q55MC9_CRYNE PRELIMINARY; PRT; 547 AA.
AC Q55MC9;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=CNB10830;
OS Cryptococcus neoformans var. neoformans B-3501A.
OC Eukaryota; Fungi; Basidiomycota; Hymenymycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
OX NCBI_TaxID=283643;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC SRRIN=B-3501A;
RA Fung E., Hyman R.W., Rowley D., Bruno D., Miranda M., Fukushima M.,
Wickes B.L., Fu J., Davis R.W.;
RT "Cryptococcus neoformans serotype D sequencing.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
DR EMBL: AA01000044; EAL18822.1; -; Genomic_DNA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR GO: GO:0006865; F:amino acid transport; IEA.
DR GO: GO:0006810; P:transport; IEA.
KM Hypothetical protein; Transmembrane; Transport.
SQ SEQUENCE 547 AA; 56918 MW; 58E526C541E342B CRC64;
Query Match 78.6%; Score 33; DB 2; Length 547;
Best Local Similarity 75.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 HOYLSRT 8
Db 369 NOYLSRT 376

RESULT 15
Q5K8E4_CRYNE
ID Q5K8E4_CRYNE PRELIMINARY; PRT; 547 AA.
AC Q5K8E4;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Gaba permease, putative.
GN ORFNames=CNL06000;
OS Cryptococcus neoformans var. neoformans JEC21.
OC Eukaryota; Fungi; Basidiomycota; Hymenymycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
OX NCBI_TaxID=214684;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC SRRIN=JEC21;
RA Loftus B., Amedeo P., Roncaglia P., Vamathavan J., Uterback T.,
Van Aken S., Fraser C.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC SRRIN=JEC21;
SQ PubMed=15653466; DOI=10.1126/science.1103773;

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RA Loftus B.J., Fung E., Roncaglia P., Rowley D., Amedeo P., Bruno D.,
RA Vamathavan J., Miranda M., Anderson I.J., Frazer J.A., Allen J.E.,
RA Bosdet I.E., Brent M.R., Chiu R., Boering T.L., Donlin M.J.,
RA D'Souza C.A., Fox D.S., Grindberg V., Fu J., Fukushima M., Haas B.J.,
RA Huang J.C., Jambon G., Jones S.J.M., Koo H.L., Kzyvinski M.I.,
RA Kwon-Chung K.J., Langeler K.B., Malti R., Marra M.A., Marra R.E.,
RA Mathewson C.A., Mitchell T.G., Parlea M., Riggs F.R., Salzberg S.L.,
RA Schein J.E., Shvartsbeyn A., Shin H., Shumway M., Specht C.A.,
RA Sun B.B., Tenney A., Utterback T.R., Wickes B.L., Wortman J.R.,
RA Wye N.H., Kronstad J.W., Lodge J.K., Heltman J., Davis R.W.,
RA Fraser C.M., Hyman R.W.;
RT "The genome of the basidiomycetous yeast and human pathogen
RT Cryptococcus neoformans.";
RL Science 307.1321-1324(2005).
DR EMBL: AE017352; AM4664.1; -, Genomic_DNA.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0016020; C: membrane; IEA.
DR GO: GO:0005279; F: amino acid-polyamine transporter activity; IEA.
DR GO: GO:0006865; P: amino acid transport; IEA.
DR GO: GO:0006810; P: transport; IEA.
DR InterPro: IPR002293; AA/rel_permease1.
DR InterPro: IPR004841; Permease_region.
DR Pfam: PF00324; AA_permease_1.
KM Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 547 AA; 58919 MW; 58EB226C541E342B CRC64;

Query Match 78.6%; Score 33; DB 2; Length 547;
Best Local Similarity 75.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HOYLSRT 8
Db 369 HOYLSRT 376

RESULT 16
Q5AR9 EMENT PRELIMINARY; PRT; 617 AA.
AC Q5AR9_2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
GN ORFNames=AN9011.2;
OS Aspergillus nidulans FGSC A4.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; Emericella.
OX NCBI_Taxid=227321;
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=FGSC A4;
RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
RA Arachchi H.M., Barna N., Bastien S., Bloom T., Boguslavsky L.,
RA Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang Y.,
RA Choepel J., Collymore A., Cook A., Cooke P., Corn B., Deaellano K.,
RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA Erickson J., Faro S., Ferreira P., Fitzgerald M., Gage D., Galagan J.,
RA Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Illiev I.,
RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
RA Ma L.-J., Mabbitt R., Maclean C., Macdonald P., Major J., Manning J.,
RA Matthews C., Mancelli E., McCarthy M., Meldrum J., Meneus L.,
RA Mihova T., Mienga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,
RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
RA Rachupka A., Ramasamy U., Raymond C., Rella R., Rise C., Rogov P.,
RA Roman J., Schauer S., Schnappack R., Seaman S., Severy P., Smitrov S.,
RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
RA Talams J., Tesfaye S., Theodore J., Topham K., Travers M.,
RA Vasilev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
RA Lander E.;
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RT "Genome Sequence of Aspergillus nidulans";
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AACD01000168; EA64343.1; -, Genomic_DNA.
DR GO: GO:0005060; F: PAD binding; IEA.
DR GO: GO:0016614; F: oxidoreductase activity, acting on CH-OH gr. .; IEA.
DR GO: GO:0006118; P: electron transport; IEA.
KM Flavoprotein; Hypothetical protein.
SQ SEQUENCE 617 AA; 66045 MW; 79AE1BC078EC25A CRC64;

Query Match 78.6%; Score 33; DB 2; Length 617;
Best Local Similarity 75.0%; Pred. No. 3.1e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HOYLSRT 8
Db 364 HOYLSRT 371

RESULT 17
Q6FQ28 CANGA PRELIMINARY; PRT; 734 AA.
AC Q6FQ28;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Candida glabrata strain CBS138 chromosome I complete sequence.
GN OrderedLocusNames=CAGL0109636g;
OS Candida glabrata (Yeast) (Torulopsis glabrata).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_Taxid=5478;
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 2001 / CBS 138;
RX PubMed=1529592; DOI=10.1038/nature02579;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthonard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
RA Boistrume A., Boyer J., Cattolico L., Confalonieri F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantuya F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicard J.-M., Nikolski M., Oztas S., Ozler-Kalogeropoulos O.,
RA Pellenz S., Portier S., Richard G.-F., Straub M.-L., Suleau A.,
RA Swennen D., Tekala F., Weslowski-Louvel M., Westhof E., Wirth B.,
RA Zenou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
RA Bouchler C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.-L.;
RT "Genome evolution in yeasts.";
RL Nature 430.35-44(2004).
DR EMBL: CR380955; CAG60603.1; -, Genomic_DNA.
DR GO: GO:0005622; C: intracellular; IEA.
DR GO: GO:0003725; F: double-stranded RNA binding; IEA.
DR GO: GO:0004525; F: ribonuclease III activity; IEA.
DR GO: GO:0006396; P: RNA processing; IEA.
DR InterPro: IPR001159; DS_RBD.
DR InterPro: IPR000999; RNase_III.
DR Pfam: PF00035; dsrm_1; RNase_III.
DR Pfam: PF00636; Ribonuclease_3; 1.
DR SMART: SM00535; RIBOC; 1.
DR PROSITE: PS50137; DS_RBD; 1.
DR PROSITE: PS00517; RNASE_3_1; 1.
DR PROSITE: PS50142; RNASE_3_2; 1.
KM Complete proteome.
SQ SEQUENCE 734 AA; 83375 MW; 1AF24B467C18D56C CRC64;

Query Match 78.6%; Score 33; DB 2; Length 734;
Best Local Similarity 85.7%; Pred. No. 3.8e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HOYLSRT 7
Db 364 HOYLSRT 371
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SQ SEQUENCE 2210 AA; 252831 MW; 620844843F1D496B CRC64;
Query Match 78.6%; Score 33; DB 2; Length 2210;
Best Local Similarity 85.7%; Pred. No. 1.2e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSSR 7
Db 1270 HOYLQSR 1276

RESULT 21
Q642U5 JUNIN PRELIMINARY; PRT; 2210 AA.
ID O642U5;
AC O642U5;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DE L protein.
OS Junin arenavirus.
OC Viruses; ssRNA negative-strand viruses; Arenaviridae; Arenavirus;
OC New world arenaviruses.
OX NCBI_TaxID=11619;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=Candid-1;
RC Walton A.H., Droll D.A., Chambers T.J.;
RA "Complete sequence analysis of the Candid-1 virus and expression of
RT encoded proteins."
RT Submitted (Aug-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; AY146354; AAU34183.1; -; Genomic RNA.
DR GO; GO:000368; F:RNA-directed RNA polymerase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0019079; P:viral genome replication; IEA.
DR InterPro; IPR010453; Arena_RNA_pol.
DR InterPro; IPR007099; RNA_pol_NSv1r.
DR Pfam; PF06317; Arena_RNA_pol; 1.
SQ SEQUENCE 2210 AA; 252616 MW; 0422065265E3E236 CRC64;

Query Match 78.6%; Score 33; DB 2; Length 2210;
Best Local Similarity 85.7%; Pred. No. 1.2e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSSR 7
Db 1270 HOYLQSR 1276

RESULT 22
Q61VU4 JUNIN PRELIMINARY; PRT; 2210 AA.
ID O61VU4 JUNIN PRELIMINARY; PRT; 2210 AA.
AC O61VU4;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE L protein.
OS Junin arenavirus.
OC Viruses; ssRNA negative-strand viruses; Arenaviridae; Arenavirus;
OC New world arenaviruses.
OX NCBI_TaxID=11619;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=Rumero;
RC Hajjaj A., Chain P.S.G., Do L.H., Smith K.L., Imbro P.M.,
RA Malfatti S.A.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY196410; AA140446.1; -; Genomic RNA.
DR GO; GO:000368; F:RNA-directed RNA polymerase activity; IEA.

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DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0019079; P:viral genome replication; IEA.
DR InterPro; IPR010453; Arena_RNA_pol.
DR InterPro; IPR007099; RNA_pol_NSv1r.
DR Pfam; PF06317; Arena_RNA_pol; 1.
SQ SEQUENCE 2210 AA; 252884 MW; 52214DE0FED7362 CRC64;

Query Match 78.6%; Score 33; DB 2; Length 2210;
Best Local Similarity 85.7%; Pred. No. 1.2e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSSR 7
Db 1270 HOYLQSR 1276

RESULT 23
Q6U7Y4 JUNIN PRELIMINARY; PRT; 2210 AA.
ID Q6U7Y4;
AC Q6U7Y4;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE L protein.
OS Junin arenavirus.
OC Viruses; ssRNA negative-strand viruses; Arenaviridae; Arenavirus;
OC New world arenaviruses.
OX NCBI_TaxID=11619;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=X13;
RC Bowen M.D., Thurman K., Minor E., Meyer R.F., Malfatti S.A., Do L.H.,
RA Smith K.L., McCreedy P.M., Chain P.S.G.;
RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY58022; AA05250.1; -; Genomic RNA.
DR GO; GO:000368; F:RNA-directed RNA polymerase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0019079; P:viral genome replication; IEA.
DR InterPro; IPR010453; Arena_RNA_pol.
DR InterPro; IPR007099; RNA_pol_NSv1r.
DR Pfam; PF06317; Arena_RNA_pol; 1.
SQ SEQUENCE 2210 AA; 252819 MW; D7DE7E07957AE17 CRC64;

Query Match 78.6%; Score 33; DB 2; Length 2210;
Best Local Similarity 85.7%; Pred. No. 1.2e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSSR 7
Db 1270 HOYLQSR 1276

RESULT 24
Q9Q0B0 NPVAG PRELIMINARY; PRT; 99 AA.
ID Q9Q0B0 NPVAG PRELIMINARY; PRT; 99 AA.
AC Q9Q0B0;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE AcMPV ORF79-like protein.
OS Anticarsia gemmatilis nuclear polyhedrosis virus (AgMPV).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolydnavirus.
OX NCBI_TaxID=31507;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=AgNPV-20;
RC MEDLINE=99449840; PubMed=10518714; DOI=10.1016/S0168-1702(99)00094-5;
RA Liu J., Maruniak J.E.;
RL "Molecular characterization of genes in the GP41 region of
RT baculoviruses and phylogenetic analysis based upon GP41 and polynedrin
RL genes."
Virus Res. 64:187-196(1999).

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DR EMBL; U37728; AAD54605.1; -; Genomic DNA.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004518; F:nuclease activity; IEA.
DR GO; GO:0006281; F:DNA repair; IEA.
DR InterPro; IPR000305; UVR_C_N.
DR Pfam; PF01541; G1Y-Y1G; 1.
DR SMART; SM00465; G1YC; 1.
SQ SEQUENCE 99 AA; 11785 MW; 485200062EC30F2A CRC64;

Query Match 76.2%; Score 32; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HOYLS 6
Db 94 HOYLS 99

RESULT 25

O6VTR5 NPVCD PRELIMINARY; PRT; 99 AA.

AC O6VTR5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Choriostoneura fumiferana defective polyhedrosis virus (Cfddef).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxId=74660;

RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20149221; PubMed=10683327; DOI=10.1006/viro.1999.0138;
RA Li X., Barrett J., Pang A., Klose R.J., Krell P.J., Arif B.M.;
RT "Characterization of an overexpressed spindle protein during a
RT baculovirus infection."
RL Virology 268:56-67(2000).

RL [2]
RN NUCLEOTIDE SEQUENCE.
RP PubMed=15784888; DOI=10.1099/vir.0.80489-0;
RX Lauzon H.A., Jamieson P.B., Krell P.J., Arif B.M.;
RT "Gene organization and sequencing of the Choriostoneura fumiferana
RT defective nucleopolyhedrovirus genome."
RL J. Gen. Virol. 86:945-961(2005).

RL [3]
RN NUCLEOTIDE SEQUENCE.

RP Lauzon H.A.M., Jamieson P.B., Krell P.J., Arif B.M.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY327402; AAQ91757.1; -; Genomic_DNA.

DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0004518; F:nuclease activity; IEA.

DR GO; GO:0006281; F:DNA repair; IEA.

DR InterPro; IPR000305; UVR_C_N.

DR Pfam; PF01541; G1Y-Y1G; 1.

DR SMART; SM00465; G1YC; 1.

KM Hypothetical protein.
SQ SEQUENCE 99 AA; 11751 MW; 5BFD852C8696A125 CRC64;

Query Match 76.2%; Score 32; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HOYLS 6
Db 94 HOYLS 99

RESULT 26

YH86 YEAST STANDARD; PRT; 134 AA.

ID YH86 YEAST
AC Q04814;
DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Hypothetical 15.6 kDa protein in HOR7-COX1 intergenic region.
CN OrderedLocustNames=YMR252C; ORFNames=YM9920.06C;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxId=4932;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=S288c / AB972;
RX MEDLINE=97313268; PubMed=9169872;
RA Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T.,
RA Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S.,
RA Jagsels K., Lyne G., Mole S., Odell C., Pearson D., Rajandream M.A.,
RA Rice P., Skelton J., Walsh S.V., Whitehead S., Barrett B.G.,
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome
RT XIII."
RL Nature 387:90-93(1997).

RL [2]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].

RC Matischky G., Rolfs A., Richardson A., Kane M., Baqui M., Taycher E.,
RA Hu Y., Vamberg F., Weger J., Kramer J., Moreira D., Kelley F.,
RA Zuo D., Raphael J., Hogle C., Jepson D., Williamson J., Camargo A.,
RA Gonzaga J., Vasconcelos A.T., Simpson A., Kolodner R., Harlow E.,
RA Labaer J.;
RT "Creation of the YFLX clone resource: cloning of Saccharomyces
RT cerevisiae ORFs in the Gateway recombinational cloning system."
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

CC EMBL; Z48639; CA88579.1; -; Genomic DNA.
DR EMBL; AY558123; AAS56449.1; -; Genomic_DNA.

DR PIR; S53074; S53074.

DR Germonline; 142927; -

DR Ensemble; YMR252C; Saccharomyces cerevisiae.

DR SGD; S000004865; YMR252C.

DR GO; GO:0005739; C:mitchondrion; IDA.

KM Complete proteome; Hypothetical protein.
SQ SEQUENCE 134 AA; 15635 MW; 09411BD5F3B8559C CRC64;

Query Match 76.2%; Score 32; DB 1; Length 134;
Best Local Similarity 75.0%; Pred. No. 99;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 HOYLSRT 8
Db 65 HOYPSRT 72

RESULT 27

O8LCX9 ARATH PRELIMINARY; PRT; 136 AA.

ID O8LCX9 ARATH PRELIMINARY;
AC O8LCX9;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Senescence-associated protein.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TaxId=3702;

RN [1]
RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=22088475; PubMed=12093376;

RA Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N.,

```

RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
RT "Full-length messenger RNA sequences greatly improve genome
RL annotation." 3:RESEARCH0029-RESEARCH0029(2002).
RN
RP NUCLEOTIDE SEQUENCE.
RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY086338; AA064406.1; -; mRNA.
DR Interpro; IPR001763; Rhodanese-like.
DR Pfam; PF00581; Rhodanese; 1.
DR SMART; SM00450; RHOD; 1.
DR PROSITE; PSS0206; RHODANSE 3; 1.
SQ SEQUENCE 136 AA; 14938 MW; DISCSE57D3656C66 CRC64;

Query Match 76.2%; Score 32; DB 2; Length 136;
Best Local Similarity 75.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
DB 30 HOYLDVRT 37

RESULT 28
O9FKM8 ARATH PRELIMINARY; PRT; 136 AA.
AC O9FKM8;
DT 01-MAR-2001 (TREMBlrel. 16; Created)
DT 01-MAR-2001 (TREMBlrel. 16; Last sequence update)
DT 10-MAY-2005 (TREMBlrel. 30; Last annotation update)
DE Senescence-associated protein sen1-like protein
(AT5G66170/KAI18_25).
GN Name=At5g66170;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98344145; PubMed=9679202;
RA Kaneo T., Kotani H., Nakamura Y., Sato S., Asamizu E., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. V. Sequence
RT features of the regions of 1,381,565 bp covered by twenty one
RT physically assigned P1 and TAC clones."
RN DNA Res. 5:131-145(1998).
[2]
RP NUCLEOTIDE SEQUENCE.
RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
RA Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,
RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,
RA Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,
RA Yamamura Y., Yu G., Yu S., Shinzaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
[3]
RP NUCLEOTIDE SEQUENCE.
RA Shinn P., Chen H., Cheuk R., Kim C.J., Meyers M.C., Banh J.,
RA Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,
RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,
RA Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,
RA Yamamura Y., Yu G., Yu S., Shinzaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
[4]
RP NUCLEOTIDE SEQUENCE.

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RA Totoki Y., Seki M., Ishida J., Nakajima M., Enju A., Kamiya A.,
RA Narusaka M., Shin-I T., Nakagawa M., Sakamoto N., Oishi K., Kohara Y.,
RA Kobayashi M., Toyoda A., Sakaki Y., Sakurai T., Iida K., Akiyama K.,
RA Satou M., Toyoda T., Konagaya A., Carninci P., Kawai J.,
RA Hayashizaki Y., Shinzaki K.;
RT "Large-scale analysis of RIKEN Arabidopsis full-length (RAFL) cDNAs."
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB011474; BAB10422.1; -; Genomic_DNA.
DR EMBL; AY065058; AAL57692.1; -; mRNA.
DR EMBL; AY091699; AAL10268.1; -; mRNA.
DR EMBL; AK22135; BAD95161.1; -; mRNA.
DR Interpro; IPR001763; Rhodanese-like.
DR Pfam; PF00581; Rhodanese; 1.
DR SMART; SM00450; RHOD; 1.
DR PROSITE; PSS0206; RHODANSE 3; 1.
SQ SEQUENCE 136 AA; 14883 MW; 6530B5E7D1B7BC64 CRC64;

Query Match 76.2%; Score 32; DB 2; Length 136;
Best Local Similarity 75.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
DB 30 HOYLDVRT 37

RESULT 29
Q4VOT7 BACCC PRELIMINARY; PRT; 172 AA.
AC Q4VOT7;
DT 13-SEP-2005 (TREMBlrel. 31; Created)
DT 13-SEP-2005 (TREMBlrel. 31; Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31; Last annotation update)
DE Hypothetical protein.
GN ORFNames=PB33J9_0001;
OS Bacillus cereus (strain ZK).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=28661;
RN
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=E33L;
RG Joint Genome Institute Microbial Sequencing, Finishing and Annotation
RG Team;
RT "Complete genome sequence of Bacillus cereus E33L."
RN Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
[2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=E33L;
RG Joint Genome Institute Microbial Sequencing, Finishing and Annotation
RG Team;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CP000044; AA160669.1; -; Genomic_DNA.
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 172 AA; 18642 MW; 237C9EAF640EC5F CRC64;

Query Match 76.2%; Score 32; DB 2; Length 172;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
DB 80 HOYSSRT 87

RESULT 30
O9OEY7 SCORO PRELIMINARY; PRT; 178 AA.
AC O9OEY7;
DT 01-MAY-2000 (TREMBlrel. 13; Created)
DT 01-MAY-2000 (TREMBlrel. 13; Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25; Last annotation update)

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DE Hypothetical protein.
 OS Porcine respiratory coronavirus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
 CC Coronaviridae; Coronavirus; Group 1 species.
 NCBI_TaxID=11146;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=BM126;
 RX MEDLINE=20403263; PubMed=10948987; DOI=10.1007/s007050070114;
 RA Kim L., Hayes J., Lewis P., Parwani A.V., Chang K.O., Saif L.J.;
 RT "Molecular characterization and pathogenesis of transmissible
 gastroenteritis coronavirus (TGEV) and porcine respiratory coronavirus
 (PRCV) field isolates co-circulating in a swine herd."
 RL Arch. Virol. 145:1133-1147(2000).
 DR EMBL: AF179887; AAF02714.1; -; Genomic_RNA.
 DR InterPro: IPR004293; Corona_NS3b.
 DR Pfam: PF03053; Corona_NS3b; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 178 AA; 20448 MW; 12C1CF4674F72A65 CRC64;
 Query Match 76.2%; Score 32; DB 2; Length 178;
 Best Local Similarity 62.5%; Pred. No. 1.3e+02;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HOVLSSRT 8
 Db 40 HQFVSART 47
 RESULT 31
 04HVO1 GIBZE PRELIMINARY; PRT; 195 AA.
 ID 04HVO1;
 AC 04HVO1;
 DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=FG09907.1;
 GN Glibberella zeae PH-1.
 OS Glibberella zeae PH-1.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocreales; Nectriaceae; Glibberella.
 OX NCBI_TaxID=229533;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PH-1;
 RA Birren B., Nisbaum C., Abouelleil A., Allen N., Anderson S.,
 RA Atarachi H.M., Barna N., Bastien V., Bloom T., Boguslavsky L.,
 RA Boukhalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
 RA Choepel Y., Collymore A., Cook A., Cooke P., Cornu B., Dearellano K.,
 RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
 RA Erickson J., Faro S., Ferreira P., Fitzgerald M., Gage D., Galagan J.,
 RA Gardyna S., Gerner S., Graham L., Grand-Pierre N., Hafez N.,
 RA Hagopian D., Haqos B., Hall J., Horton L., Hulme W., Iliev I.,
 RA Jaffe D., Johnson R., Jones C., Kamat M., Kamat A., Karatas A.,
 RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
 RA Ma L.-J., Mabbitt R., Maclean C., Macdonald P., Major J., Manning J.,
 RA Matthews C., Mancelli E., McCarthy M., Meldrum J., Meneus L.,
 RA Mihova T., Mienga V., Murphy T., Naylor J., Nguyen C., Nicot R.,
 RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,
 RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
 RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
 RA Roman J., Schauer S., Schupack R., Seaman S., Severy S., Smirnov S.,
 RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
 RA Talamas J., Testaye S., Theodore J., Topham K., Travers M.,
 RA Vasiliev H., Venkataaraman V.S., Viel R., Vo A., Wang S., Wilson B.,
 RA Wu X., Wyman D., Young G., Zainoun J., Zemek L., Zimmer A., Zody M.,
 RA Lander E.;
 RT "Fusarium graminearum genome sequence."
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CATION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 DR EMBL: AAC01000411; EAA70133.1; -; Genomic_DNA.

KW Hypothetical protein.
 SQ SEQUENCE 195 AA; 2123 MW; 3A9C7C6C26F8AB07 CRC64;
 Query Match 76.2%; Score 32; DB 2; Length 195;
 Best Local Similarity 85.7%; Pred. No. 1.5e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 HOVLSSRT 7
 Db 94 HSYLSSR 100
 RESULT 32
 09F3M7 STRCO PRELIMINARY; PRT; 212 AA.
 ID 09F3M7;
 AC 09F3M7;
 DT 01-MAR-2001 (TReMBLrel. 16, Created)
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
 DE Putative secreted protein.
 GN OrderedLocustNames=SC010F4.34;
 OS Streptomyces coelicolor.
 CC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 CC Streptomycinae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=A3(2) / M145;
 RC MEDLINE=2196410; PubMed=12000953; DOI=10.1038/417141a;
 RX Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kleser T., Larke L., Murphy L.D., Oliver K., O'Neill S.,
 RA Rabinowitsch E., Rajandream M.A., Rutherford K.M., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 coelicolor A3(2)."
 RL Nature 417:141-147(2002).
 DR EMBL: AL939132; CAC16994.1; -; Genomic_DNA.
 DR GO: GO:0008703; F:5-amino-6-(5-phosphoribosylamino)uracil red. .; IEA.
 DR GO: GO:0016491; F:oxidoreductase activity; IEA.
 DR GO: GO:0009231; P:riboflavin biosynthesis; IEA.
 DR InterPro: IPR002734; RibDG_C.
 DR Pfam: PF01872; RibD_C; 1.
 KW Complete proteome.
 SQ SEQUENCE 212 AA; 23246 MW; 588B8C9351CED2BC CRC64;
 Query Match 76.2%; Score 32; DB 2; Length 212;
 Best Local Similarity 62.5%; Pred. No. 1.6e+02;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HOVLSSRT 8
 Db 100 HKTVASRT 107
 RESULT 33
 08ODU1 9HIV1 PRELIMINARY; PRT; 225 AA.
 ID 08ODU1;
 AC 08ODU1;
 DT 01-JUN-2002 (TReMBLrel. 21, Created)
 DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
 DE Gag protein (Fragment).
 GN Name=gag;
 OS Human immunodeficiency virus 1.
 OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
 OC Lentivirus; Primate lentivirus group.
 OX NCBI_TaxID=11676;
 RN [1]

```
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21665446; PubMed=11807313;
DOI=10.1097/00002030-200201250-00018;
RA Vitreli D.L., Kaleebu P., Morgan D., Watera C., Magambo B.,
Lyagoba F., Whitworth J.;
RT "Inter- and intra-genic interubtype HIV-1 recombination in rural and
semi-urban Uganda.";
RL AIDS 16:279-286(2002).
DR EMBL; AY051288; AAL16395.1; -; Genomic_DNA.
DR HSSP; Q724971 1L6N.
DR SMR; Q8QD01; 1-225.
DR GO; GO:0019013; C:Viral nucleocapsid; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR GO; GO:0016032; P:Viral life cycle; IEA.
DR InterPro; IPR000721; Gag_p24.
DR InterPro; IPR000771; Imm_lentv_matrix.
DR InterPro; IPR008919; Retrov_capsid_N.
DR Pfam; PF00540; Gag_p17; 1.
DR Pfam; PF00607; Gag_p24; 1.
DR PRINTS; PR00234; HIV1MATR1X.
KM AIDS; Core protein.
FT NON_TER 1
SQ SEQUENCE 225 AA; 24694 MW; B77F721F7686CF4F CRC64;

Query Match 76.2%; Score 32; DB 2; Length 225;
Best Local Similarity 75.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HOYLSRT 8
Db 112 HQHLSPT 119

RESULT 34
Q9QEV6_9COCO PRELIMINARY; PRT; 239 AA.
ID Q9QEV6_9COCO PRELIMINARY;
AC Q9QEV6;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Porcine respiratory coronavirus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirinae; Group 1 species.
OX NCBI_TaxId=11146;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BM154;
RX MEDLINE=20403263; PubMed=10948987; DOI=10.1007/s007050070114;
RA Kim L., Hayes J., Lewis P., Parwani A.V., Chang K.O., Saif L.J.;
RT "Molecular characterization and pathogenesis of transmissible
gastroenteritis coronavirus (TGEV) and porcine respiratory coronavirus
(RPCV) field isolates co-circulating in a swine herd.";
RL Arch. Virol. 145:1133-1147(2000).
DR EMBL; AF179888; AAF02716.1; -; Genomic_RNA.
DR InterPro; IPR004293; Corona_NS3b.
DR Pfam; PF03053; Corona_NS3b; 1.
KM Hypothetical protein.
SQ SEQUENCE 239 AA; 27198 MW; EF97BB42551D28F2 CRC64;

Query Match 76.2%; Score 32; DB 2; Length 239;
Best Local Similarity 62.5%; Pred. No. 1.8e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HOYLSRT 8
Db 40 HQFVSART 47

RESULT 35
VNS3_CVCAI STANDARD; PRT; 250 AA.
ID_VNS3_CVCAI
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AC P36995;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Nonstructural protein 3-B (ORF 3B).
OS Canine enteric coronavirus (strain InsaVC-1) (CCoV) (CCV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirinae; Group 1 species.
OX NCBI_TaxId=36391;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC RNA].
RX MEDLINE=93057357; PubMed=1431811;
RA Horsburgh B.C., Brierley I., Brown T.D.K.;
RT "Analysis of a 9.6 kb sequence from the 3' end of canine coronavirus
J. Gen. Virol. 73:2849-2862(1992).
CC -1- SIMILARITY: Belongs to the coronaviruses NS3b protein family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC
CC EMBL; D13096; BAA02411.1; ALT TERM; Genomic_RNA.
DR InterPro; IPR004293; Corona_NS3b.
DR Pfam; PF03053; Corona_NS3b; 1.
SQ SEQUENCE 250 AA; 28426 MW; FCB7ABFP83DD9CFE CRC64;

Query Match 76.2%; Score 32; DB 1; Length 250;
Best Local Similarity 62.5%; Pred. No. 1.9e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HOYLSRT 8
Db 39 HQFVSART 46

RESULT 36
082G95_STRAW PRELIMINARY; PRT; 270 AA.
ID 082G95_STRAW PRELIMINARY;
AC 082G95;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Putative Arac-family transcriptional regulator.
GN OrderedLocustNames=SAV4003;
OS Streptomyces avermitilis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomycetes.
OX NCBI_TaxId=33903;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=22608306; PubMed=12692562; DOI=10.1038/nbt820;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
Sakaki Y., Hattori M., Omura S.;
RT "Complete genome sequence and comparative analysis of the industrial
microorganism Streptomyces avermitilis.";
RL Nat. Biotechnol. 21:526-531(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osomoe T.,
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RT "Genome sequence of an industrial microorganism Streptomyces
S. avermitilis: deducing the ability of producing secondary
metabolites.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
DR EMBL; BA000030; BAC71715.1; -; Genomic_DNA.
DR GO; GO:0005622; C:intracellular; IEA.
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DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR003313; Arac binding.
DR InterPro; IPR012287; Homedomain-rel.
DR Pfam; PF02311; Arac_binding; 1.
DR Pfam; PF00165; HTH_Arac; 2.
DR PRINTS; PR00032; HTHARAC.
DR SMART; SM00342; HTH_ARAC; 1.
DR PROSITE; PS01124; HTH_ARAC_FAMILY_2; 1.
KM Complete proteome.
SQ SEQUENCE 270 AA; 30423 MW; DD29560D044B19B9 CRC64;

Query Match 76.2%; Score 32; DB 2; Length 270;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSSR 7
DB 214 HOYLMSR 220

RESULT 37
Q9FCG3_STRCO PRELIMINARY; PRT; 271 AA.
ID Q9FCG3_STRCO
AC Q9FCG3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative Arac-family transcriptional regulator.
GN OrderedLocustNames=SCO4206; ORFNames=2SCD46.20c;
OC Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomycetes.
OX NCBI_TaxID=1902;
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; Pubmed=12000953; DOI=10.1038/41714a;
RA Bentley S.D., Chater K.F., Cerdano-Parraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieseer H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Gobie A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieseer T., Larke L., Murphy L.D., Oliver K., O'Neill S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K.M., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
EMBL: AL939119; CAC04042.1; -; Genomic_DNA.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR003313; Arac binding.
DR InterPro; IPR012287; Homedomain-rel.
DR InterPro; IPR000005; HTHARAC.
DR Pfam; PF02311; Arac_binding; 1.
DR Pfam; PF00165; HTH_Arac; 2.
DR PRINTS; PR00032; HTHARAC.
DR SMART; SM00342; HTH_ARAC; 1.
DR PROSITE; PS01124; HTH_ARAC_FAMILY_2; 1.
KM Complete proteome.
SQ SEQUENCE 271 AA; 29783 MW; A0930A7873081BE2 CRC64;

Query Match 76.2%; Score 32; DB 2; Length 271;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSSR 7
DB 213 HOYLMSR 219

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- RESULT 38
Q8ED48_SHEON PRELIMINARY; PRT; 296 AA.
ID Q8ED48_SHEON
AC Q8ED48;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein SO2922.
GN OrderedLocustNames=SO2922;
OC Shewanella oneidensis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Shewanellaceae; Shewanella.
OX NCBI_TaxID=70863;
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=NR-1;
RX MEDLINE=22297666; Pubmed=12368813; DOI=10.1038/nbt749;
RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
RA Read T.D., Eissen J.A., Seshadri R., Ward N.L., Mathe B.A.,
RA Clayton R.A., Meyer T., Tsapin A., Scott J., Beaman M.J.,
RA Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S.,
RA Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A.,
RA White O., Wolf A.M., Vamathevan J.J., Weidman J.F., Impraim M.,
RA Lee K., Berry K.J., Lee C., Mueller J., Khouri H.M., Gill J.,
RA Utechbek T.R., McDonald L.A., Feldblyum T.V., Smith H.O.,
RA Venter J.C., Neilson K.H., Fraser C.M.;
RT "Genome sequence of the dissimilatory metal ion-reducing bacterium
RT Shewanella oneidensis.";
RL Nat. Biotechnol. 20:1118-1123(2002).
EMBL: AE015731; AAN5936.1; -; Genomic_DNA.
DR TIGR; SO2922;
DR InterPro; IPR010099; Cone_hypoth_yfch.
DR InterPro; IPR001509; Epimerase_Dh.
DR Pfam; PF01370; Epimerase; 1.
DR TIGRPFAM; TIGR01777; yfch; 1.
KM Complete proteome.
SQ SEQUENCE 296 AA; 32596 MW; 0D292DDC08B163F8 CRC64;

Query Match 76.2%; Score 32; DB 2; Length 296;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYLSS 6
DB 44 HOYLSS 49

RESULT 39
Q5P9T3_ANAMM PRELIMINARY; PRT; 299 AA.
ID Q5P9T3_ANAMM
AC Q5P9T3;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Pantocate-beta-alanine ligase (EC 6.3.2.1).
GN Name=panc; OrderedLocustNames=AM1089;
OS Anaplasma marginale (Strain St. Maries).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Anaplasmataceae; Anaplasma.
OX NCBI_TaxID=234826;
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP PubMed=15618402; DOI=10.1073/pnas.040656102.
RX Brayton K.A., Kappmeyer L.S., Herndon D.R., Dark M.J., Tibbals D.L.,
RA Palmer G.H., McGuire T.C., Knowles D.P., Jr.;
RT "Complete genome sequencing of Anaplasma marginale reveals that the
RT surface is skewed to two superfamilies of outer membrane proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 102:844-849(2005).
EMBL: CP0000030; AAV86947.1; -; Genomic_DNA.
DR GO; GO:0016874; F:Ligase activity; IEA.
DR GO; GO:0004592; F:pantocate-beta-alanine ligase activity; IEA.

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GN ORFNames=AN0281.2;
OS Aspergillus nidulans FGSC A4.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; Emicellia.
OX NCBI_TaxID=227321;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FGSC A4;
RA Birren B., Nisbaum C., Abouelleil A., Allen N., Anderson S.,
RA Archchi H.M., Barna N., Bastien V., Bloom T., Boguslavsky L.,
RA Boukhalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA Choepel Y., Collymore A., Cook A., Cooke P., Corum B., Deatellano K.,
RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA Erickson J., Faro S., Ferreira P., Fitzgerald M., Gage D., Galagan J.,
RA Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA Jaffe D., Johnson R., Jones C., Kamat M., Kamat A., Karatas A.,
RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
RA Ma L.-J., Mabbitt R., Maclean C., Macdonald P., Major J., Manning J.,
RA Matthews C., Mauceli E., McCarthy M., Meldrum J., Menues L.,
RA Mahova T., Menga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,
RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
RA Rachupka A., Ramasamy U., Raymond C., Rella R., Rise C., Rogov P.,
RA Roman J., Schauer S., Schupack R., Seaman S., Severy P., Smlirnov S.,
RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
RA Talamas J., Testaye S., Theodore J., Topham K., Travers M.,
RA Vassiliou H., Venkatarman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA Wu X., Wyman D., Young G., Zannou J., Zembek L., Zimmer A., Zody M.,
RA Lander E.;
RT "Genome Sequence of Aspergillus nidulans."
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAC0100005; EAA6154.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 453 AA; 50401 MW; CA3368C47E404A7C CRC64;

Query Match 76.2%; Score 32; DB 2; Length 453;
Best Local Similarity 85.7%; Pred. No. 3.7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HOYLSRT 7
Db 34 HQHLSR 40

RESULT 43
Q73V57 MYCPA PRELIMINARY; PRT; 486 AA.
AC Q73V57;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS OrderedLocuNames=MAP3159;
OC Mycobacterium paratuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium;
OC Mycobacterium avium complex (MAC).
OX NCBI_TaxID=1770;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=k10;
RA Li L., Bannantine J., Zhang Q., Amonsin A., Alt D., Kapur V.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB017238; AAS05707.1; -; Genomic_DNA.
DR GO; GO:0003824; P: catalytic activity; IEA.
DR GO; GO:0008152; P: metabolism; IEA.
DR InterPro; IPR001735; PLD.
DR Pfam; PF00614; PLDc; 2.
DR SMART; SM00155; PLDc; 2.

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DR PROSITE; PS50035; PLD; 2.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 486 AA; 54173 MW; 0537791dFAE313C4 CRC64;

Query Match 76.2%; Score 32; DB 2; Length 486;
Best Local Similarity 75.0%; Pred. No. 4e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HOYLSRT 8
Db 276 NOYLSRT 283

RESULT 44
Q4UBW9 SULAC PRELIMINARY; PRT; 493 AA.
AC Q4UBW9;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Glycosyl transferase (EC 2.-.-.-).
GN OrderedLocuNames=Sac1_0294;
OS Sulfolobus acidocaldarius.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=2285;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 33909 / NCIB 11770 / DSM 639;
RX PubMed=15959215; DOI=10.1128/JB.187.14.4992-4999.2005;
RA Chen L., Bruegger K., Skovgaard M., Redder P., She O., Torarinnsson E.,
RA Greve B., Aweyer M., Zibat A., Klenk H.-P., Garrett R.A.;
RT "The genome of Sulfolobus acidocaldarius, a model organism of the
RT Crenarchaeota."
RL J. Bacteriol. 187:4992-4999(2005).
DR EMBL; CP000077; AAY7910.1; -; Genomic_DNA.
KW Complete proteome; Transferase.
SQ SEQUENCE 493 AA; 56780 MW; BC907E5278B6CC97 CRC64;

Query Match 76.2%; Score 32; DB 2; Length 493;
Best Local Similarity 75.0%; Pred. No. 4e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HOYLSRT 8
Db 185 HPYFSRT 192

RESULT 45
Q6NVU4 BRARE PRELIMINARY; PRT; 711 AA.
AC Q6NVU4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein zgc:76890.
GN ORFNames=zgc:76890;
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo A.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshitaki S., Carninci P., Prange C.,

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RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Mowley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RA Strausberg R.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC068016; AAH68016.1; -, mRNA.
DR ZFIN; ZDB-GENE-040426-2085; zgc:76890.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:Protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:Protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:Protein amino acid phosphorylation; IEA.
DR InterPro; IPR000095; PAKbox/Rhodning.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser Thr kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00786; PBD.1.
DR Pfam; PF00069; Pkinase.1.
DR ProDom; PD000001; Prot_kinase.1.
DR SMART; SM00285; PBD.1.
DR SMART; SM00220; S_TKc.1.
DR SMART; SM00219; Ty_TKc.1.
DR PROSITE; PSS0108; CRIB.1.
DR PROSITE; PSS0107; PROTEIN_KINASE_ATP.1.
DR PROSITE; PSS0011; PROTEIN_KINASE_DOM.1.
DR HypoProtein; HYP00001; PROTEIN_KINASE_DOM.1.
KW Hypothetical protein.
SQ SEQUENCE 711 AA; 78614 MW; D09E7BD579D211B CRC64;

Query Match 76.2%; Score 32; DB 2; Length 711;
Best Local Similarity 75.0%; Pred. No. 6e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HOXLSRT 8
DB 182 HAYLESRT 189

RESULT 46
065106 JPICO
ID 065106 JPICO PRELIMINARY; PRT; 758 AA.
AC 065106;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Figure 2. The structural protein coding region from FMDV SAT3.
DE precursor (fragment).
OS Foot-and-mouth disease virus SAT 3.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Aphthovirus; Foot-and-mouth disease virus.
OX NCBI_TaxID=12123;
[1]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=89232753; PubMed=2541051; DOI=10.1016/0378-1119(89)90268-0;
RA Brown A.V., Campbell R.O., Clarke B.E.;
RT "The nucleotide sequence of the structural-protein-coding region of
RT foot-and-mouth disease virus serotype SAT3."
RL Gene 75:225-233(1989).
DR EMBL; M28719; AAA53370.1; -, Genomic_RNA.
DR PIR; J0198; J0198.
DR HSSP; Q88590; ITMF.
DR SMR; Q65106; 17-62.

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DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0008234; F:cysteine-type peptidase activity; IEA.
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006410; F:transcription, RNA-dependent; IEA.
DR InterPro; IPR004080; FMDVPIcoat.
DR InterPro; IPR001676; Rhv.
DR Pfam; PF00073; Rhv.3.
DR PRINTS; PR01542; FMDVPICOAT.
KW Signal.
FT SIGNAL 3
FT CHAIN 1
FT CHAIN 87
FT CHAIN 88
FT CHAIN 305
FT CHAIN 525
FT CHAIN 526
FT CHAIN 742
FT CHAIN 743
FT CHAIN >758
FT NON_TER 1
FT NON_TER 758
FT NON_TER 758
SQ SEQUENCE 758 AA; 83424 MW; 172622D436E7B95B CRC64;

Query Match 76.2%; Score 32; DB 2; Length 758;
Best Local Similarity 62.5%; Pred. No. 4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOXLSRT 8
DB 232 HOXINERT 239

RESULT 47
054208 DICDI
ID 054208 DICDI PRELIMINARY; PRT; 850 AA.
AC 054208;
DT 11-SEP-2005 (TEMBLrel. 31, Created)
DT 13-SEP-2005 (TEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
DE ORFNames=DDB0204337;
GN Dictyostelium discoideum (Slime mold).
OS Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
[1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
RA Sugeng R., Berriman M., Song J., Olsen R., Szafranski K., Xu Q.,
RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
RA Kerhornou A., Nle X., Hall N., Anjard C., Hemphill L., Bason N.,
RA Farbrother P., Deasy B., Just E., Morio T., Roat R., Churcher C.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Muzny D., Moutier T., Pain A., Lu M., Harper D., Lindsay I.,
RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
RA Mardopero A., Felder M., Thangavelu M., Johnson D., Knights A.,
RA Loubegeed H., Mungall K., Oliver K., Price C., Quail M.A.,
RA Uneshihara H., Hernandez J., Rabinowitsch E., Steffen D., Sanders M.,
RA Ma J., Kohara Y., Sharp S., Simons M., Spiegler S., Tivey A.,
RA Suga S., White B., Walker D., Woodward J., Winkler T., Yanaka Y.,
RA Shaulsky G., Schleicher M., Weinstein G., Rosenthal A., Cox E.C.,
RA Chisholm R.L., Gibbs R., Loomis W.F., Platzner M., Kay R.R.,
RA Williams J., Dear P.H., Noegel A.A., Batirel B., Kuapa A.;
RT "The genome of the social amoeba Dictyostelium discoideum."
RL Nature 0:0-0(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC preliminary data.
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
DR EMBL; AAF01000052; EAL68161.1; -, Genomic_DNA.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0006396; P:RNA processing; IEA.
DR InterPro; IPR003107; HAT.
DR InterPro; IPR011990; TPR-like_helical.

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DR SMART; SM00386; HAT; 10.
KM Hypothetical protein; Repeat.
SQ SEQUENCE 850 AA; 101312 MW; 031FDA89110C2A6D CRC64;

Query Match 76.2%; Score 32; DB 2; Length 850;
Best Local Similarity 75.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
DB 82 HOYLSRT 89

RESULT 48

080612_9EMTO PRELIMINARY; PRT; 861 AA.

ID 080612_9EMTO PRELIMINARY; PRT; 861 AA.
AC 080612;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Polypeptide (Fragment).
OS Human enterovirus 77.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae; Enterovirus.
OX NCBI_TaxID=222887;
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=Jafewille;
RX MEDLINE=22541853; PubMed=12655083; DOI=10.1099/vir.0.18647-0;
RA Nordier H., Bjerregaard L., Magnus L., Lima B., Aymard M., Chomel J.J.;
RT "Sequencing of 'untypable' enteroviruses reveals two new types, EV-77 and EV-78, within human enterovirus type B and substitutions in the BC loop of the VP1 protein for known types."
RL J. Gen. Virol. 84:827-836(2003).
RN NUCLEOTIDE SEQUENCE.
RC Oberste S.M., Michale S.M., Maher K., Schmitt D., Cisterna D., Juntila N., Uddin M., Chomel J.-J., Lau C.-S., Rida W., al-Busaidy S., Nordier H., Magnus L., Pallansch M.A.;
RT "Molecular identification and characterization of two proposed new enterovirus serotypes, EV74 and EV75."
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY208119; AF059358.2; -; Genomic_RNA.
DR GO: GO:0019028; C:Viral capsid; IEA.
DR GO: GO:0008234; F:Cysteine-type peptidase activity; IEA.
DR GO: GO:0003368; F:RNA-directed RNA polymerase activity; IEA.
DR GO: GO:0005198; F:Structural molecule activity; IEA.
DR GO: GO:0016740; F:transcription activity; IEA.
DR GO: GO:0006410; P:transcription, RNA-dependent; IEA.
DR InterPro: IPR001956; CBD_3.
DR InterPro: IPR012282; Cytochrome_c_R.
DR InterPro: IPR011992; EF-Hand_type.
DR InterPro: IPR002563; Flv_red_FMN_bind.
DR InterPro: IPR012287; Homodomain-rel.
DR InterPro: IPR001093; IMPH/GMPase.
DR InterPro: IPR000070; Pectinesterase.
DR InterPro: IPR003138; Pico_P1A.
DR InterPro: IPR008976; PLAT_LH2.
DR InterPro: IPR001676; Rbv.
DR InterPro: IPR011991; Wing_hlx_DNA_bol.
DR Pfam: PF02236; Pico_P1A; I.
DR Pfam: PF00073; Rbv_3.
KM Polypeptide.
FT CHAIN 1 67 VP4.
FT CHAIN 68 330 VP2.
FT CHAIN 331 571 VP3.
FT CHAIN 572 >861 VP1.
FT NON_TER 861 861
SQ SEQUENCE 861 AA; 95296 MW; 868D4B0915842A80 CRC64;

Query Match 76.2%; Score 32; DB 2; Length 861;

Best Local Similarity 62.5%; Pred. No. 7.3e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
DB 257 HOYLSRT 264

RESULT 49

04PH70_USTMA PRELIMINARY; PRT; 1353 AA.

ID 04PH70_USTMA PRELIMINARY; PRT; 1353 AA.
AC 04PH70;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
OS ORFNames=UM00543.1;
GN Ustilago maydis 521.
OU Ustilago maydis 521.
OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes; Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
OX NCBI_TaxID=237631;
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=521;
RA Birren B., Nusbaum C., Abebe A., Abouelell A., Adekoya E., Alt-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S., Arachchi H., Armbruster J., Bachantang P., Baldwin J., Barry A., Bayul T., Blitsheteyn B., Bloom T., Blye J., Boguslavsky L., Borowsky M., Boukhalter B., Brunache A., Butler J., Calixte N., Calvo S., Camarata J., Campo K., Chang J., Cheshtang Y., Citroen M., Collymore A., Considine T., Cook A., Coko P., Corum B., Cuomo C., David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P., Dorje K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R., Erickson J., Farina A., Faro S., Ferreira P., Fischer H., Gierre S., Fitzgerald W., Foley K., Gage D., Galagan J., Geatin G., Gierre S., Guitre A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N., Hagopian D., Hagos B., Hall J., Hatchet B., Heller A., Higgins H., Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I., Jaffe D., Jones C., Kamel M., Kamat A., Kamysseis M., Karlsson E., Kells C., Kieu A., Kiser P., Kodira C., Kulbokas E., Labutti K., Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T., Lindblad-toh K., Liu X., Lokysang T., Lokysang Y., Lucien O., Lui A., Ma L.J., Mabbitt R., MacDonald J., Maclean C., Major J., Manning J., Maraballa R., Marr K., Matthews C., Mancelli E., McCarthy M., McDonough S., Mcghee T., Meldrum J., Menes L., Mesirov J., Minahey A., Mihova T., Mikkelsen T., Mlenga V., Moru K., Mozes J., Mulrain L., Munson G., Naylor J., Neves C., Nguyen C., Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C., Norbu N., O'donnell P., Okoawo O., O'leary S., Omotosho B., O'Neill K., Osman S., Parker S., Peritt D., Phunkhang P., Pignani B., Purcell S., Rachupka T., Ramassamy U., Rameau R., Ray V., Raymond C., Rector R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P., Rutman M., Schubach R., Seaman C., Settipalli S., Sharpe T., Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnez C., Spencer B., Stalker J., Stange-thomann N., Stavropoulos S., Stetson K., Stone C., Stone S., Stubbs W., Talamas J., Tchinga P., Tenzing P., Tesfaye S., Theodore J., Thoulutang Y., Topham K., Towey S., Tsamta T., Tsomo N., Vallee D., Vassiliev H., Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T., Wang S., Yang X., Yeager S., Wilkison J., Wu Y., Wyman D., Yadav S., Zimmer A., Zody M., Lander E.;
RT "The genome sequence of Ustilago maydis".
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -i- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.
CC EMBL: AACP0100012; EAK80995.1; -; Genomic_DNA.
KM Hypothetical protein.
SQ SEQUENCE 1353 AA; 143888 MW; 17A51E5430B31E0A CRC64;

Query Match 76.2%; Score 32; DB 2; Length 1353;
Best Local Similarity 62.5%; Pred. No. 1.2e+03;

Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
|:|:|:|
Db 72 HKYLSNKT 79

RESULT 50

Q5KTM2_BOMMO
ID Q5KTM2_BOMMO PRELIMINARY; PRT; 1401 AA.
AC Q5KTM2;
DT 10-MAY-2005 (TReMBLrel. 30, Created)
DT 10-MAY-2005 (TReMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TReMBLrel. 30, Last annotation update)
DE Reverse transcriptase.
GN Name=gag;
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PS0;
RA Abe H., Mita K., Yasukochi Y., Oshiki T., Shimada T.;
RT "The Retrotransposable Elements on the W chromosome of the Silkworm,
RT Bombyx mori.";
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB126055; BAD8655.1; -; Genomic_DNA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR GO; GO:0006310; P:DNA recombination; IEA.
DR GO; GO:0006278; P:RNA-dependent DNA replication; IEA.
DR InterPro; IPR001584; Rve.
DR InterPro; IPR00477; RVTse.
DR InterPro; IPR001878; Znf_CCHC.
DR Pfam; PF00665; Rve; 1.
DR Pfam; PF00078; RVT_1; 1.
DR Pfam; PF00098; Zf-CCHC; 1.
KW RNA-directed DNA polymerase.
SQ SEQUENCE 1401 AA; 157466 MW; 697495E47392BB68 CRC64;

Query Match 76.2%; Score 32; DB 2; Length 1401;
Best Local Similarity 75.0%; Pred. No. 1.2e+03;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
|:|:|:|
Db 781 HOYLYGRT 788

Search completed: May 4, 2006, 13:06:26
Job time : 115.921 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 4, 2006, 13:09:53 ; Search time 18.0317 Seconds
(without alignments)
36.680 Million cell updates/sec

Title: US-10-700-632-6
Perfect score: 42
Sequence: 1 HOX15SRT 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 1000 summaries

Database :

1: Issued_Patents_AA: *
2: /cgn2_6/ptodata/1/iaa/5_COMB.pep: *
3: /cgn2_6/ptodata/1/iaa/6_COMB.pep: *
4: /cgn2_6/ptodata/1/iaa/H_COMB.pep: *
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep: *
6: /cgn2_6/ptodata/1/iaa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	88.1	162	2	US-09-522-217-2
2	37	88.1	162	2	US-09-923-246-2
3	37	88.1	162	2	US-10-295-723-2
4	37	88.1	162	2	US-09-825-561A-10
5	37	88.1	162	2	US-10-282-622-2
6	37	88.1	162	2	US-10-282-622-6
7	37	88.1	174	2	US-09-949-016-10307
8	37	88.1	519	2	US-09-522-217-85
9	37	88.1	519	2	US-09-923-246-85
10	37	88.1	519	2	US-10-295-723-85
11	34	81.0	112	2	US-08-435-516-4
12	34	81.0	112	2	US-08-435-516-28
13	34	81.0	113	1	US-08-690-102A-2
14	34	81.0	113	1	US-08-690-102A-6
15	34	81.0	113	1	US-09-127-902-2
16	34	81.0	113	2	US-09-127-902-6
17	34	81.0	113	2	US-09-155-107-2
18	34	81.0	113	2	US-09-155-107-6
19	34	81.0	113	2	US-09-155-107-20
20	34	81.0	113	4	PCT-US95-09641-2
21	34	81.0	113	4	PCT-US95-09641-6
22	34	81.0	301	1	US-08-661-052-14
23	34	81.0	301	2	US-09-188-082-14
24	34	81.0	301	2	US-09-364-088-14
25	34	81.0	301	2	US-09-102-716-14
26	34	81.0	352	2	US-09-203-958A-2
27	34	81.0	553	1	US-08-661-052-16

28	34	81.0	553	2	US-09-188-082-16	Sequence 16, Appl
29	34	81.0	553	2	US-09-364-088-16	Sequence 16, Appl
30	34	81.0	553	2	US-09-102-716-16	Sequence 16, Appl
31	31	73.8	63	2	US-09-134-001C-3543	Sequence 3543, Ap
32	31	73.8	309	2	US-09-540-236-2027	Sequence 2027, Ap
33	31	73.8	403	1	US-08-118-674-1	Sequence 1, Appl
34	31	73.8	720	2	US-09-624-693A-13	Sequence 13, Appl
35	31	73.8	1642	1	US-08-447-411-45	Sequence 45, Appl
36	31	73.8	1642	1	US-08-662-427-2	Sequence 2, Appl
37	31	73.8	1642	1	US-09-017-447-2	Sequence 2, Appl
38	31	73.8	1642	2	US-09-925-442-2	Sequence 2, Appl
39	31	73.8	1648	1	US-08-662-427-35	Sequence 35, Appl
40	31	73.8	1648	1	US-09-017-947-35	Sequence 35, Appl
41	31	73.8	1648	2	US-09-925-442-35	Sequence 35, Appl
42	30	71.4	192	2	US-10-290-579A-202	Sequence 202, App
43	30	71.4	216	2	US-09-198-452A-627	Sequence 627, App
44	30	71.4	221	2	US-09-248-796A-24110	Sequence 24110, A
45	30	71.4	313	2	US-09-328-352-7010	Sequence 7010, Ap
46	30	71.4	462	2	US-09-166-350-18	Sequence 18, Appl
47	30	71.4	472	2	US-09-252-991A-22840	Sequence 22840, A
48	30	71.4	571	2	US-09-248-796A-18791	Sequence 18791, A
49	30	71.4	635	1	US-09-014-969-11	Sequence 11, Appl
50	30	71.4	635	2	US-09-949-016-6991	Sequence 6991, Ap
51	30	71.4	673	2	US-09-252-991A-28817	Sequence 28817, A
52	30	71.4	686	2	US-09-949-016-7874	Sequence 7874, Ap
53	30	71.4	691	2	US-09-902-540-14477	Sequence 14477, A
54	30	71.4	810	2	US-09-583-110-4352	Sequence 4352, Ap
55	30	71.4	866	2	US-09-107-433-4504	Sequence 4504, Ap
56	30	71.4	1482	2	US-09-410-951B-21	Sequence 21, Appl
57	30	71.4	1482	2	US-09-940-316B-21	Sequence 21, Appl
58	30	71.4	1488	2	US-09-410-951B-17	Sequence 17, Appl
59	30	71.4	1488	2	US-09-940-316B-17	Sequence 17, Appl
60	30	71.4	1509	2	US-09-410-951B-23	Sequence 23, Appl
61	30	71.4	1509	2	US-09-940-316B-23	Sequence 23, Appl
62	30	71.4	1517	2	US-09-410-951B-19	Sequence 19, Appl
63	30	71.4	1517	2	US-09-940-316B-19	Sequence 19, Appl
64	30	71.4	1517	2	US-09-410-951B-27	Sequence 27, Appl
65	30	71.4	1557	2	US-09-940-316B-27	Sequence 27, Appl
66	30	71.4	1574	2	US-09-410-951B-25	Sequence 25, Appl
67	30	71.4	1574	2	US-09-940-316B-25	Sequence 25, Appl
68	30	71.4	1578	2	US-09-410-951B-31	Sequence 31, Appl
69	30	71.4	1578	2	US-09-940-316B-31	Sequence 31, Appl
70	30	71.4	1588	2	US-09-410-951B-29	Sequence 29, Appl
71	30	71.4	1588	2	US-09-940-316B-29	Sequence 29, Appl
72	30	71.4	1605	2	US-09-410-951B-33	Sequence 33, Appl
73	30	71.4	1605	2	US-09-940-316B-33	Sequence 33, Appl
74	30	71.4	6396	2	US-09-410-951B-72	Sequence 72, Appl
75	30	71.4	6396	2	US-09-940-316B-72	Sequence 72, Appl
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77	29	69.0	76	2	US-09-621-976-6303	Sequence 6303, Ap
78	29	69.0	118	2	US-09-270-767-36428	Sequence 36428, A
79	29	69.0	118	2	US-09-270-767-51645	Sequence 51645, A
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81	29	69.0	138	2	US-09-270-767-56946	Sequence 56946, A
82	29	69.0	143	2	US-09-270-767-42327	Sequence 42327, A
83	29	69.0	149	2	US-09-252-991A-35070	Sequence 35070, A
84	29	69.0	153	2	US-09-198-452A-329	Sequence 329, App
85	29	69.0	153	2	US-09-438-188A-314	Sequence 314, App
86	29	69.0	161	2	US-09-605-703B-1884	Sequence 1884, Ap
87	29	69.0	256	2	US-09-252-991A-21475	Sequence 21475, A
88	29	69.0	263	2	US-09-792-024-79	Sequence 79, Appl
89	29	69.0	295	2	US-09-248-796A-16714	Sequence 16714, A
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92	29	69.0	527	2	US-09-830-218-16	Sequence 16, Appl
93	29	69.0	530	2	US-09-252-986-2	Sequence 2, Appl
94	29	69.0	532	2	US-09-181-336-15	Sequence 15, Appl
95	29	69.0	543	1	US-08-922-170B-10	Sequence 10, Appl
96	29	69.0	543	2	US-09-071-739B-2	Sequence 2, Appl
97	29	69.0	543	2	US-09-181-336-13	Sequence 13, Appl
98	29	69.0	543	2	US-09-260-038B-2	Sequence 2, Appl
99	29	69.0	543	2	US-09-635-923-2	Sequence 2, Appl
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102	29	69.0	543	2	US-09-186-200-1	Sequence 1, Appli	175	28	66.7	460	2	US-09-248-796A-14306	Sequence 14306, A
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105	29	69.0	543	2	US-09-704-772A-2	Sequence 2, Appli	178	28	66.7	494	2	US-10-290-579A-179	Sequence 179, App
106	29	69.0	543	2	US-09-968-113-10	Sequence 10, Appli	179	28	66.7	503	2	US-09-914-259-13	Sequence 13, Appli
107	29	69.0	543	2	US-09-944-602-2	Sequence 2, Appli	180	28	66.7	518	2	US-09-107-570A-7248	Sequence 7248, Ap
108	29	69.0	543	2	US-10-368-044A-1	Sequence 1, Appli	181	28	66.7	528	2	US-08-637-670-27	Sequence 27, App
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115	29	69.0	608	2	US-08-843-572E-2	Sequence 2, Appli	188	27	64.3	42	2	US-08-905-233-482	Sequence 482, App
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117	29	69.0	761	2	US-09-949-016-6880	Sequence 6880, Ap	190	27	64.3	58	2	US-09-471-276-1064	Sequence 1064, Ap
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122	28	66.7	26	2	US-09-774-639-309	Sequence 309, App	195	27	64.3	155	2	US-09-710-279-1874	Sequence 1874, Ap
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127	28	66.7	88	2	US-09-270-767-60354	Sequence 60354, A	200	27	64.3	212	2	US-09-786-4808-29	Sequence 29, Appli
128	28	66.7	114	2	US-09-489-039A-13622	Sequence 13622, A	201	27	64.3	220	2	US-09-915-789A-23	Sequence 23, Appli
129	28	66.7	119	2	US-09-270-767-47348	Sequence 47348, A	202	27	64.3	223	2	US-09-489-039A-10718	Sequence 10718, A
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132	28	66.7	120	2	US-10-101-464A-128	Sequence 128, App	205	27	64.3	245	2	US-09-413-814-20	Sequence 20, Appli
133	28	66.7	131	2	US-09-311-021-44	Sequence 44, Appli	206	27	64.3	245	2	US-09-645-069-2	Sequence 2, Appli
134	28	66.7	149	2	US-09-774-639-304	Sequence 304, App	207	27	64.3	245	2	US-09-644-934-2	Sequence 2, Appli
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137	28	66.7	176	2	US-09-270-767-42909	Sequence 42909, A	210	27	64.3	277	2	US-09-252-991A-15919	Sequence 15919, A
138	28	66.7	210	2	US-09-252-991A-28362	Sequence 28362, A	211	27	64.3	280	2	US-09-134-000C-5418	Sequence 5418, Ap
139	28	66.7	227	2	US-09-270-767-35605	Sequence 35605, A	212	27	64.3	283	2	US-08-956-171E-5503	Sequence 5203, Ap
140	28	66.7	227	2	US-09-270-767-50822	Sequence 50822, A	213	27	64.3	283	2	US-08-781-986A-5503	Sequence 5203, Ap
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144	28	66.7	232	2	US-09-731-126-7	Sequence 7, Appli	217	27	64.3	290	2	US-09-620-461-8	Sequence 8, Appli
145	28	66.7	243	2	US-09-270-767-35979	Sequence 35979, A	218	27	64.3	290	2	US-09-451-291-1	Sequence 1, Appli
146	28	66.7	243	2	US-09-270-767-51196	Sequence 51196, A	219	27	64.3	290	2	US-09-645-069-4	Sequence 4, Appli
147	28	66.7	259	2	US-09-198-452A-1121	Sequence 1121, Ap	220	27	64.3	290	2	US-09-915-789A-17	Sequence 17, Appli
148	28	66.7	260	2	US-09-543-681A-5505	Sequence 5505, Ap	221	27	64.3	290	2	US-09-644-934-4	Sequence 4, Appli
149	28	66.7	266	2	US-09-538-092-313	Sequence 313, App	222	27	64.3	303	2	US-10-104-047-3897	Sequence 3897, Ap
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156	28	66.7	331	2	US-09-478-816-4	Sequence 4, Appli	229	27	64.3	364	2	US-09-949-016-7730	Sequence 7730, Ap
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162	28	66.7	348	2	US-09-671-950-10	Sequence 10, Appli	235	27	64.3	446	2	US-09-041-780-10	Sequence 10, Appli
163	28	66.7	348	2	US-09-671-950-12	Sequence 12, Appli	236	27	64.3	470	1	US-08-514-014-2	Sequence 2, Appli
164	28	66.7	348	2	US-09-671-950-14	Sequence 14, Appli	237	27	64.3	470	1	US-08-813-823-2	Sequence 2, Appli
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169	28	66.7	423	2	US-09-270-767-42815	Sequence 42815, A	242	27	64.3	474	2	US-09-297-703C-47	Sequence 47, Appli
170	28	66.7	457	2	US-09-416-213-2	Sequence 2, Appli	243	27	64.3	481	2	US-09-297-703C-51	Sequence 51, Appli
171	28	66.7	457	2	US-09-416-214-2	Sequence 2, Appli	244	27	64.3	481	2	US-10-290-579A-182	Sequence 182, App
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252	27	64.3	658	2	US-09-720-317A-24	Sequence 24, App1	325	26	61.9	170	2	US-08-817-441-67	Sequence 67, App1
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258	27	64.3	799	2	US-09-731-166-12	Sequence 12, App1	331	26	61.9	196	2	US-09-270-767-48180	Sequence 48180, A
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261	27	64.3	836	2	US-09-297-703C-29	Sequence 29, App1	334	26	61.9	206	2	US-09-270-767-33867	Sequence 33867, A
262	27	64.3	844	2	US-09-786-480B-18	Sequence 18, App1	335	26	61.9	206	2	US-09-270-767-49084	Sequence 49084, A
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265	27	64.3	848	2	US-09-297-703C-53	Sequence 53, App1	338	26	61.9	213	2	US-08-679-493A-25	Sequence 25, App1
266	27	64.3	848	2	US-09-297-703C-56	Sequence 56, App1	339	26	61.9	222	2	US-09-640-211A-807	Sequence 807, App
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275	27	64.3	1144	2	US-09-270-767-11849	Sequence 41849, A	348	26	61.9	242	2	US-09-640-211A-623	Sequence 623, App
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287	26	61.9	21	1	US-08-127-499A-12	Sequence 12, App1	360	26	61.9	275	1	US-08-389-459A-4	Sequence 4, App1
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296	26	61.9	40	2	US-09-270-767-35377	Sequence 35377, A	369	26	61.9	304	1	US-09-370-368-3	Sequence 3, App1
297	26	61.9	40	2	US-09-270-767-50594	Sequence 50594, A	370	26	61.9	300	2	US-08-946-928-7	Sequence 7, App1
298	26	61.9	51	1	US-09-057-762-10	Sequence 10, App1	371	26	61.9	300	2	US-09-248-796A-20598	Sequence 20598, A
299	26	61.9	51	2	US-08-326-119A-10	Sequence 10, App1	372	26	61.9	305	1	US-08-946-928-1	Sequence 1, App1
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303	26	61.9	65	2	US-09-716-129-186	Sequence 186, App	376	26	61.9	310	2	US-10-070-464-3	Sequence 3, App1
304	26	61.9	72	2	US-09-248-796A-27929	Sequence 27929, A	377	26	61.9	328	2	US-08-776-188A-77	Sequence 77, App1
305	26	61.9	73	2	US-09-311-021-18	Sequence 18, App1	378	26	61.9	328	2	US-09-502-540-12995	Sequence 12995, A
306	26	61.9	77	2	US-09-248-796A-22840	Sequence 22840, A	379	26	61.9	339	2	US-09-710-279-1460	Sequence 1460, App
307	26	61.9	84	4	PCT-US93-08386-15	Sequence 15, App1	380	26	61.9	333	6	5204259-7	Patent No. 5204259
308	26	61.9	98	2	US-09-248-796A-22701	Sequence 22701, A	381	26	61.9	335	2	US-09-949-016-11462	Sequence 11462, A
309	26	61.9	102	2	US-09-513-999C-5312	Sequence 5312, App	382	26	61.9	337	1	US-07-648-796A-1	Sequence 1, App1
310	26	61.9	108	2	US-09-640-211A-2182	Sequence 2182, App	383	26	61.9	350	2	US-09-489-039A-13799	Sequence 13799, A
311	26	61.9	109	2	US-09-583-110-5342	Sequence 4342, App	384	26	61.9	350	2	US-09-134-000C-5321	Sequence 5321, App
312	26	61.9	117	2	US-09-270-767-56852	Sequence 36852, A	385	26	61.9	351	2	US-09-949-016-7853	Sequence 7853, App
313	26	61.9	117	2	US-09-270-767-52069	Sequence 52069, A	386	26	61.9	353	2	US-09-134-001C-4252	Sequence 4252, App
314	26	61.9	132	2	US-09-621-625A-29	Sequence 29, App1	387	26	61.9	355	2	US-09-265-630-9	Sequence 9, App1
315	26	61.9	136	2	US-09-270-767-44230	Sequence 44230, A	388	26	61.9	360	2	US-10-070-464-7	Sequence 7, App1
316	26	61.9	136	2	US-09-270-767-49447	Sequence 44447, A	389	26	61.9	363	1	US-08-850-049-130	Sequence 130, App
317	26	61.9	146	2	US-09-270-767-48829	Sequence 48829, A	390	26	61.9	363	1	US-08-050-478-130	Sequence 130, App
318	26	61.9	152	2	US-09-270-767-59655	Sequence 39655, A	391	26	61.9	363	1	US-09-814-117-130	Sequence 130, App
319	26	61.9	152	2	US-09-270-767-54872	Sequence 54872, A	392	26	61.9	363	2	US-09-678-437-130	Sequence 130, App

393	25	61.9	363	2	US-09-943-722-130	Sequence 130, App	466	25	61.9	500	2	US-09-393-795-5	Sequence 5, Appl1
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395	26	61.9	377	2	US-08-248-796A-25454	Sequence 25454, A	468	26	61.9	502	2	US-09-323-9988-20	Sequence 20, Appl1
396	26	61.9	384	1	US-08-220-958-2	Sequence 2, Appl1	469	26	61.9	502	2	US-09-323-9988-56	Sequence 56, Appl1
397	26	61.9	388	2	US-09-265-630-11	Sequence 11, Appl1	470	26	61.9	503	2	US-08-358-2878-36	Sequence 36, Appl1
398	26	61.9	398	2	US-09-270-767-42084	Sequence 42084, A	471	26	61.9	503	2	US-08-368-704C-36	Sequence 36, Appl1
399	26	61.9	398	2	US-10-104-047-2010	Sequence 2010, Ap	472	26	61.9	503	2	US-09-323-9988-61	Sequence 61, Appl1
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407	26	61.9	447	2	US-09-394-142B-24	Sequence 24, Appl1	480	26	61.9	511	2	US-09-323-9988-60	Sequence 60, Appl1
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411	26	61.9	450	2	US-09-265-630-1	Sequence 1, Appl1	484	26	61.9	512	2	US-08-463-209-8	Sequence 8, Appl1
412	26	61.9	450	2	US-09-265-630-6	Sequence 6, Appl1	485	26	61.9	514	1	US-08-660-022-14	Sequence 14, Appl1
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416	26	61.9	458	1	US-07-648-796A-5	Sequence 5, Appl1	489	26	61.9	576	2	US-09-543-681A-4990	Sequence 4990, Ap
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418	26	61.9	459	2	US-09-606-304-4	Sequence 4, Appl1	491	26	61.9	604	2	US-09-820-809-13	Sequence 13, Appl1
419	26	61.9	472	2	US-09-543-681A-6560	Sequence 6560, Ap	492	26	61.9	608	2	US-09-570-856B-32	Sequence 32, Appl1
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421	26	61.9	477	2	US-09-289-180-1	Sequence 1, Appl1	494	26	61.9	641	1	US-08-836-567-10	Sequence 10, Appl1
422	26	61.9	477	2	US-09-978-709-1	Sequence 1, Appl1	495	26	61.9	641	2	US-09-606-304-10	Sequence 10, Appl1
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437	26	61.9	498	1	US-08-702-598-2	Sequence 2, Appl1	510	26	61.9	803	2	US-09-543-681A-4312	Sequence 4312, Ap
438	26	61.9	498	2	US-09-109-916-59	Sequence 59, Appl1	511	26	61.9	818	2	US-09-786-480B-34	Sequence 34, Appl1
439	26	61.9	498	2	US-09-109-916-60	Sequence 60, Appl1	512	26	61.9	836	2	US-09-538-092-173	Sequence 173, App
440	26	61.9	498	2	US-09-886-156-59	Sequence 59, Appl1	513	26	61.9	854	2	US-09-833-466-12	Sequence 12, Appl1
441	26	61.9	498	2	US-09-886-156-60	Sequence 60, Appl1	514	26	61.9	858	2	US-09-775-252A-6	Sequence 6, Appl1
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443	26	61.9	498	2	US-09-886-149-60	Sequence 60, Appl1	516	26	61.9	871	2	US-09-134-001C-3979	Sequence 3979, Ap
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447	26	61.9	498	2	US-09-886-159-60	Sequence 60, Appl1	520	26	61.9	880	1	US-08-445-640-10	Sequence 10, Appl1
448	26	61.9	498	2	US-09-323-998E-57	Sequence 57, Appl1	521	26	61.9	880	2	US-08-447-314-10	Sequence 10, Appl1
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453	26	61.9	500	1	US-08-375-510-1	Sequence 1, Appl1	526	26	61.9	882	2	US-10-070-464-1	Sequence 1, Appl1
454	26	61.9	500	1	US-08-487-657-1	Sequence 1, Appl1	527	26	61.9	888	2	US-09-786-480B-54	Sequence 54, Appl1
455	26	61.9	500	1	US-08-816-155B-45	Sequence 45, Appl1	528	26	61.9	890	1	US-08-445-640-2	Sequence 2, Appl1
456	26	61.9	500	2	US-09-079-587-45	Sequence 45, Appl1	529	26	61.9	890	2	US-08-170-58-2	Sequence 2, Appl1
457	26	61.9	500	2	US-09-265-630-13	Sequence 13, Appl1	530	26	61.9	890	2	US-08-447-314-2	Sequence 2, Appl1
458	26	61.9	500	2	US-09-309-572-16	Sequence 16, Appl1	531	26	61.9	890	2	US-08-445-641-2	Sequence 2, Appl1
459	26	61.9	500	2	US-09-718-096-16	Sequence 16, Appl1	532	26	61.9	890	2	US-09-223-490-2	Sequence 2, Appl1
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461	26	61.9	500	2	US-09-323-998E-59	Sequence 59, Appl1	534	26	61.9	911	1	US-08-441-104A-1	Sequence 1, Appl1
462	26	61.9	500	2	US-10-230-579A-174	Sequence 174, App	535	26	61.9	911	1	US-08-440-816A-1	Sequence 1, Appl1
463	26	61.9	500	2	US-10-230-579A-177	Sequence 177, App	536	26	61.9	911	1	US-09-417-381A-1	Sequence 1, Appl1
464	26	61.9	500	2	US-10-230-579A-178	Sequence 178, App	537	26	61.9	912	2	US-08-617-785-2	Sequence 2, Appl1
465	26	61.9	500	2	US-09-393-795-3	Sequence 3, Appl1	538	26	61.9	912	2	US-09-641-318-2	Sequence 2, Appl1

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540	26	61.9	912	4	PCT-US91-09422-19	Sequence 19, App1	613	25	59.5	159	2	US-09-690-454-205	Sequence 205, App
541	26	61.9	1350	2	US-09-953-060-35	Sequence 35, App1	614	25	59.5	180	2	US-09-252-991A-20686	Sequence 20686, A
542	26	61.9	1394	2	US-09-902-540-16497	Sequence 16497, A	615	25	59.5	151	2	US-09-328-352-7245	Sequence 7245, App
543	26	61.9	1420	1	US-08-540-804-14	Sequence 14, App1	616	25	59.5	133	2	US-09-252-991A-32167	Sequence 32167, A
544	26	61.9	1420	1	US-08-218-265-14	Sequence 14, App1	617	25	59.5	138	2	US-09-252-991A-17332	Sequence 17332, A
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546	26	61.9	1420	2	US-08-590-399-14	Sequence 396, App	619	25	59.5	160	2	US-09-270-767-31151	Sequence 31151, A
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548	26	61.9	1481	1	US-08-616-844-40	Sequence 40, App1	621	25	59.5	160	2	US-09-949-016-8123	Sequence 8123, App
549	26	61.9	1481	1	US-08-599-654-40	Sequence 40, App1	622	25	59.5	166	2	US-09-690-454-204	Sequence 204, App
550	26	61.9	1481	2	US-08-944-868A-40	Sequence 40, App1	623	25	59.5	166	2	US-09-540-236-2413	Sequence 2413, App
551	26	61.9	1481	2	US-08-944-423A-40	Sequence 40, App1	624	25	59.5	167	2	US-09-710-279-132	Sequence 132, App
552	26	61.9	1481	2	US-08-944-496-40	Sequence 40, App1	625	25	59.5	173	2	US-09-134-001C-2944	Sequence 2944, App
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558	25	59.5	10	1	US-08-764-640-74	Sequence 74, App1	631	25	59.5	180	1	US-08-933-750C-48	Sequence 48, App1
559	25	59.5	10	2	US-08-973-225-74	Sequence 74, App1	632	25	59.5	180	2	US-09-234-613-48	Sequence 48, App1
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563	25	59.5	10	2	US-09-832-230A-74	Sequence 74, App1	636	25	59.5	184	2	US-09-991-181-221	Sequence 221, App
564	25	59.5	17	2	US-09-440-781-48	Sequence 48, App1	637	25	59.5	184	2	US-09-997-444-221	Sequence 221, App
565	25	59.5	18	2	US-09-205-658-273	Sequence 273, App	638	25	59.5	184	2	US-09-997-444-221	Sequence 221, App
566	25	59.5	20	1	US-07-894-063A-4	Sequence 4, App1	639	25	59.5	184	2	US-09-992-598-221	Sequence 221, App
567	25	59.5	21	1	US-08-102-738-2	Sequence 2, App1	640	25	59.5	185	2	US-09-107-532A-6334	Sequence 6334, App
568	25	59.5	37	2	US-09-270-767-36923	Sequence 36923, A	641	25	59.5	188	2	US-09-134-001C-2938	Sequence 2938, App
569	25	59.5	37	2	US-09-270-767-52140	Sequence 52140, A	642	25	59.5	189	2	US-09-252-991A-1010	Sequence 1010, A
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572	25	59.5	52	2	US-08-906-769-85	Sequence 85, App1	645	25	59.5	193	2	US-09-489-039A-7493	Sequence 7493, App
573	25	59.5	52	2	US-08-906-769-85	Sequence 85, App1	646	25	59.5	195	2	US-09-949-016-10851	Sequence 10851, A
574	25	59.5	52	2	US-08-817-795-85	Sequence 85, App1	647	25	59.5	196	1	US-08-481-814A-9	Sequence 9, App1
575	25	59.5	52	2	US-08-639-075A-85	Sequence 85, App1	648	25	59.5	196	2	US-09-489-039A-14010	Sequence 14010, A
576	25	59.5	52	2	US-09-012-431-85	Sequence 85, App1	649	25	59.5	207	2	US-09-328-352-5708	Sequence 5708, App
577	25	59.5	52	2	US-09-012-692-85	Sequence 85, App1	650	25	59.5	210	1	US-08-781-560-4	Sequence 4, App1
578	25	59.5	52	2	US-08-906-613-85	Sequence 85, App1	651	25	59.5	210	1	US-08-933-750C-6	Sequence 6, App1
579	25	59.5	52	4	PCT-US95-14442A-85	Sequence 85, App1	652	25	59.5	210	2	US-08-792-014-4	Sequence 4, App1
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581	25	59.5	53	2	US-10-004-860-983	Sequence 983, App	654	25	59.5	210	2	US-09-443-948-4	Sequence 4, App1
582	25	59.5	57	2	US-09-640-211A-2285	Sequence 2285, App	655	25	59.5	210	2	US-09-690-196-4	Sequence 4, App1
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594	25	59.5	106	2	US-08-150-204E-82	Sequence 82, App1	667	25	59.5	245	2	US-09-858-664A-7	Sequence 7, App1
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596	25	59.5	106	2	US-08-150-204E-84	Sequence 84, App1	669	25	59.5	245	2	US-10-697-261-8	Sequence 8, App1
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601	25	59.5	123	2	US-09-270-767-49463	Sequence 49463, A	674	25	59.5	257	2	US-09-134-001C-3539	Sequence 3539, App
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714	25	59.5	313	2	US-10-104-047-5545	Sequence 3545, Ap	787	25	59.5	479	1	US-09-888-243-6	Sequence 6, Appli
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717	25	59.5	317	2	US-09-605-703B-2286	Sequence 2286, Ap	790	25	59.5	482	1	US-08-142-839A-7	Sequence 7, Appli
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747	25	59.5	409	2	US-09-248-796A-16363	Sequence 16363, A	820	25	59.5	537	2	US-09-271-815-2	Sequence 2, Appli
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755	25	59.5	428	2	US-09-252-991A-29094	Sequence 29094, A	828	25	59.5	537	1	US-08-454-439-22	Sequence 22, Appli
756	25	59.5	425	2	US-09-134-001C-3793	Sequence 3793, Ap	829	25	59.5	537	2	US-08-464-954A-6	Sequence 6, Appli
757	25	59.5	428	2	US-09-252-991A-33081	Sequence 33081, A	830	25	59.5	537	4	PCT-US94-10487-13	Sequence 13, Appli

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833	25	59.5	577	1	US-08-663-566A-11	Sequence 11, Appl	906	25	59.5	817	2	US-10-434-034-4	Sequence 4, Appl
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844	25	59.5	577	4	PCT-US93-00324-30	Sequence 30, Appl	917	25	59.5	937	2	US-09-005-180A-4	Sequence 4, Appl
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846	25	59.5	577	6	5310678-3	Patent No. 5310678	919	25	59.5	952	2	US-09-538-092-452	Sequence 452, App
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848	25	59.5	581	2	US-08-477-459-13	Sequence 13, Appl	921	25	59.5	960	2	US-09-949-016-5894	Sequence 5894, Ap
849	25	59.5	581	2	US-08-479-869-13	Sequence 13, Appl	922	25	59.5	960	2	US-09-248-796A-20230	Sequence 20230, A
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852	25	59.5	581	4	PCT-US94-02252A-13	Sequence 13, Appl	925	25	59.5	998	2	US-09-991-181-33	Sequence 33, Appl
853	25	59.5	581	4	PCT-US94-02252A-13	Sequence 13, Appl	926	25	59.5	1003	2	US-09-990-444-33	Sequence 33, Appl
854	25	59.5	583	2	US-09-949-016-8740	Sequence 14, Appl	927	25	59.5	1003	2	US-09-997-333-33	Sequence 33, Appl
855	25	59.5	590	1	US-08-221-817-14	Sequence 14, Appl	928	25	59.5	1003	2	US-09-992-398-33	Sequence 33, Appl
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859	25	59.5	590	2	US-09-771-161A-207	Sequence 207, App	932	25	59.5	1188	2	US-09-590-101A-8	Sequence 8, Appl
860	25	59.5	590	2	US-09-771-161A-208	Sequence 208, App	933	25	59.5	1151	2	US-09-590-101A-10	Sequence 10, Appl
861	25	59.5	590	4	PCT-US94-10487-14	Sequence 14, Appl	934	25	59.5	1236	2	US-09-769-787-109	Sequence 109, App
862	25	59.5	614	2	US-09-270-767-56832	Sequence 36832, A	935	25	59.5	1257	2	US-09-220-641-3	Sequence 3, Appl
863	25	59.5	614	2	US-09-270-767-52049	Sequence 52049, A	936	25	59.5	1296	2	US-08-728-6903-15	Sequence 15, Appl
864	25	59.5	617	2	US-09-252-991A-23472	Sequence 23472, A	937	25	59.5	1401	2	US-09-750-5908-12	Sequence 2, Appl
865	25	59.5	625	2	US-10-003-392-21	Sequence 21, Appl	938	25	59.5	1433	2	US-09-716-964A-184	Sequence 184, App
866	25	59.5	626	2	US-09-019-385-2	Sequence 2, Appl	939	25	59.5	1469	2	US-09-713-273A-16	Sequence 16, Appl
867	25	59.5	636	2	US-10-104-047-2449	Sequence 2449, Ap	940	25	59.5	1493	2	US-09-713-273A-20	Sequence 20, Appl
868	25	59.5	638	2	US-09-687-538A-4	Sequence 4, Appl	941	25	59.5	1626	1	US-08-771-6020-2	Sequence 2, Appl
869	25	59.5	638	2	US-10-309-437-4	Sequence 4, Appl	942	25	59.5	1656	2	US-09-232-446B-2	Sequence 2, Appl
870	25	59.5	642	2	US-09-270-767-42873	Sequence 42873, A	943	25	59.5	1657	2	US-09-270-767-41425	Sequence 41425, A
871	25	59.5	667	2	US-09-315-127-5	Sequence 5, Appl	944	25	59.5	1745	2	US-09-800-729-89	Sequence 89, Appl
872	25	59.5	667	2	US-09-315-127-6	Sequence 6, Appl	945	25	59.5	1766	2	US-08-444-818-54	Sequence 54, Appl
873	25	59.5	667	2	US-09-070-630-13	Sequence 13, Appl	946	25	59.5	1861	2	US-09-233-086-3	Sequence 3, Appl
874	25	59.5	669	2	US-10-104-047-2373	Sequence 2373, Ap	947	25	59.5	2232	2	US-09-091-219-25	Sequence 25, Appl
875	25	59.5	670	1	US-08-243-542-3	Sequence 3, Appl	948	25	59.5	2232	2	US-09-660-541-25	Sequence 25, Appl
876	25	59.5	670	1	US-08-477-407-3	Sequence 3, Appl	949	25	59.5	2247	2	US-09-091-219-2	Sequence 2, Appl
877	25	59.5	670	1	US-08-464-355-3	Sequence 3, Appl	950	25	59.5	2247	2	US-09-660-541-2	Sequence 2, Appl
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879	25	59.5	713	2	US-09-624-693A-17	Sequence 17, Appl	952	25	59.5	2436	2	US-08-444-818-75	Sequence 75, Appl
880	25	59.5	724	2	US-09-562-737-30	Sequence 30, Appl	953	25	59.5	2772	2	US-08-444-818-89	Sequence 89, Appl
881	25	59.5	726	2	US-09-949-016-5916	Sequence 5916, Ap	954	25	59.5	2894	1	US-08-466-975A-23	Sequence 23, Appl
882	25	59.5	728	2	US-09-543-681A-812	Sequence 8132, Ap	955	25	59.5	2894	1	US-08-391-671A-23	Sequence 23, Appl
883	25	59.5	737	2	US-09-949-016-11607	Sequence 11607, A	956	25	59.5	2894	2	US-08-467-902A-23	Sequence 23, Appl
884	25	59.5	742	1	US-07-921-807B-2	Sequence 2, Appl	957	25	59.5	2894	2	US-09-275-265-23	Sequence 23, Appl
885	25	59.5	742	1	US-08-441-944A-2	Sequence 2, Appl	958	25	59.5	2894	2	US-09-941-611-23	Sequence 23, Appl
886	25	59.5	742	1	US-10-104-047-2807	Sequence 2807, Ap	959	25	59.5	2894	2	US-10-044-995-23	Sequence 23, Appl
887	25	59.5	743	2	US-09-248-796A-17817	Sequence 17817, A	960	25	59.5	2955	1	US-08-443-260-3	Sequence 3, Appl
888	25	59.5	749	2	US-09-562-737-100	Sequence 100, App	961	25	59.5	2955	2	US-08-442-805A-3	Sequence 3, Appl
889	25	59.5	749	2	US-09-710-279-138	Sequence 138, App	962	25	59.5	2955	2	US-08-443-900A-3	Sequence 3, Appl
890	25	59.5	754	1	US-08-941-262-1	Sequence 1, Appl	963	25	59.5	2955	2	US-08-444-818-124	Sequence 124, App
891	25	59.5	759	1	US-09-949-016-6340	Sequence 6340, Ap	964	25	59.5	2955	2	US-08-249-843-3	Sequence 3, Appl
892	25	59.5	763	1	US-08-677-862-2	Sequence 2, Appl	965	25	59.5	2995	2	US-08-444-818-138	Sequence 138, App
893	25	59.5	763	1	US-09-252-571-2	Sequence 2, Appl	966	25	59.5	3011	1	US-08-440-103-36	Sequence 36, Appl
894	25	59.5	763	2	US-09-434-065-2	Sequence 2, Appl	967	25	59.5	3011	1	US-08-440-542-36	Sequence 36, Appl
895	25	59.5	763	2	US-08-789-275-4	Sequence 4, Appl	968	25	59.5	3011	1	US-07-910-760-10	Sequence 10, Appl
896	25	59.5	763	2	US-08-789-275-5	Sequence 5, Appl	969	25	59.5	3011	1	US-08-440-919-10	Sequence 10, Appl
897	25	59.5	769	2	US-09-540-636A-3110	Sequence 3110, Ap	970	25	59.5	3011	1	US-08-231-368-36	Sequence 36, Appl
898	25	59.5	770	2	US-09-543-681A-4291	Sequence 4291, Ap	971	25	59.5	3011	1	US-08-440-210-36	Sequence 36, Appl
899	25	59.5	798	2	US-08-867-611-36	Sequence 36, Appl	972	25	59.5	3011	2	US-08-833-678A-6	Sequence 6, Appl
900	25	59.5	802	2	US-09-690-359-36	Sequence 36, Appl	973	25	59.5	3011	2	US-08-811-566-20	Sequence 20, Appl
901	25	59.5	802	2	US-09-173-151A-33	Sequence 33, Appl	974	25	59.5	3011	2	US-08-444-818-177	Sequence 177, App
902	25	59.5	815	2	US-09-134-001C-3614	Sequence 3614, Ap	975	25	59.5	3011	2	US-09-014-416-1	Sequence 1, Appl
903	25	59.5	816	2	US-09-949-016-10904	Sequence 10904, A	976	25	59.5	3011	2	US-09-014-416-5	Sequence 5, Appl

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977 25 59.5 3011 2 US-08-529-169A-6 Sequence 6, Appli
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979 25 59.5 3011 2 US-09-046-604-36 Sequence 36, Appli
980 25 59.5 3011 2 US-08-440-549-10 Sequence 10, Appli
981 25 59.5 3011 2 US-08-850-328-1 Sequence 1, Appli
982 25 59.5 3011 2 US-09-034-756-20 Sequence 20, Appli
983 25 59.5 3011 2 US-09-483-799-6 Sequence 6, Appli
984 25 59.5 3011 2 US-09-916-359-2 Sequence 2, Appli
985 25 59.5 3011 2 US-10-104-966-1 Sequence 1, Appli
986 25 59.5 3011 2 US-09-952-572-9 Sequence 9, Appli
987 25 59.5 3011 2 US-09-929-955-1 Sequence 1, Appli
988 25 59.5 3011 2 US-10-259-275-20 Sequence 20, Appli
989 25 59.5 3011 4 PCT-US91-02225-10 Sequence 10, Appli
990 25 59.5 3012 2 US-08-811-566-2 Sequence 2, Appli
991 25 59.5 3012 2 US-09-034-756-2 Sequence 2, Appli
992 24.5 58.3 1512 2 US-09-328-352-5163 Sequence 5163, Ap
993 24 57.1 9 1 US-07-822-043-26 Sequence 26, Appli
994 24 57.1 9 1 US-07-988-925-6 Sequence 6, Appli
995 24 57.1 9 1 US-08-346-455B-26 Sequence 26, Appli
996 24 57.1 9 1 US-08-362-780-6 Sequence 6, Appli
997 24 57.1 9 2 US-08-977-221-26 Sequence 26, Appli
998 24 57.1 9 2 US-08-483-831B-26 Sequence 26, Appli
999 24 57.1 9 2 US-08-478-684G-6 Sequence 6, Appli
1000 24 57.1 9 4 PCT-US95-06613-26 Sequence 26, Appli
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ALIGNMENTS

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RESULT 1
US-09-522-217-2
; Sequence 2, Application US/09522217
; Patent No. 6307024
; GENERAL INFORMATION:
; APPLICANT: No. 6307024a, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/522,217
; EARLIER FILING DATE: 2000-03-09
; EARLIER APPLICATION NUMBER: US 60/123,547
; EARLIER FILING DATE: 1999-03-09
; EARLIER APPLICATION NUMBER: US 60/123,904
; EARLIER FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: US 60/142,013
; EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-522-217-2
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Best Local Similarity 87.5%; Pred. No. 2.3;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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RESULT 2
US-09-923-246-2
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; Sequence 2, Application US/09923246
; Patent No. 6605272
; GENERAL INFORMATION:
; APPLICANT: No. 6605272a, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/923,246
; EARLIER FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-923-246-2
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Query Match 88.1%; Score 37; DB 2; Length 162;
Best Local Similarity 87.5%; Pred. No. 2.3;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 1 HOYLSRT 8
Db 149 HOHLSRT 156
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RESULT 3
US-10-295-723-2
; Sequence 2, Application US/10295723
; Patent No. 6686178
; GENERAL INFORMATION:
; APPLICANT: No. 6686178a, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/295,723
; EARLIER FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/123,547
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-10-295-723-2

Query Match 88.1%; Score 37; DB 2; Length 162;
Best Local Similarity 87.5%; Pred. No. 2.3;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
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Db 149 HOHLSRT 156

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US-09-825-561A-10
; Sequence 10, Application US/09825561A
; Patent No. 677539
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: No. 677539ak, Julia E.
; APPLICANT: West, James W.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Holly, Richard D.
; APPLICANT: Nelson, Andrew J.
; TITLE OF INVENTION: SOLUBLE ZALPHAL1 CYTOKINE RECEPTORS
; FILE REFERENCE: 00-22
; CURRENT APPLICATION NUMBER: US/09/825,561A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/194,731
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/222,121
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-825-561A-10

Query Match 88.1%; Score 37; DB 2; Length 162;
Best Local Similarity 87.5%; Pred. No. 2.3;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
||:|||||
Db 149 HOHLSRT 156

RESULT 5

US-10-282-622-2
; Sequence 2, Application US/10282622
; Patent No. 6929932
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: West, James W.
; APPLICANT: No. 6929932ak, Julia E.
; TITLE OF INVENTION: ZALPHAL1 LIGAND ANTAGONISTS
; FILE REFERENCE: 01-37
; CURRENT APPLICATION NUMBER: US/10/282,622
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 60/337,586
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-622-2

Query Match 88.1%; Score 37; DB 2; Length 162;
Best Local Similarity 87.5%; Pred. No. 2.3;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
||:|||||
Db 149 HOHLSRT 156

RESULT 6

US-10-282-622-6
; Sequence 6, Application US/10282622
; Patent No. 6929932
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: West, James W.
; APPLICANT: No. 6929932ak, Julia E.
; TITLE OF INVENTION: ZALPHAL1 LIGAND ANTAGONISTS
; FILE REFERENCE: 01-37
; CURRENT APPLICATION NUMBER: US/10/282,622
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 60/337,586
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: zalphal1 ligand Q153D/1156D
US-10-282-622-6

Query Match 88.1%; Score 37; DB 2; Length 162;
Best Local Similarity 87.5%; Pred. No. 2.3;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
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Db 149 HOHLSRT 156

RESULT 7

US-09-949-016-10307
; Sequence 10307, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10307
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10307

Query Match 88.1%; Score 37; DB 2; Length 174;
Best Local Similarity 87.5%; Pred. No. 2.5;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
||:|||||
Db 161 HOHLSRT 168

RESULT 8

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US-09-522-217-85
; Sequence 85, Application US/09522217
; Patent No. 6307024
; GENERAL INFORMATION:
; APPLICANT: No. 6307024ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/522,217
; CURRENT FILING DATE: 2000-03-09
; EARLIER APPLICATION NUMBER: US 60/123,547
; EARLIER FILING DATE: 1999-03-09
; EARLIER APPLICATION NUMBER: US 60/123,904
; EARLIER FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: US 60/142,013
; EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 85
; LENGTH: 519
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MBP-human zalpha11 ligand fusion polypeptide
US-09-522-217-85
Query Match      88.1%; Score 37; DB 2; Length 519;
Best Local Similarity 87.5%; Pred. No. 8.4;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MBP-human zalpha11 ligand fusion polypeptide
US-09-923-246-85
Query Match      88.1%; Score 37; DB 2; Length 519;
Best Local Similarity 87.5%; Pred. No. 8.4;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cy      1 HOYLSRT 8
Db      506 HOHLSRT 513

RESULT 10
US-10-295-723-85
; Sequence 85, Application US/10295723
; Patent No. 6686178
; GENERAL INFORMATION:
; APPLICANT: No. 6686178ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/295,723
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/123,547
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 85
; LENGTH: 519
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MBP-human zalpha11 ligand fusion polypeptide
US-10-295-723-85
Query Match      88.1%; Score 37; DB 2; Length 519;
Best Local Similarity 87.5%; Pred. No. 8.4;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cy      1 HOYLSRT 8
Db      506 HOHLSRT 513

RESULT 11
US-08-435-516-4
; Sequence 4, Application US/08435516
; Patent No. 6500931
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANIZED ANTIBODIES TO PC RECEPTORS FOR
; TITLE OF INVENTION: IMMUNOBLOULIN G ON HUMAN MONONUCLEAR PHAGOCYTES
; NUMBER OF SEQUENCES: 28
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,516
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UK 92 23377.4, PCT/US93/10384
FILING DATE: 04-NOV-1992; -02-NOV-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MXI-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-435-516-4

Query Match 81.0%; Score 34; DB 2; Length 112;
Best Local Similarity 87.5%; Pred. No. 6.7;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
DB 95 HOYLSWT 102

RESULT 12
US-08-435-516-28
Sequence 28, Application US/08435516
Patent No. 6500931
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: HUMANIZED ANTIBODIES TO FC RECEPTORS FOR
NUMBER OF SEQUENCES: 28
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,516
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UK 92 23377.4, PCT/US93/10384
FILING DATE: 04-NOV-1992; -02-NOV-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MXI-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-435-516-28

Query Match 81.0%; Score 34; DB 2; Length 112;

Best Local Similarity 87.5%; Pred. No. 6.7;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
DB 95 HOYLSWT 102

RESULT 13
US-08-690-102A-2
Sequence 2, Application US/08690102A
Patent No. 5789554
GENERAL INFORMATION:
APPLICANT: LEUNG, Shui-on
TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/690,102A
FILING DATE: 01-JUL-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,576
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Saxe, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 18733/463/IMIN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-690-102A-2

Query Match 81.0%; Score 34; DB 1; Length 113;
Best Local Similarity 87.5%; Pred. No. 6.8;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
DB 95 HOYLSWT 102

RESULT 14
US-08-690-102A-6
Sequence 6, Application US/08690102A
Patent No. 5789554
GENERAL INFORMATION:
APPLICANT: LEUNG, Shui-on
TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/690,102A
FILING DATE: 01-JUL-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,576
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 18733/463/IMIN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-690-102A-6

Query Match 81.0%; Score 34; DB 1; Length 113;
Best Local Similarity 87.5%; Pred. No. 6.8;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HOYLSSRT 8
Db 95 HOYLSSWT 102

RESULT 15
US-09-127-902-2
Sequence 2, Application US/09127902
Patent No. 6187287
GENERAL INFORMATION:
APPLICANT: LEUNG, Shui-on
APPLICANT: HANSEN, Hans
TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR B-CELL LYMPHOMA AND LEUKEMIA CELLS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/127,902
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/690,102
FILING DATE: 01-JUL-1996
APPLICATION NUMBER: US 08/289,576
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.

REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 18733/463/IMIN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-127-902-2

Query Match 81.0%; Score 34; DB 2; Length 113;
Best Local Similarity 87.5%; Pred. No. 6.8;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HOYLSSRT 8
Db 95 HOYLSSWT 102

RESULT 16
US-09-127-902-6
Sequence 6, Application US/09127902
Patent No. 6187287
GENERAL INFORMATION:
APPLICANT: LEUNG, Shui-on
APPLICANT: HANSEN, Hans
TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR B-CELL LYMPHOMA AND LEUKEMIA CELLS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/127,902
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/690,102
FILING DATE: 01-JUL-1996
APPLICATION NUMBER: US 08/289,576
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 18733/463/IMIN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-127-902-6

Query Match 81.0%; Score 34; DB 2; Length 113;
Best Local Similarity 87.5%; Pred. No. 6.8;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
Db 95 HOYLSWT 102

RESULT 17

US-09-155-107-2
; Sequence 2, Application US/09155107
; Patent No. 6254868
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; APPLICANT: QU, Zhengxing
; TITLE OF INVENTION: GLYCOSYLATED HUMANIZED B-CELL SPECIFIC ANTIBODIES
; FILE REFERENCE: 018733/0879
; CURRENT APPLICATION NUMBER: US/09/155,107
; EARLIER FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: WO PCT/US97/04196
; EARLIER FILING DATE: 1997-03-19
; EARLIER APPLICATION NUMBER: US 60/013,709
; EARLIER FILING DATE: 1996-03-20
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Murine
US-09-155-107-2

Query Match 81.0%; Score 34; DB 2; Length 113;
Best Local Similarity 87.5%; Pred. No. 6.8;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
Db 95 HOYLSWT 102

RESULT 18

US-09-155-107-6
; Sequence 6, Application US/09155107
; Patent No. 6254868
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; APPLICANT: QU, Zhengxing
; TITLE OF INVENTION: GLYCOSYLATED HUMANIZED B-CELL SPECIFIC ANTIBODIES
; FILE REFERENCE: 018733/0879
; CURRENT APPLICATION NUMBER: US/09/155,107
; EARLIER FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: WO PCT/US97/04196
; EARLIER FILING DATE: 1997-03-19
; EARLIER APPLICATION NUMBER: US 60/013,709
; EARLIER FILING DATE: 1996-03-20
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-155-107-6

Query Match 81.0%; Score 34; DB 2; Length 113;
Best Local Similarity 87.5%; Pred. No. 6.8;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
Db 95 HOYLSWT 102

RESULT 19
US-09-155-107-20

; Sequence 20, Application US/09155107
; Patent No. 6254868
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; APPLICANT: QU, Zhengxing
; TITLE OF INVENTION: GLYCOSYLATED HUMANIZED B-CELL SPECIFIC ANTIBODIES
; FILE REFERENCE: 018733/0879
; CURRENT APPLICATION NUMBER: US/09/155,107
; EARLIER FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: WO PCT/US97/04196
; EARLIER FILING DATE: 1997-03-19
; EARLIER APPLICATION NUMBER: US 60/013,709
; EARLIER FILING DATE: 1996-03-20
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-155-107-20

Query Match 81.0%; Score 34; DB 2; Length 113;
Best Local Similarity 87.5%; Pred. No. 6.8;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
Db 95 HOYLSWT 102

RESULT 20

PCT-US95-09641-2
; Sequence 2, Application PC/TUS9509641
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR B-CELL LYMPHOMA AND LEUKEMIA CELLS
; NUMBER OF SEQUENCES: 21
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/09641
; FILING DATE: 11-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/289,576
; FILING DATE: 12-AUG-1994
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-09641-2

Query Match 81.0%; Score 34; DB 4; Length 113;
Best Local Similarity 87.5%; Pred. No. 6.8;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
Db 95 HOYLSWT 102

RESULT 21

PCT-US95-09641-6
; Sequence 6, Application PC/TUS9509641
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED

TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR B-CELL LYMPHOMA AND LEUKEMIA CELLS
NUMBER OF SEQUENCES: 21
COMPUTER READABLE FORM: disk
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09641
FILING DATE: 11-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,576
FILING DATE: 12-AUG-1994
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-09641-6

Query Match 81.0%; Score 34; DB 4; Length 113;
Best Local Similarity 87.5%; Pred. No. 6.8;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HOYLSRT 8
Db 95 HOYLSWT 102

RESULT 22
US-08-661-052-14
Sequence 14, Application US/08661052
Patent No. 5837243
GENERAL INFORMATION:
APPLICANT: Yashwant M. Deo
APPLICANT: Joel Goldstein
APPLICANT: Robert Graziano
APPLICANT: Chezian Somasundaram
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/661,052
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/484,172
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MXI-043CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 301 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-661-052-14

Query Match 81.0%; Score 34; DB 1; Length 301;
Best Local Similarity 87.5%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HOYLSRT 8
Db 249 HOYLSWT 256

RESULT 23
US-09-188-082-14
Sequence 14, Application US/09188082
Patent No. 6270765
GENERAL INFORMATION:
APPLICANT: Yashwant M. Deo
APPLICANT: Joel Goldstein
APPLICANT: Robert Graziano
APPLICANT: Chezian Somasundaram
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/188,082
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/661,052
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MXI-043CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 301 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-188-082-14

Query Match 81.0%; Score 34; DB 2; Length 301;
Best Local Similarity 87.5%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HOYLSRT 8
Db 249 HOYLSWT 256

RESULT 24
US-09-364-088-14
Sequence 14, Application US/09364088
Patent No. 6365161
GENERAL INFORMATION:
APPLICANT: Yashwant M. Deo, et al.
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES

NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street, 24th Floor
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/364,088
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/188,082
FILING DATE: 07-JUNE-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/484,172
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Remillard, Jane E.
REGISTRATION NUMBER: 38,872
REFERENCE/DOCKET NUMBER: MXI-043CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-7414
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 301 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-364-088-14

Query Match 81.0%; Score 34; DB 2; Length 301;
Best Local Similarity 87.5%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
Db 249 HOYLSWT 256

RESULT 25
US-09-102-716-14
Sequence 14, Application US/09102716
Patent No. 6395272
GENERAL INFORMATION:
APPLICANT: Yashwant M. Deo
Robert Graziano
Joel Goldstein
Chezian Somasundaram
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
OF ANTI-FC RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/102,716
FILING DATE: 22-Jun-1998

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/661,052
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MXI-043CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 301 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-102-716-14

Query Match 81.0%; Score 34; DB 2; Length 301;
Best Local Similarity 87.5%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
Db 249 HOYLSWT 256

RESULT 26
US-09-203-958A-2
Sequence 2, Application US/09203958A
Patent No. 6682928
GENERAL INFORMATION:
APPLICANT: KELLER, Tibor
APPLICANT: GOLDSTEIN, Joel
APPLICANT: GRAZIANO, Robert
APPLICANT: DEO, Yashwant M.
TITLE OF INVENTION: CELLS EXPRESSING ANTI-FC RECEPTOR
FILE REFERENCE: MXI-099CPA
CURRENT APPLICATION NUMBER: US/09/203,958A
CURRENT FILING DATE: 1998-12-02
PRIOR APPLICATION NUMBER: 60/067232
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 352
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic construct
US-09-203-958A-2

Query Match 81.0%; Score 34; DB 2; Length 352;
Best Local Similarity 87.5%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
Db 132 HOYLSWT 139

RESULT 27
US-08-661-052-16
Sequence 16, Application US/08661052
Patent No. 5837243
GENERAL INFORMATION:
APPLICANT: Yashwant M. Deo
APPLICANT: Joel Goldstein
APPLICANT: Robert Graziano
APPLICANT: Chezian Somasundaram
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED

TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/661,052
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/484,172
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MXI-043CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
FAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-661-052-16

Query Match 81.0%; Score 34; DB 1; Length 553;
Best Local Similarity 87.5%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
DB 249 HOYLSWT 256

RESULT 28
US-09-188-082-16
Sequence 16, Application US/09188082
Patent No. 6270765
GENERAL INFORMATION:
APPLICANT: Yashwant M. Deo
APPLICANT: Joel Goldstein
APPLICANT: Robert Graziano
APPLICANT: Chetian Somasundaram
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/188,082
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/661,052

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MXI-043CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
FAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-188-082-16

Query Match 81.0%; Score 34; DB 2; Length 553;
Best Local Similarity 87.5%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
DB 249 HOYLSWT 256

RESULT 29
US-09-364-088-16
Sequence 16, Application US/09364088
Patent No. 6365161
GENERAL INFORMATION:
APPLICANT: Yashwant M. Deo, et al.
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street, 24th Floor
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/364,088
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/188,082
FILING DATE: 07-JUNE-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/484,172
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Remillard, Jane E.
REGISTRATION NUMBER: 38,872
REFERENCE/DOCKET NUMBER: MXI-043CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
FAX: (617)742-7414
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-364-088-16

Query Match 81.0%; Score 34; DB 2; Length 553;
Best Local Similarity 87.5%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
Db 249 HOYLSRT 256

RESULT 30
US-09-102-716-16
; Sequence 16, Application US/09102716
; Patent No. 6395272
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deso
; Robert Graziano
; Chezian Somasundaram
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
; OF ANTI-FC RECEPTOR ANTIBODIES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; City: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/09/102,716
; FILING DATE: 22-Jun-1998
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/661,052
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-043CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-102-716-16
Query Match 81.0%; Score 34; DB 2; Length 553;
Best Local Similarity 87.5%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 HOYLSRT 8
Db 249 HOYLSRT 256
RESULT 31
US-09-134-001C-3543
; Sequence 3543, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; FILING DATE: 1998-08-13
; PRIORITY APPLICATION NUMBER: US 60/064,964

; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3543
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3543

Query Match 73.8%; Score 31; DB 2; Length 63;
Best Local Similarity 71.4%; Pred. No. 16;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 HOYLSR 7
Db 13 HOYLSR 19

RESULT 32
US-09-540-236-2027
; Sequence 2027, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARR
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2027
; LENGTH: 309
; TYPE: PRT
; ORGANISM: M.catarrhalis
US-09-540-236-2027

Query Match 73.8%; Score 31; DB 2; Length 309;
Best Local Similarity 85.7%; Pred. No. 92;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSR 7
Db 299 HOYLSR 305

RESULT 33
US-08-118-674-1
; Sequence 1, Application US/08118674
; Patent No. 5714344
; GENERAL INFORMATION:
; APPLICANT: OILBERT, MARKUS W.
; APPLICANT: ZIEGELMULLER, PATRICK
; APPLICANT: GRUMWALD, THOMAS
; APPLICANT: BREDEHORST, REINHARD
; APPLICANT: VOGEL, CARL-WILHELM
; TITLE OF INVENTION: PROTEASE-DERIVED CVP
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OILON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; City: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/118,674

FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/043,747
FILING DATE: 07-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Obion, No. 5714344man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 1126-104-68 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELETYPE: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 403 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-118-674-1

Query Match 73.8%; Score 31; DB 1; Length 403;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HOYLSR 7
Db 322 HOYLSR 328

RESULT 34
US-09-624-693A-13
Sequence 13, Application US/09624693A
Patent No. 6355468
GENERAL INFORMATION:
APPLICANT: Yoshida, Roberta
TITLE OF INVENTION: Phenylalanine Ammonia Lyase Polypeptide and
TITLE OF INVENTION: Polynucleotide Sequences and Methods of Obtaining and
TITLE OF INVENTION: Using Same
FILE REFERENCE: 29479/500NSC
CURRENT APPLICATION NUMBER: US/09/624,693A
CURRENT FILING DATE: 2000-07-24
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 13
LENGTH: 720
TYPE: PRT
ORGANISM: Rhodotorula graminis
US-09-624-693A-13

Query Match 73.8%; Score 31; DB 2; Length 720;
Best Local Similarity 75.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HOYLSR 8
Db 659 HAYLSRPT 666

RESULT 35
US-08-447-411-45
Sequence 45, Application US/08447411
Patent No. 5773243
GENERAL INFORMATION:
APPLICANT: FRITZINGER, DAVID C.
APPLICANT: BREDEHORST, REINHARD
APPLICANT: VOGEL, CARL-WILHELM
TITLE OF INVENTION: DNA ENCODING COBRA C3, CVF1, AND CVF2
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBION, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.

STREET: 1755 S. Jefferson Davis Highway, Suite 400
City: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,411

FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/043,747
FILING DATE: 07-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Obion, No. 5773243man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 1126-101-0

TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELETYPE: 248855 OPAT UR

INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 1642 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-447-411-45

Query Match 73.8%; Score 31; DB 1; Length 1642;
Best Local Similarity 71.4%; Pred. No. 5.9e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HOYLSR 7
Db 1561 HOYLSR 1567

RESULT 36
US-08-662-227-2
Sequence 2, Application US/08662227
Patent No. 5922320
GENERAL INFORMATION:
APPLICANT: VOGEL, CARL-WILHELM
APPLICANT: BREDEHORST, REINHORST
APPLICANT: KOCK, MICHAEL

APPLICANT: FRITZINGER, DAVID
TITLE OF INVENTION: RECOMBINANT PROCVF
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBION, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.

STREET: 1755 S. JEFFERSON DAVIS HIGHWAY
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/662,227
FILING DATE: 14-JUN-1996
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
NAME: OBION, NORMAN F.
REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 1126-0107-0X
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1642 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-662-227-2

Query Match 73.8%; Score 31; DB 1; Length 1642;
Best Local Similarity 71.4%; Pred. No. 5.9e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSR 7
DB 1561 HOYISOR 1567

RESULT 37
US-09-017-947-2
Sequence 2, Application US/09017947
Patent No. 6303754
GENERAL INFORMATION:
APPLICANT: VOGEL, CARL-WILHELM
APPLICANT: BREDEHORST, REINHORST
APPLICANT: KOCK, MICHAEL
APPLICANT: FRITZINGER, DAVID
TITLE OF INVENTION: RECOMBINANT PROCVF
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESSES:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/017,947
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/662,227
FILING DATE: 14-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 1126-0107-0X
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1642 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-017-947-2

Query Match 73.8%; Score 31; DB 2; Length 1642;
Best Local Similarity 71.4%; Pred. No. 5.9e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSR 7
DB 1561 HOYISOR 1567

RESULT 38
US-09-925-442-2
Sequence 2, Application US/09925442
Patent No. 6607897
GENERAL INFORMATION:
APPLICANT: VOGEL, CARL-WILHELM
APPLICANT: BREDEHORST, REINHORST
APPLICANT: KOCK, MICHAEL
APPLICANT: FRITZINGER, DAVID
TITLE OF INVENTION: RECOMBINANT PROCVF
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESSES:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/925,442
FILING DATE: 10-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/017,947
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 1126-0107-0X
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1642 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-925-442-2

Query Match 73.8%; Score 31; DB 2; Length 1642;
Best Local Similarity 71.4%; Pred. No. 5.9e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSR 7
DB 1561 HOYISOR 1567

RESULT 39
US-08-662-227-35
Sequence 35, Application US/08662227
Patent No. 5922320
GENERAL INFORMATION:
APPLICANT: VOGEL, CARL-WILHELM
APPLICANT: BREDEHORST, REINHORST
APPLICANT: KOCK, MICHAEL
APPLICANT: FRITZINGER, DAVID
TITLE OF INVENTION: RECOMBINANT PROCVF
NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/662,227
FILING DATE: 14-JUN-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 1126-0107-0X
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 1648 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-662-227-35

Query Match 73.8%; Score 31; DB 1; Length 1648;
Best Local Similarity 71.4%; Pred. No. 5.9e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSR 7
DB 1561 HOYLSR 1567

RESULT 40
US-09-017-947-35
Sequence 35, Application US/09017947
Patent No. 6303754
GENERAL INFORMATION:
APPLICANT: VOGEL, CARL-WILHELM
APPLICANT: BREDEHORST, REINHORST
APPLICANT: KOCK, MICHAEL
APPLICANT: FRITZINGER, DAVID
TITLE OF INVENTION: RECOMBINANT PROCV
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/017,947
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/662,227
FILING DATE: 14-JUN-1996

ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 1126-0107-0X
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 1648 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-017-947-35

Query Match 73.8%; Score 31; DB 2; Length 1648;
Best Local Similarity 71.4%; Pred. No. 5.9e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSR 7
DB 1561 HOYLSR 1567

RESULT 41
US-09-925-442-35
Sequence 35, Application US/09925442
Patent No. 6607897
GENERAL INFORMATION:
APPLICANT: VOGEL, CARL-WILHELM
APPLICANT: BREDEHORST, REINHORST
APPLICANT: KOCK, MICHAEL
APPLICANT: FRITZINGER, DAVID
TITLE OF INVENTION: RECOMBINANT PROCV
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/925,442
FILING DATE: 10-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/017,947
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 1126-0107-0X
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 1648 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-09-925-442-35

Query Match 73.8%; Score 31; DB 2; Length 1648;
Best Local Similarity 71.4%; Pred. No. 5.9e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSR 7
DB 1561 HOYLSR 1567

RESULT 42

US-10-290-579A-202
; Sequence 202, Application US/10290579A
; Patent No. 6897301
; GENERAL INFORMATION:
; APPLICANT: Hahn, Beatrice
; APPLICANT: Gao, Feng
; APPLICANT: Shaw, George
; TITLE OF INVENTION: CLONING AND SEQUENCES FOR NON-SUBTYPE B ISOLATES OF HUMAN
; FILE REFERENCE: D6287D
; CURRENT APPLICATION NUMBER: US/10/290,579A
; CURRENT FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: US 09/184,418
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 270
; SEQ ID NO 202
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; FEATURE:
; OTHER INFORMATION: isolate=96ZM751.3; gene=vif
US-10-290-579A-202

Query Match 71.4%; Score 30; DB 2; Length 192;
Best Local Similarity 62.5%; Pred. No. 89;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HOYLSR 8
DB 28 HMYVSKRT 35

RESULT 43

US-09-198-452A-627
; Sequence 627, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 627
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-627

Query Match 71.4%; Score 30; DB 2; Length 216;
Best Local Similarity 62.5%; Pred. No. 1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSR 8
DB 2 HSFLSTR 9

RESULT 44

US-09-248-796A-24110
; Sequence 24110, Application US/09248796A

; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 24110
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-24110

Query Match 71.4%; Score 30; DB 2; Length 221;
Best Local Similarity 71.4%; Pred. No. 1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYLSR 7
DB 117 HOYLSQ 123

RESULT 45

US-09-328-352-7010
; Sequence 7010, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 7010
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-7010

Query Match 71.4%; Score 30; DB 2; Length 313;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSR 7
DB 281 HOYESSR 287

RESULT 46

US-09-166-350-18
; Sequence 18, Application US/09166350A
; Patent No. 6440663
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew
; APPLICANT: Chen, Yao
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Old, Lloyd
; APPLICANT: Jager, Elke
; APPLICANT: Knuth, Alex
; TITLE OF INVENTION: Renal Cancer Associated Antigens and
; FILE REFERENCE: L0461/7051
; CURRENT APPLICATION NUMBER: US/09/166,350A
; CURRENT FILING DATE: 1998-10-05
; EARLIER APPLICATION NUMBER: US 09/166,350
; EARLIER FILING DATE: 1998-10-05

NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-166-350-18

Query Match 71.4%; Score 30; DB 2; Length 462;
Best Local Similarity 71.4%; Pred. No. 2.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HOYLSRT 7
Db 117 HXYLSQR 123

RESULT 47
US-09-252-991A-22840
; Sequence 22840, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 22840
; LENGTH: 472
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22840

Query Match 71.4%; Score 30; DB 2; Length 472;
Best Local Similarity 62.5%; Pred. No. 2.4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HOYLSRT 8
Db 81 HOYLAART 88

RESULT 48
US-09-248-796A-18791
; Sequence 18791, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 18791
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Candida albicans
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (284)
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unkno
US-09-248-796A-18791

Query Match 71.4%; Score 30; DB 2; Length 571;
Best Local Similarity 62.5%; Pred. No. 3e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HOYLSRT 8
Db 393 HXYLSQT 400

RESULT 49
US-09-014-969-11
; Sequence 11, Application US/09014969
; Patent No. 5965397
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: Lavallee, Edward R.
; APPLICANT: Racie, Lisa A.
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; APPLICANT: Agostino, Michael J.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/014,969
; CURRENT FILING DATE: 1999-02-18
; ADDRESS: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/014,969
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sprunger, Suzanne A.
; REGISTRATION NUMBER: 41,323
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8284
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 635 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-014-969-11

Query Match 71.4%; Score 30; DB 1; Length 635;
Best Local Similarity 85.7%; Pred. No. 3.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QYLSRT 8
Db 280 RYLSRT 286

RESULT 50
US-09-949-016-6991
; Sequence 6991, Application US/09949016
; Patent No. 681239
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
US-09-949-016-6991

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6991
; LENGTH: 635
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6991

Query Match 71.4%; Score 30; DB 2; Length 635;
Best Local Similarity 85.7%; Pred. No. 3.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYLSRT 8
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Db 280 RYLSRT 286

Search completed: May 4, 2006, 13:12:38
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 4, 2006, 13:43:49 ; Search time 59.0317 Seconds
(without alignments)
57.600 Million cell updates/sec

Title: US-10-700-632-6

Perfect score: 42

Sequence: 1 HOYLSRT 8

Scoring table:

Bioscore62

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 1000 summaries

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4: /cgn2_6/ptodaca/1/pubpaa/US10_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	42	100.0	113	US-10-700-632-8	Sequence 8, Appl1
3	42	100.0	113	US-10-700-632-10	Sequence 10, Appl1
4	42	100.0	114	US-10-700-632-62	Sequence 62, Appl1
5	37	88.1	112	US-10-056-052-6	Sequence 6, Appl1
6	37	88.1	111	US-10-867-992-2	Sequence 2, Appl1
7	37	88.1	131	US-10-867-992-4	Sequence 4, Appl1
8	37	88.1	131	US-10-867-992-6	Sequence 6, Appl1
9	37	88.1	131	US-10-867-992-8	Sequence 8, Appl1
10	37	88.1	131	US-10-867-992-10	Sequence 10, Appl1
11	37	88.1	133	US-10-867-992-12	Sequence 12, Appl1
12	37	88.1	133	US-10-867-992-14	Sequence 14, Appl1
13	37	88.1	133	US-10-867-992-16	Sequence 16, Appl1
14	37	88.1	133	US-10-867-992-18	Sequence 18, Appl1
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16	37	88.1	133	US-10-867-992-22	Sequence 22, Appl1
17	37	88.1	133	US-10-867-992-24	Sequence 24, Appl1
18	37	88.1	133	US-10-867-992-26	Sequence 26, Appl1
19	37	88.1	133	US-10-867-992-28	Sequence 28, Appl1
20	37	88.1	133	US-10-867-992-30	Sequence 30, Appl1
21	37	88.1	133	US-10-867-992-32	Sequence 32, Appl1
22	37	88.1	133	US-10-867-992-34	Sequence 34, Appl1
23	37	88.1	133	US-10-867-992-36	Sequence 36, Appl1
24	37	88.1	133	US-10-867-992-38	Sequence 38, Appl1
25	37	88.1	133	US-10-867-992-40	Sequence 40, Appl1
26	37	88.1	133	US-10-867-992-42	Sequence 42, Appl1
27	37	88.1	133	US-10-867-992-44	Sequence 44, Appl1

28	37	88.1	162	US-10-775-204-2177	Sequence 2177, Ap
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31	37	88.1	519	US-10-659-684-85	Sequence 85, Appl
32	37	88.1	742	US-10-787-442-85	Sequence 85, Appl
33	37	88.1	165	US-10-775-204-2167	Sequence 2167, Ap
34	36	85.7	165	US-10-425-115-34136	Sequence 34136, A
35	35	83.3	8	US-11-013-537-10	Sequence 10, Appl
36	35	83.3	58	US-10-425-115-318736	Sequence 318736, A
37	35	83.3	112	US-10-056-052-10	Sequence 10, Appl
38	35	83.3	112	US-10-056-052-12	Sequence 12, Appl
39	35	83.3	112	US-10-056-052-14	Sequence 14, Appl
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41	35	83.3	112	US-10-056-052-18	Sequence 18, Appl
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61	34	81.0	112	US-10-056-052-58	Sequence 58, Appl
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64	34	81.0	112	US-10-056-052-64	Sequence 64, Appl
65	34	81.0	112	US-10-056-052-66	Sequence 66, Appl
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68	34	81.0	112	US-10-056-052-72	Sequence 72, Appl
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70	34	81.0	112	US-10-056-052-76	Sequence 76, Appl
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75	34	81.0	112	US-10-056-052-86	Sequence 86, Appl
76	34	81.0	112	US-10-056-052-88	Sequence 88, Appl
77	34	81.0	112	US-10-056-052-90	Sequence 90, Appl
78	34	81.0	112	US-10-056-052-92	Sequence 92, Appl
79	34	81.0	112	US-10-056-052-94	Sequence 94, Appl
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81	34	81.0	112	US-10-056-052-98	Sequence 98, Appl
82	34	81.0	112	US-10-056-052-100	Sequence 100, Appl
83	34	81.0	112	US-10-056-052-102	Sequence 102, Appl
84	34	81.0	112	US-10-056-052-104	Sequence 104, Appl
85	34	81.0	112	US-10-056-052-106	Sequence 106, Appl
86	34	81.0	112	US-10-056-052-108	Sequence 108, Appl
87	34	81.0	112	US-10-056-052-110	Sequence 110, Appl
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92	34	81.0	112	US-10-056-052-120	Sequence 120, Appl
93	34	81.0	112	US-10-056-052-122	Sequence 122, Appl
94	34	81.0	112	US-10-056-052-124	Sequence 124, Appl
95	34	81.0	112	US-10-056-052-126	Sequence 126, Appl
96	34	81.0	112	US-10-056-052-128	Sequence 128, Appl
97	34	81.0	112	US-10-056-052-130	Sequence 130, Appl
98	34	81.0	112	US-10-056-052-132	Sequence 132, Appl
99	34	81.0	112	US-10-056-052-134	Sequence 134, Appl
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101	31	73.8	661	5	US-10-723-003-28	Sequence 28, Appl	174	30	71.4	1274	4	US-10-408-7654-1849	Sequence 1849, Ap
102	31	73.8	661	5	US-10-723-003-44	Sequence 34, Appl	175	30	71.4	1317	4	US-10-071-275-2	Sequence 2, Appl
103	31	73.8	661	5	US-11-004-639-28	Sequence 28, Appl	176	30	71.4	1317	4	US-10-193-452-95	Sequence 95, Appl
104	31	73.8	661	6	US-11-004-639-54	Sequence 34, Appl	177	30	71.4	1351	5	US-10-494-940-39	Sequence 39, Appl
105	31	73.8	720	3	US-09-939-4084-13	Sequence 13, Appl	178	30	71.4	1482	3	US-09-940-3168-21	Sequence 21, Appl
106	31	73.8	744	4	US-10-320-787-3279	Sequence 3279, Ap	179	30	71.4	1488	3	US-09-940-3168-17	Sequence 17, Appl
107	31	73.8	920	5	US-10-732-923-1107	Sequence 7107, Ap	180	30	71.4	1509	3	US-09-940-3168-23	Sequence 23, Appl
108	31	73.8	920	5	US-10-732-923-1110	Sequence 7110, Ap	181	30	71.4	1517	3	US-09-940-3168-19	Sequence 19, Appl
109	31	73.8	952	5	US-10-732-923-7087	Sequence 7087, Ap	182	30	71.4	1557	3	US-09-940-3168-27	Sequence 27, Appl
110	31	73.8	952	5	US-10-732-923-7088	Sequence 7088, Ap	183	30	71.4	1574	3	US-09-940-3168-25	Sequence 25, Appl
111	31	73.8	954	4	US-10-425-114-62396	Sequence 62396, A	184	30	71.4	1588	3	US-09-940-3168-31	Sequence 31, Appl
112	31	73.8	1147	4	US-10-337-481A-38	Sequence 38, Appl	185	30	71.4	1588	3	US-09-940-3168-29	Sequence 29, Appl
113	31	73.8	1638	5	US-10-884-813-8	Sequence 8, Appl	186	30	71.4	1604	3	US-09-888-615-73	Sequence 73, Appl
114	31	73.8	1638	5	US-10-884-813-12	Sequence 12, Appl	187	30	71.4	1605	3	US-09-940-3168-33	Sequence 33, Appl
115	31	73.8	1642	5	US-09-925-442-2	Sequence 2, Appl	188	30	71.4	1637	3	US-09-808-602-83	Sequence 83, Appl
116	31	73.8	1642	5	US-10-884-813-4	Sequence 4, Appl	189	30	71.4	1731	1	US-09-800-198-71	Sequence 71, Appl
117	31	73.8	1648	3	US-09-925-442-35	Sequence 35, Appl	190	30	71.4	2144	5	US-10-723-860-2303	Sequence 2303, Ap
118	31	73.8	1663	5	US-10-884-813-6	Sequence 6, Appl	191	30	71.4	2551	4	US-10-144-194A-80	Sequence 80, Appl
119	31	73.8	1663	5	US-10-884-813-10	Sequence 10, Appl	192	30	71.4	2551	5	US-10-491-566-80	Sequence 80, Appl
120	30	71.4	46	4	US-10-425-115-362031	Sequence 362031,	193	30	71.4	2633	4	US-10-144-194A-82	Sequence 82, Appl
121	30	71.4	56	3	US-09-764-869-1001	Sequence 1001, Ap	194	30	71.4	2633	5	US-10-491-566-82	Sequence 82, Appl
122	30	71.4	56	4	US-10-091-504-1001	Sequence 1001, Ap	195	30	71.4	2724	3	US-09-808-602-13	Sequence 13, Appl
123	30	71.4	56	4	US-10-227-577-1001	Sequence 1001, Ap	196	30	71.4	2724	3	US-09-800-198-13	Sequence 13, Appl
124	30	71.4	56	4	US-10-424-599-200741	Sequence 200741,	197	30	71.4	2733	3	US-09-808-602-8	Sequence 8, Appl
125	30	71.4	78	4	US-10-425-115-263908	Sequence 263908,	198	30	71.4	2733	4	US-09-808-602-8	Sequence 8, Appl
126	30	71.4	81	4	US-10-437-963-15166	Sequence 15166,	199	30	71.4	2739	4	US-10-072-012-144	Sequence 144, Ap
127	30	71.4	82	4	US-10-437-963-159419	Sequence 159419,	200	30	71.4	2764	3	US-09-808-602-80	Sequence 80, Appl
128	30	71.4	87	4	US-10-425-115-189673	Sequence 189673,	201	30	71.4	2764	3	US-09-800-198-68	Sequence 68, Appl
129	30	71.4	93	4	US-10-425-115-360240	Sequence 360240,	202	30	71.4	2764	4	US-10-072-012-487	Sequence 487, Appl
130	30	71.4	94	4	US-10-425-115-261186	Sequence 261186,	203	30	71.4	2764	5	US-10-631-467-1514	Sequence 1514, Ap
131	30	71.4	103	4	US-10-029-386-29158	Sequence 29158, A	204	30	71.4	2765	3	US-09-808-602-84	Sequence 84, Appl
132	30	71.4	155	4	US-10-424-599-179985	Sequence 179985,	205	30	71.4	2765	3	US-09-800-198-72	Sequence 72, Appl
133	30	71.4	160	4	US-10-425-115-196271	Sequence 196271,	206	30	71.4	2765	3	US-10-072-012-488	Sequence 488, Appl
134	30	71.4	192	4	US-10-130-435-168	Sequence 168, App	207	30	71.4	6396	3	US-09-940-3168-72	Sequence 72, Appl
135	30	71.4	192	6	US-11-135-537-202	Sequence 202, App	208	30	70.2	88	4	US-10-424-599-191310	Sequence 191310, Ap
136	30	71.4	216	6	US-10-289-762-627	Sequence 627, App	209	29	69.0	14	4	US-10-308-128-50	Sequence 50, Appl
137	30	71.4	272	4	US-10-207-655-14	Sequence 14, Appl	210	29	69.0	14	4	US-10-722-502-10	Sequence 10, Appl
138	30	71.4	272	6	US-11-089-511-14	Sequence 14, Appl	211	29	69.0	14	4	US-10-645-659-10	Sequence 10, Appl
139	30	71.4	272	6	US-11-089-190-14	Sequence 14, Appl	212	29	69.0	15	5	US-10-916-598-21	Sequence 21, Appl
140	30	71.4	272	6	US-11-088-570-14	Sequence 14, Appl	213	29	69.0	31	4	US-10-391-172-574	Sequence 574, App
141	30	71.4	272	6	US-11-088-737-14	Sequence 14, Appl	214	29	69.0	31	4	US-10-321-978-574	Sequence 574, App
142	30	71.4	272	6	US-11-088-569-14	Sequence 14, Appl	215	29	69.0	36	4	US-10-424-599-198466	Sequence 198466,
143	30	71.4	272	6	US-11-088-693-14	Sequence 14, Appl	216	29	69.0	49	4	US-10-424-599-226105	Sequence 226105,
144	30	71.4	272	6	US-11-089-367-14	Sequence 14, Appl	217	29	69.0	52	4	US-10-425-115-205778	Sequence 205778,
145	30	71.4	272	6	US-11-089-367-14	Sequence 14, Appl	218	29	69.0	57	4	US-10-424-599-244592	Sequence 244592,
146	30	71.4	272	6	US-11-089-368-14	Sequence 14, Appl	219	29	69.0	57	4	US-10-425-115-264643	Sequence 264643,
147	30	71.4	391	4	US-10-282-122A-44655	Sequence 44655, A	220	29	69.0	58	4	US-10-425-115-336772	Sequence 336772,
148	30	71.4	399	4	US-10-425-115-196274	Sequence 196274,	221	29	69.0	63	4	US-10-767-701-50121	Sequence 50121, A
149	30	71.4	415	4	US-10-425-114-62725	Sequence 62725, A	222	29	69.0	66	4	US-10-425-115-340883	Sequence 340883,
150	30	71.4	421	4	US-10-156-761-13612	Sequence 13612, A	223	29	69.0	67	4	US-10-425-115-204392	Sequence 204392,
151	30	71.4	422	4	US-10-437-963-158439	Sequence 158439,	224	29	69.0	68	4	US-10-424-599-143670	Sequence 143670,
152	30	71.4	439	4	US-10-437-963-111003	Sequence 111003,	225	29	69.0	71	4	US-10-029-386-29386	Sequence 29386, A
153	30	71.4	635	4	US-10-032-585-7695	Sequence 7695, Ap	226	29	69.0	76	5	US-10-450-763-33364	Sequence 33364, A
154	30	71.4	635	5	US-10-241-220-85	Sequence 85, Appl	227	29	69.0	77	4	US-10-424-599-210992	Sequence 210992,
155	30	71.4	635	5	US-10-872-972-85	Sequence 85, Appl	228	29	69.0	84	4	US-10-184-648-56	Sequence 56, Appl
156	30	71.4	635	5	US-10-872-991-85	Sequence 85, Appl	229	29	69.0	84	4	US-10-425-115-358392	Sequence 358392,
157	30	71.4	670	3	US-09-893-519A-32	Sequence 32, Appl	230	29	69.0	86	4	US-10-242-355-411	Sequence 411, App
158	30	71.4	701	4	US-10-437-963-107501	Sequence 107501	231	29	69.0	100	4	US-10-425-115-337369	Sequence 337369,
159	30	71.4	718	3	US-09-815-242-14036	Sequence 14036, A	232	29	69.0	103	4	US-10-425-115-250089	Sequence 250089,
160	30	71.4	726	4	US-10-282-122A-75909	Sequence 75909, A	233	29	69.0	111	4	US-10-424-599-234411	Sequence 234411,
161	30	71.4	726	4	US-10-282-122A-75135	Sequence 75135, A	234	29	69.0	112	4	US-10-437-963-179754	Sequence 179754,
162	30	71.4	762	4	US-10-282-122A-74229	Sequence 74229, A	235	29	69.0	113	4	US-10-424-599-173708	Sequence 173708,
163	30	71.4	762	5	US-10-732-923-6749	Sequence 6749, Ap	236	29	69.0	115	4	US-10-437-963-168959	Sequence 168959,
164	30	71.4	796	5	US-10-732-923-3291	Sequence 3291, A	237	29	69.0	117	4	US-10-767-701-51240	Sequence 51240, A
165	30	71.4	810	3	US-09-815-242-13636	Sequence 13636, A	238	29	69.0	127	4	US-10-425-115-237950	Sequence 237950,
166	30	71.4	810	3	US-09-769-744A-74	Sequence 74, Appl	239	29	69.0	128	4	US-10-291-172-198	Sequence 198, App
167	30	71.4	810	5	US-10-427-928-6608	Sequence 4608, Ap	240	29	69.0	128	4	US-10-321-878-198	Sequence 103853,
168	30	71.4	810	5	US-10-732-923-6746	Sequence 6746, Ap	241	29	69.0	128	4	US-10-424-599-153853	Sequence 153853,
169	30	71.4	816	5	US-10-617-320-4504	Sequence 4504, Ap	242	29	69.0	128	4	US-10-424-599-153853	Sequence 153853,
170	30	71.4	847	5	US-10-094-749-3045	Sequence 3045, Ap	243	29	69.0	124	3	US-09-925-501-1022	Sequence 1022, Ap
171	30	71.4	870	5	US-10-732-923-6870	Sequence 6870, Ap	244	29	69.0	124	3	US-09-796-692-1206	Sequence 1206, Ap
172	30	71.4	1059	5	US-10-473-451-8	Sequence 8, Appl	245	29	69.0	134	3	US-09-796-692-1985	Sequence 1985, Ap
173	30	71.4	1160	4	US-10-437-963-116762	Sequence 116762,	246	29	69.0	134	3	US-09-796-692-2226	Sequence 2226, Ap

247	29	69.0	134	4	US-10-040-862-1206	Sequence 1206, Ap	320	29	69.0	533	3	US-09-776-874A-10	Sequence 10, Appl
248	29	69.0	134	4	US-10-040-862-1985	Sequence 1985, Ap	321	29	69.0	533	3	US-09-944-602-2	Sequence 2, Appl1
249	29	69.0	134	4	US-10-040-862-2226	Sequence 2226, Ap	322	29	69.0	533	3	US-09-322-977-2	Sequence 2, Appl1
250	29	69.0	134	4	US-10-057-475B-1206	Sequence 1206, Ap	323	29	69.0	533	3	US-09-988-113-10	Sequence 10, Appl
251	29	69.0	134	4	US-10-057-475B-1985	Sequence 1985, Ap	324	29	69.0	533	4	US-10-137-351-2	Sequence 2, Appl1
252	29	69.0	134	4	US-10-057-475B-2226	Sequence 2226, Ap	325	29	69.0	533	4	US-10-341-582-10	Sequence 10, Appl
253	29	69.0	134	4	US-10-154-884B-1206	Sequence 1206, Ap	326	29	69.0	533	4	US-10-384-451-10	Sequence 10, Appl
254	29	69.0	134	4	US-10-154-884B-1985	Sequence 1985, Ap	327	29	69.0	533	4	US-10-384-451-10	Sequence 3, Appl1
255	29	69.0	134	4	US-10-154-884B-2226	Sequence 2226, Ap	328	29	69.0	533	4	US-10-368-044A-1	Sequence 1, Appl1
256	29	69.0	134	4	US-10-764-324-1206	Sequence 1206, Ap	329	29	69.0	533	4	US-10-384-450-10	Sequence 10, Appl
257	29	69.0	134	4	US-10-764-324-1985	Sequence 1985, Ap	330	29	69.0	533	4	US-10-371-218A-10	Sequence 10, Appl
258	29	69.0	134	4	US-10-764-324-2226	Sequence 2226, Ap	331	29	69.0	533	4	US-10-456-573-10	Sequence 10, Appl
259	29	69.0	134	4	US-10-108-605-165	Sequence 165, App	332	29	69.0	533	4	US-10-676-079-2	Sequence 2, Appl1
260	29	69.0	141	6	US-10-437-963-176994	Sequence 176994, A	333	29	69.0	533	4	US-10-785-115-10	Sequence 10, Appl
261	29	69.0	141	6	US-11-097-143-11550	Sequence 11550, A	334	29	69.0	533	4	US-10-781-758-10	Sequence 10, Appl
262	29	69.0	143	4	US-10-425-114-11663	Sequence 41663, A	335	29	69.0	533	4	US-10-186-149-9	Sequence 2, Appl1
263	29	69.0	153	4	US-10-289-762-329	Sequence 329, App	336	29	69.0	533	4	US-10-168-195A-5	Sequence 5, Appl1
264	29	69.0	156	3	US-09-738-626-4097	Sequence 4097, Ap	337	29	69.0	533	4	US-10-122-502-4	Sequence 4, Appl1
265	29	69.0	158	4	US-10-029-386-29054	Sequence 29054, A	338	29	69.0	533	4	US-10-645-659-4	Sequence 4, Appl1
266	29	69.0	185	5	US-10-732-923-15797	Sequence 15797, A	339	29	69.0	533	5	US-10-651-135-2	Sequence 2, Appl1
267	29	69.0	208	5	US-10-732-923-16092	Sequence 16092, A	340	29	69.0	543	5	US-10-916-598-8	Sequence 8, Appl1
268	29	69.0	225	4	US-10-767-701-56655	Sequence 56655, A	341	29	69.0	543	5	US-10-938-661A-9	Sequence 9, Appl1
269	29	69.0	226	4	US-10-282-122A-43888	Sequence 43888, A	342	29	69.0	545	3	US-09-899-440-18	Sequence 18, Appl
270	29	69.0	226	5	US-10-470-048B-342	Sequence 342, App	343	29	69.0	545	4	US-10-115-479-42	Sequence 42, Appl
271	29	69.0	227	5	US-10-343-477A-50	Sequence 50, Appl1	344	29	69.0	545	5	US-10-483-009A-18	Sequence 18, Appl
272	29	69.0	227	5	US-10-732-923-16335	Sequence 16335, A	345	29	69.0	544	4	US-10-314-683-2	Sequence 2, Appl1
273	29	69.0	229	5	US-10-732-923-15855	Sequence 15855, A	346	29	69.0	567	5	US-10-450-763-54049	Sequence 54049, A
274	29	69.0	235	3	US-09-815-242-5455	Sequence 5455, Ap	347	29	69.0	574	4	US-10-425-114-42248	Sequence 42248, A
275	29	69.0	235	3	US-09-815-242-12684	Sequence 12684, A	348	29	69.0	568	4	US-10-107-859-2	Sequence 2, Appl1
276	29	69.0	253	4	US-10-032-585-1103	Sequence 7103, Ap	349	29	69.0	552	3	US-09-776-874A-14	Sequence 14, Appl
277	29	69.0	263	5	US-10-882-104-79	Sequence 79, Appl1	350	29	69.0	552	3	US-09-988-113-14	Sequence 14, Appl
278	29	69.0	267	4	US-10-369-493-15566	Sequence 15566, A	351	29	69.0	552	4	US-10-341-582-14	Sequence 14, Appl
279	29	69.0	267	4	US-10-369-493-15939	Sequence 15939, A	352	29	69.0	552	4	US-10-384-450-14	Sequence 14, Appl
280	29	69.0	267	4	US-10-369-493-16305	Sequence 16305, A	353	29	69.0	552	4	US-10-384-450-14	Sequence 14, Appl
281	29	69.0	267	4	US-10-425-114-37464	Sequence 37464, A	354	29	69.0	552	4	US-10-371-218A-14	Sequence 14, Appl
282	29	69.0	301	4	US-10-369-493-33105	Sequence 23105, A	355	29	69.0	552	4	US-10-456-573-14	Sequence 14, Appl
283	29	69.0	308	4	US-10-437-963-199801	Sequence 199801, A	356	29	69.0	552	4	US-10-785-116-14	Sequence 14, Appl
284	29	69.0	327	4	US-10-282-122A-68681	Sequence 68681, A	357	29	69.0	552	4	US-10-781-758-14	Sequence 14, Appl
285	29	69.0	334	4	US-10-437-963-122368	Sequence 122368, A	358	29	69.0	604	4	US-10-437-963-150085	Sequence 150085, A
286	29	69.0	337	5	US-10-732-923-20559	Sequence 20559, A	359	29	69.0	608	4	US-10-325-066A-1096	Sequence 1096, Ap
287	29	69.0	339	4	US-10-369-493-3060	Sequence 3060, Ap	360	29	69.0	608	4	US-10-225-067-34	Sequence 34, Appl
288	29	69.0	332	4	US-10-451-374-15	Sequence 15, Appl	361	29	69.0	608	4	US-10-374-780A-36	Sequence 36, Appl
289	29	69.0	371	4	US-10-425-115-294673	Sequence 294673, A	362	29	69.0	608	4	US-10-412-699B-128	Sequence 128, App
290	29	69.0	374	4	US-10-425-114-68067	Sequence 68067, A	363	29	69.0	608	4	US-10-412-699B-1744	Sequence 1744, App
291	29	69.0	379	3	US-09-864-761-43232	Sequence 43232, A	364	29	69.0	608	5	US-10-325-066A-1096	Sequence 1096, Ap
292	29	69.0	384	4	US-10-425-114-65273	Sequence 65273, A	365	29	69.0	611	4	US-10-424-599-234141	Sequence 234141, Ap
293	29	69.0	386	4	US-10-722-502-1	Sequence 1, Appl1	366	29	69.0	624	4	US-10-108-260A-3446	Sequence 3446, Ap
294	29	69.0	386	4	US-10-645-659-1	Sequence 1, Appl1	367	29	69.0	643	4	US-10-437-963-171515	Sequence 171515, A
295	29	69.0	386	5	US-10-916-598-33	Sequence 33, Appl	368	29	69.0	648	4	US-10-425-115-300974	Sequence 34, Appl
296	29	69.0	406	4	US-10-425-115-218260	Sequence 218260, A	369	29	69.0	662	4	US-10-429-160-34	Sequence 160, App
297	29	69.0	430	4	US-10-437-963-164464	Sequence 164464, A	370	29	69.0	662	4	US-10-308-128-160	Sequence 128, App
298	29	69.0	459	5	US-10-389-566-2195	Sequence 2195, Ap	371	29	69.0	664	4	US-10-425-115-237968	Sequence 237968, A
299	29	69.0	459	5	US-10-732-923-2760	Sequence 2760, Ap	372	29	69.0	731	4	US-10-437-963-204439	Sequence 204439, A
300	29	69.0	460	4	US-10-602-268-7	Sequence 7, Appl1	373	29	69.0	760	4	US-10-139-092-8	Sequence 8, Appl1
301	29	69.0	460	5	US-10-916-598-37	Sequence 37, Appl1	374	29	69.0	761	4	US-10-755-889-428	Sequence 428, App
302	29	69.0	488	6	US-11-097-143-5514	Sequence 5514, Ap	375	29	69.0	761	5	US-10-723-860-3307	Sequence 3307, Ap
303	29	69.0	494	4	US-10-437-963-148377	Sequence 148377, A	376	29	69.0	761	5	US-10-631-467-632	Sequence 632, App
304	29	69.0	506	4	US-10-425-115-294674	Sequence 294674, A	377	29	69.0	761	5	US-10-631-467-1429	Sequence 1429, Ap
305	29	69.0	508	5	US-10-916-598-34	Sequence 34, Appl	378	29	69.0	792	4	US-10-437-963-168186	Sequence 168186, A
306	29	69.0	515	4	US-10-139-092-1	Sequence 1, Appl1	379	29	69.0	795	4	US-10-112-944-267	Sequence 267, App
307	29	69.0	516	4	US-10-296-734-1469	Sequence 1469, Ap	380	29	69.0	826	4	US-10-108-128-2	Sequence 2, Appl1
308	29	69.0	517	4	US-10-437-963-168578	Sequence 168578, A	381	29	69.0	827	4	US-10-282-122A-61760	Sequence 61760, A
309	29	69.0	518	4	US-10-767-701-39270	Sequence 39270, A	382	29	69.0	827	4	US-10-108-128-9	Sequence 9, Appl1
310	29	69.0	525	4	US-10-139-092-3	Sequence 3, Appl1	383	29	69.0	828	3	US-09-935-280-2	Sequence 2, Appl1
311	29	69.0	526	5	US-10-495-918-134	Sequence 134, App	384	29	69.0	828	4	US-10-288-152-6	Sequence 6, Appl1
312	29	69.0	527	3	US-09-930-218-16	Sequence 16, Appl	385	29	69.0	828	4	US-10-114-270-128	Sequence 128, App
313	29	69.0	527	4	US-10-431-338-16	Sequence 16, Appl	386	29	69.0	828	4	US-10-308-128-10	Sequence 10, Appl
314	29	69.0	528	5	US-10-901-943-4	Sequence 4, Appl1	387	29	69.0	828	4	US-10-287-226-428	Sequence 428, App
315	29	69.0	539	4	US-10-424-599-170370	Sequence 170370, A	388	29	69.0	828	4	US-10-287-226-430	Sequence 430, App
316	29	69.0	540	4	US-10-139-092-9	Sequence 9, Appl1	389	29	69.0	828	4	US-10-416-914A-25	Sequence 25, Appl
317	29	69.0	543	3	US-09-759-207-2	Sequence 2, Appl1	390	29	69.0	828	4	US-10-398-038-6	Sequence 6, Appl1
318	29	69.0	543	3	US-09-930-218-3	Sequence 3, Appl1	391	29	69.0	828	5	US-10-976-440-6	Sequence 6, Appl1
319	29	69.0	543	3	US-09-186-200-1	Sequence 1, Appl1	392	29	69.0	831	4	US-10-342-844-76	Sequence 76, Appl

393	29	69.0	841	5	US-10-739-930-6310	Sequence 6310, App	466	28	66.7	76	4	US-10-424-599-197916	Sequence 197916,
394	29	69.0	852	4	US-10-211-162-63	Sequence 63, App1	467	28	66.7	77	4	US-10-437-963-139639	Sequence 139639,
395	29	69.0	887	5	US-10-450-763-54043	Sequence 54043, A	468	28	66.7	80	4	US-10-425-114-63004	Sequence 63004, A
396	29	69.0	949	4	US-10-282-122A-59089	Sequence 59089, A	469	28	66.7	80	4	US-10-437-963-202693	Sequence 202693,
397	29	69.0	957	4	US-10-437-963-107121	Sequence 107121, A	470	28	66.7	80	4	US-10-425-115-33251	Sequence 33251, A
398	29	69.0	987	4	US-10-437-963-119332	Sequence 119332, A	471	28	66.7	81	4	US-10-425-115-35350	Sequence 35350, A
399	29	69.0	1020	4	US-10-437-963-120996	Sequence 120996, A	472	28	66.7	83	4	US-10-425-115-255689	Sequence 255689, A
400	29	69.0	1078	4	US-10-170-385-295	Sequence 295, App	473	28	66.7	84	4	US-10-425-115-33209	Sequence 33209, A
401	29	69.0	1083	5	US-10-450-763-35011	Sequence 35011, A	474	28	66.7	85	4	US-10-425-115-313140	Sequence 313140, A
402	29	69.0	1100	4	US-10-139-092-7	Sequence 7, App1	475	28	66.7	85	4	US-10-425-115-338038	Sequence 338038, A
403	29	69.0	1113	5	US-10-450-763-37061	Sequence 37061, A	476	28	66.7	87	4	US-10-425-115-291459	Sequence 291459, A
404	29	69.0	1167	4	US-10-274-409-2	Sequence 2, App1	477	28	66.7	88	4	US-10-425-115-230091	Sequence 230091, A
405	29	69.0	1167	5	US-10-932-135-2	Sequence 2, App1	478	28	66.7	90	5	US-10-450-763-33178	Sequence 33178, A
406	29	69.0	1178	4	US-10-369-493-21997	Sequence 21997, A	479	28	66.7	91	4	US-10-424-599-173283	Sequence 173283, A
407	29	69.0	1253	4	US-10-139-092-2	Sequence 2, App1	480	28	66.7	91	4	US-10-425-115-297988	Sequence 297988, A
408	29	69.0	1365	4	US-10-437-963-169650	Sequence 169650, A	481	28	66.7	94	4	US-10-424-599-185967	Sequence 185967, A
409	29	69.0	1366	4	US-10-437-963-170621	Sequence 170621, A	482	28	66.7	94	4	US-10-425-115-235113	Sequence 235113, A
410	29	69.0	1376	6	US-11-097-143-5979	Sequence 5979, App	483	28	66.7	95	4	US-10-424-599-181354	Sequence 181354, A
411	29	69.0	1388	5	US-10-840-512-202	Sequence 202, App	484	28	66.7	98	4	US-10-424-599-258313	Sequence 258313, A
412	29	69.0	1529	4	US-10-437-963-204162	Sequence 204162, A	485	28	66.7	99	5	US-10-700-632-60	Sequence 60, App1
413	29	69.0	1558	4	US-10-437-963-204394	Sequence 204394, A	486	28	66.7	101	4	US-10-767-701-50044	Sequence 50044, A
414	29	69.0	1565	4	US-10-437-963-204400	Sequence 204400, A	487	28	66.7	101	4	US-10-425-115-337215	Sequence 337215, A
415	29	69.0	1628	4	US-10-437-963-170587	Sequence 170587, A	488	28	66.7	109	3	US-09-867-550-1608	Sequence 1608, App
416	29	69.0	1651	4	US-10-437-963-171937	Sequence 171937, A	489	28	66.7	110	4	US-10-425-115-261824	Sequence 261824, A
417	29	69.0	1665	4	US-10-437-963-168678	Sequence 168678, A	490	28	66.7	111	3	US-09-864-408A-4298	Sequence 4298, App
418	29	69.0	1740	4	US-10-437-963-204284	Sequence 204284, A	491	28	66.7	111	4	US-10-029-386-30414	Sequence 30414, A
419	29	69.0	1863	4	US-10-437-963-170953	Sequence 170953, A	492	28	66.7	111	4	US-10-437-963-128568	Sequence 128568, A
420	29	69.0	1874	4	US-10-437-963-172543	Sequence 172543, A	493	28	66.7	117	4	US-10-425-115-216306	Sequence 216306, A
421	29	69.0	1893	4	US-10-437-963-169461	Sequence 169461, A	494	28	66.7	119	4	US-10-101-464A-832	Sequence 832, App
422	29	69.0	1999	4	US-10-437-963-170499	Sequence 170499, A	495	28	66.7	119	5	US-10-864-252-832	Sequence 832, App
423	29	69.0	2009	4	US-10-437-963-204241	Sequence 204241, A	496	28	66.7	120	4	US-10-101-464A-128	Sequence 128, App
424	29	69.0	2158	4	US-10-437-963-171980	Sequence 171980, A	497	28	66.7	120	5	US-10-864-252-128	Sequence 128, App
425	29	69.0	2264	4	US-10-437-963-169538	Sequence 169538, A	498	28	66.7	122	4	US-10-425-115-327129	Sequence 327129, A
426	29	69.0	2275	4	US-10-285-027-928	Sequence 928, App	499	28	66.7	126	4	US-10-424-599-148994	Sequence 148994, A
427	29	69.0	2275	4	US-10-029-020-52	Sequence 52, App1	500	28	66.7	126	4	US-10-424-599-190576	Sequence 190576, A
428	29	69.0	2275	4	US-10-408-765A-1687	Sequence 1687, App	501	28	66.7	126	4	US-10-437-963-124758	Sequence 124758, A
429	29	69.0	2275	5	US-10-723-860-4102	Sequence 4102, App	502	28	66.7	132	4	US-10-425-114-44340	Sequence 44340, A
430	29	69.0	2758	4	US-10-467-535-10	Sequence 10, App1	503	28	66.7	136	4	US-10-425-115-327125	Sequence 327125, A
431	29	69.0	2769	4	US-10-383-201-44	Sequence 44, App1	504	28	66.7	149	3	US-09-774-639-304	Sequence 304, App
432	29	69.0	2769	4	US-10-029-020-14	Sequence 14, App1	505	28	66.7	149	3	US-09-969-720-231	Sequence 231, App
433	29	69.0	2771	3	US-09-808-602-82	Sequence 82, App1	506	28	66.7	149	4	US-10-621-363-231	Sequence 231, App
434	29	69.0	2771	3	US-09-800-198-70	Sequence 70, App1	507	28	66.7	150	4	US-10-424-599-174813	Sequence 174813, A
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712	27	64.3	69	4	US-10-424-599-277737	Sequence 277737,	785	27	64.3	161	4	US-10-970-713-282	Sequence 282, App
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ALIGNMENTS

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RESULT 1
US-10-700-632-6
; Sequence 6, Application US/10700632
; Publication No. US20050118183A1
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; GENERAL INFORMATION:
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; TITLE OF INVENTION: ANTI-CD33 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID
; FILE REFERENCE: A8427
; CURRENT APPLICATION NUMBER: US/10/700,632
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US-10-700-632-6
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; Sequence 8, Application US/10700632
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; FILE REFERENCE: A8427
; CURRENT APPLICATION NUMBER: US/10/700,632
; CURRENT FILING DATE: 2003-11-05
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; SEQ ID NO 8
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-700-632-8
```

```
Query Match          100.0%; Score 42; DB 5; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.96;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 HOYLSRT 8
Db 95 HOYLSRT 102
```

```
RESULT 3
US-10-700-632-10
; Sequence 10, Application US/10700632
; Publication No. US20050118183A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Immunogen, Inc.
; TITLE OF INVENTION: ANTI-CD33 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID
; FILE REFERENCE: A8427
; CURRENT APPLICATION NUMBER: US/10/700,632
; CURRENT FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: US 60/424,332
; PRIOR FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized My9-6 antibody light chain variable region
US-10-700-632-10
```

```
Query Match          100.0%; Score 42; DB 5; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.96;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 HOYLSRT 8
Db 95 HOYLSRT 102
```

```
RESULT 4
US-10-700-632-62
; Sequence 62, Application US/10700632
; Publication No. US20050118183A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Immunogen, Inc.
; TITLE OF INVENTION: ANTI-CD33 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID
; FILE REFERENCE: A8427
; CURRENT APPLICATION NUMBER: US/10/700,632
; CURRENT FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: US 60/424,332
; PRIOR FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 62
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-700-632-62
```

```
Query Match          100.0%; Score 42; DB 5; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.97;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

OY 1 HOYLSRT 8
Db 95 HOYLSRT 102

RESULT 5

US-10-056-052-6
; Sequence 6, Application US/10056052
; Publication No. US20030099656A1
; GENERAL INFORMATION:
; APPLICANT: PATTI, Joseph M
; APPLICANT: HUTCHINS, Jeff T
; APPLICANT: DOMANSKI, Paul
; APPLICANT: PATEL, Prakisha
; APPLICANT: HALL, Andrea
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLPA PROTEIN . . .
; FILE REFERENCE: P07069US04/BAS
; CURRENT APPLICATION NUMBER: US/10/056,052
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/308,116
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/298,413
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/274,611
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/264,072
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-056-052-6

Query Match 88.1%; Score 37; DB 4; Length 112;
Best Local Similarity 87.5%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 HOYLSRT 8
Db 95 HOYLSRT 102

RESULT 6

US-10-867-992-2
; Sequence 2, Application US/10867992
; Publication No. US2005012404A1
; GENERAL INFORMATION:
; APPLICANT: Cunningham, Mark R.; Heavner, George A.; Luo, Jinquan; Song, Xiao-yu R.
; TITLE OF INVENTION: Interleukin-21 Analogs
; FILE REFERENCE: CEN5029 NP
; CURRENT APPLICATION NUMBER: US/10/867,992
; CURRENT FILING DATE: 2004-06-15
; PRIOR APPLICATION NUMBER: US 60/427,772
; PRIOR FILING DATE: 2003-06-19
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Analog #1
US-10-867-992-2

Query Match 88.1%; Score 37; DB 5; Length 131;
Best Local Similarity 87.5%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 HOYLSRT 8
Db 118 HOYLSRT 125

RESULT 7

US-10-867-992-4
; Sequence 4, Application US/10867992
; Publication No. US2005012404A1
; GENERAL INFORMATION:
; APPLICANT: Cunningham, Mark R.; Heavner, George A.; Luo, Jinquan; Song, Xiao-yu R.
; TITLE OF INVENTION: Interleukin-21 Analogs
; FILE REFERENCE: CEN5029 NP
; CURRENT APPLICATION NUMBER: US/10/867,992
; CURRENT FILING DATE: 2004-06-15
; PRIOR APPLICATION NUMBER: US 60/427,772
; PRIOR FILING DATE: 2003-06-19
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Analog #2
US-10-867-992-4

Query Match 88.1%; Score 37; DB 5; Length 131;
Best Local Similarity 87.5%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 HOYLSRT 8
Db 118 HOYLSRT 125

RESULT 8

US-10-867-992-6
; Sequence 6, Application US/10867992
; Publication No. US2005012404A1
; GENERAL INFORMATION:
; APPLICANT: Cunningham, Mark R.; Heavner, George A.; Luo, Jinquan; Song, Xiao-yu R.
; TITLE OF INVENTION: Interleukin-21 Analogs
; FILE REFERENCE: CEN5029 NP
; CURRENT APPLICATION NUMBER: US/10/867,992
; CURRENT FILING DATE: 2004-06-15
; PRIOR APPLICATION NUMBER: US 60/427,772
; PRIOR FILING DATE: 2003-06-19
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Analog #3
US-10-867-992-6

Query Match 88.1%; Score 37; DB 5; Length 131;
Best Local Similarity 87.5%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 HOYLSRT 8
Db 118 HOYLSRT 125

RESULT 9

US-10-867-992-8
; Sequence 8, Application US/10867992
; Publication No. US2005012404A1
; GENERAL INFORMATION:
; APPLICANT: Cunningham, Mark R.; Heavner, George A.; Luo, Jinquan; Song, Xiao-yu R.
; TITLE OF INVENTION: Interleukin-21 Analogs
; FILE REFERENCE: CEN5029 NP
; CURRENT APPLICATION NUMBER: US/10/867,992

```
/ CURRENT FILING DATE: 2004-06-15
/ PRIOR APPLICATION NUMBER: US 60/427,772
/ PRIOR FILING DATE: 2003-06-19
/ NUMBER OF SEQ ID NOS: 19
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 8
/ LENGTH: 131
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Analog #4
US-10-867-992-8
```

```
Query Match      88.1%; Score 37; DB 5; Length 131;
Best Local Similarity 87.5%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 HOYLSRT 8
      ||:|||||
Db      118 HOHLSRT 125
```

```
RESULT 10
US-10-867-992-10
/ Sequence 10, Application US/10867992
/ Publication No. US20050124044A1
/ GENERAL INFORMATION:
/ APPLICANT: Cunningham, Mark R.; Heavner, George A.; Luo, Jinqun; Song, Xiao-yu R.
/ TITLE OF INVENTION: Interleukin-21 Analogs
/ FILE REFERENCE: CEN5029 NP
/ CURRENT APPLICATION NUMBER: US/10/867,992
/ CURRENT FILING DATE: 2004-06-15
/ PRIOR APPLICATION NUMBER: US 60/427,772
/ PRIOR FILING DATE: 2003-06-19
/ NUMBER OF SEQ ID NOS: 19
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 10
/ LENGTH: 131
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Analog #10A
US-10-867-992-10
```

```
Query Match      88.1%; Score 37; DB 5; Length 131;
Best Local Similarity 87.5%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 HOYLSRT 8
      ||:|||||
Db      118 HOHLSRT 125
```

```
RESULT 11
US-10-867-992-16
/ Sequence 16, Application US/10867992
/ Publication No. US20050124044A1
/ GENERAL INFORMATION:
/ APPLICANT: Cunningham, Mark R.; Heavner, George A.; Luo, Jinqun; Song, Xiao-yu R.
/ TITLE OF INVENTION: Interleukin-21 Analogs
/ FILE REFERENCE: CEN5029 NP
/ CURRENT APPLICATION NUMBER: US/10/867,992
/ CURRENT FILING DATE: 2004-06-15
/ PRIOR APPLICATION NUMBER: US 60/427,772
/ PRIOR FILING DATE: 2003-06-19
/ NUMBER OF SEQ ID NOS: 19
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 16
/ LENGTH: 131
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-867-992-16
```

```
Query Match      88.1%; Score 37; DB 5; Length 131;
Best Local Similarity 87.5%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 HOYLSRT 8
      ||:|||||
Db      118 HOHLSRT 125
```

```
RESULT 12
US-10-867-992-12
/ Sequence 12, Application US/10867992
/ Publication No. US20050124044A1
/ GENERAL INFORMATION:
/ APPLICANT: Cunningham, Mark R.; Heavner, George A.; Luo, Jinqun; Song, Xiao-yu R.
/ TITLE OF INVENTION: Interleukin-21 Analogs
/ FILE REFERENCE: CEN5029 NP
/ CURRENT APPLICATION NUMBER: US/10/867,992
/ CURRENT FILING DATE: 2004-06-15
/ PRIOR APPLICATION NUMBER: US 60/427,772
/ PRIOR FILING DATE: 2003-06-19
/ NUMBER OF SEQ ID NOS: 19
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 12
/ LENGTH: 133
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Analog #10B
US-10-867-992-12
```

```
Query Match      88.1%; Score 37; DB 5; Length 133;
Best Local Similarity 87.5%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 HOYLSRT 8
      ||:|||||
Db      120 HOHLSRT 127
```

```
RESULT 13
US-10-867-992-14
/ Sequence 14, Application US/10867992
/ Publication No. US20050124044A1
/ GENERAL INFORMATION:
/ APPLICANT: Cunningham, Mark R.; Heavner, George A.; Luo, Jinqun; Song, Xiao-yu R.
/ TITLE OF INVENTION: Interleukin-21 Analogs
/ FILE REFERENCE: CEN5029 NP
/ CURRENT APPLICATION NUMBER: US/10/867,992
/ CURRENT FILING DATE: 2004-06-15
/ PRIOR APPLICATION NUMBER: US 60/427,772
/ PRIOR FILING DATE: 2003-06-19
/ NUMBER OF SEQ ID NOS: 19
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 14
/ LENGTH: 133
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Analog #4A
US-10-867-992-14
```

```
Query Match      88.1%; Score 37; DB 5; Length 133;
Best Local Similarity 87.5%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 HOYLSRT 8
      ||:|||||
Db      120 HOHLSRT 127
```

```
RESULT 14
US-10-867-992-19
```


; Sequence 19, Application US/10867992
; Publication No. US20050124044A1
; GENERAL INFORMATION:
; APPLICANT: Cunningham, Mark R.; Heavner, George A.; Luo, Jinqun; Song, Xiao-yu R.
; TITLE OF INVENTION: Interleukin-21 Analogs
; FILE REFERENCE: CEN5029 NP
; CURRENT APPLICATION NUMBER: US/10/867,992
; CURRENT FILING DATE: 2004-06-15
; PRIOR APPLICATION NUMBER: US 60/427,772
; PRIOR FILING DATE: 2003-06-19
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-867-992-19

Query Match 88.1%; Score 37; DB 5; Length 133;
Best Local Similarity 87.5%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
Db 120 HOHLSRT 127

RESULT 15
US-09-923-246-2
; Sequence 2, Application US/09923246
; Patent No. US20020128446A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020128446A1ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/923,246
; PRIOR APPLICATION NUMBER: 2001-08-03
; PRIOR FILING DATE: EARLIER APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-923-246-2

Query Match 88.1%; Score 37; DB 3; Length 162;
Best Local Similarity 87.5%; Pred. No. 15;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
Db 149 HOHLSRT 156

RESULT 16
US-09-825-561A-10
; Sequence 10, Application US/09825561A
; Patent No. US20020137677A1

; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: No. US20020137677A1ak, Julia E.
; APPLICANT: West, James W.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Holly, Richard D.
; APPLICANT: Nelson, Andrew J.
; TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECEPTORS
; FILE REFERENCE: 00-22
; CURRENT APPLICATION NUMBER: US/09/825,561A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/194,731
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/222,121
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-825-561A-10

Query Match 88.1%; Score 37; DB 3; Length 162;
Best Local Similarity 87.5%; Pred. No. 15;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
Db 149 HOHLSRT 156

RESULT 17
US-09-972-218A-19
; Sequence 19, Application US/09972218A
; Publication No. US20030049798A1
; GENERAL INFORMATION:
; APPLICANT: Carter, Laura
; APPLICANT: Whiters, Matthew J
; APPLICANT: Collins, Mary
; APPLICANT: Young, Deborah A.
; APPLICANT: Donaldson, Debra D.
; APPLICANT: Lowe, Leslie D.
; APPLICANT: Unger, Michelle
; TITLE OF INVENTION: MU-1, Member of the Cytokine Receptor Family
; FILE REFERENCE: 22058-552CIP2
; CURRENT APPLICATION NUMBER: US/09/972,218A
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: 09/569384
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: 09/560766
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US/6057128
; PRIOR FILING DATE: 1998-03-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Human
US-09-972-218A-19

Query Match 88.1%; Score 37; DB 3; Length 162;
Best Local Similarity 87.5%; Pred. No. 15;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
Db 149 HOHLSRT 156

RESULT 18
US-10-264-634-19

```
; Sequence 19, Application US/10264634
; Publication No. US20030108549A1
; GENERAL INFORMATION:
; APPLICANT: Donaldson, Debra et al.
; TITLE OF INVENTION: Methods and Compositions for Modulating Interleukin-21 Receptor A
; FILE REFERENCE: G15320-P3
; CURRENT APPLICATION NUMBER: US/10/264,634
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: 09/040,005
; PRIOR FILING DATE: 1998-03-17
; PRIOR APPLICATION NUMBER: 09/560,766
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/569,384
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: 09/972,218
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/373,746
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Human
US-10-264-634-19
```

```
Query Match      88.1%; Score 37; DB 4; Length 162;
Best Local Similarity 87.5%; Pred. No. 15;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 HOYLSRT 8
Db      149 HQHLSRT 156
```

```
RESULT 19
US-10-295-723-2
; Sequence 2, Application US/10295723
; Publication No. US20030125524A1
; GENERAL INFORMATION:
; APPLICANT: No. US20030125524A1ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAL1 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/295,723
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/123,547
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-723-2
```

```
Query Match      88.1%; Score 37; DB 4; Length 162;
Best Local Similarity 87.5%; Pred. No. 15;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 HOYLSRT 8
Db      149 HQHLSRT 156

RESULT 20
US-10-282-622-2
; Sequence 2, Application US/10282622
; Publication No. US20030134390A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: West, James W.
; APPLICANT: No. US20030134390A1ak, Julia E.
; TITLE OF INVENTION: ZALPHAL1 LIGAND ANTAGONISTS
; FILE REFERENCE: 01-37
; CURRENT APPLICATION NUMBER: US/10/282,622
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 60/337,586
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-622-2
```

```
Query Match      88.1%; Score 37; DB 4; Length 162;
Best Local Similarity 87.5%; Pred. No. 15;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 HOYLSRT 8
Db      149 HQHLSRT 156
```

```
RESULT 21
US-10-282-622-6
; Sequence 6, Application US/10282622
; Publication No. US20030134390A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: West, James W.
; APPLICANT: No. US20030134390A1ak, Julia E.
; TITLE OF INVENTION: ZALPHAL1 LIGAND ANTAGONISTS
; FILE REFERENCE: 01-37
; CURRENT APPLICATION NUMBER: US/10/282,622
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 60/337,586
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: zalphal1 ligand Q153D/I156D
US-10-282-622-6
```

```
Query Match      88.1%; Score 37; DB 4; Length 162;
Best Local Similarity 87.5%; Pred. No. 15;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 HOYLSRT 8
Db      149 HQHLSRT 156
```

```
RESULT 22
US-10-456-780-2
; Sequence 2, Application US/10456780
```

Publication No. US2004009150A1
GENERAL INFORMATION:
APPLICANT: Nelson, Andrew J.
APPLICANT: Hughes, Steven D.
APPLICANT: Holly, Richard D.
TITLE OF INVENTION: USE OF IL-21 IN CANCER AND
OTHER THERAPEUTIC APPLICATIONS
FILE REFERENCE: 03-08
CURRENT APPLICATION NUMBER: US/10/456,780
CURRENT FILING DATE: 2003-06-06
PRIOR APPLICATION NUMBER: US 60/387,127
PRIOR FILING DATE: 2002-06-07
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 162
TYPE: PRT
ORGANISM: Homo sapiens
US-10-456-780-2

Query Match 88.1%; Score 37; DB 4; Length 162;
Best Local Similarity 87.5%; Pred. No. 15;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
||:|||||
Db 149 HOHLSRT 156

RESULT 23
US-10-659-684-2
Sequence 2, Application US/10659684
Publication No. US20040110932A1
GENERAL INFORMATION:

APPLICANT: Novak, Julia E.
APPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Gross, Jane A.
APPLICANT: Johnston, Janet V.
APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAL1 LIGAND
FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/10/659,684
CURRENT FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: US/09/522,217
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,547
PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09
PRIOR APPLICATION NUMBER: US 60/123,904
PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 162
TYPE: PRT
ORGANISM: Homo sapiens
US-10-659-684-2

Query Match 88.1%; Score 37; DB 4; Length 162;
Best Local Similarity 87.5%; Pred. No. 15;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
||:|||||
Db 149 HOHLSRT 156

RESULT 24
US-10-620-169-2
Sequence 2, Application US/10620169
Publication No. US20040136954A1
GENERAL INFORMATION:
APPLICANT: Grubby, Michael J
APPLICANT: Wurster, Andrea
APPLICANT: Young, Deborah
APPLICANT: Collins, Mary
APPLICANT: Whitters, Matthew
TITLE OF INVENTION: Methods and Compositions for Modulating T Helper (TH)
FILE REFERENCE: 22058-585
CURRENT APPLICATION NUMBER: US/10/620,169
CURRENT FILING DATE: 2003-07-15
PRIOR APPLICATION NUMBER: 60/396,160
PRIOR FILING DATE: 2002-07-15
PRIOR APPLICATION NUMBER: 60/403,001
PRIOR FILING DATE: 2002-08-12
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 162
TYPE: PRT
ORGANISM: Homo sapiens
US-10-620-169-2

Query Match 88.1%; Score 37; DB 4; Length 162;
Best Local Similarity 87.5%; Pred. No. 15;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
||:|||||
Db 149 HOHLSRT 156

RESULT 25
US-10-872-087-10
Sequence 10, Application US/10872087
Publication No. US20040235743A1
GENERAL INFORMATION:
APPLICANT: Sprecher, Cindy A.
APPLICANT: Novak, Julia E.
APPLICANT: West, James W.
APPLICANT: Holly, Richard D.
APPLICANT: Nelson, Andrew J.
TITLE OF INVENTION: SOLUBLE ZALPHAL1 CYTOKINE RECEPTORS
FILE REFERENCE: 00-22D1
CURRENT APPLICATION NUMBER: US/10/872,087
CURRENT FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: US 60/194,731
PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/222,121
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: US 09/825,561
PRIOR FILING DATE: 2001-04-03
NUMBER OF SEQ ID NOS: 86
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 162
TYPE: PRT
ORGANISM: Homo sapiens
US-10-872-087-10

Query Match 88.1%; Score 37; DB 5; Length 162;
Best Local Similarity 87.5%; Pred. No. 15;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
||:|||||
Db 149 HOHLSRT 156

RESULT 26
US-10-787-442-2
; Sequence 2, Application US/10787442
; Publication No. US2004026065A1
; GENERAL INFORMATION:
; APPLICANT: Novak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALP1A1 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/787,442
; CURRENT FILING DATE: 2004-02-26
; PRIOR APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/123,547
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-787-442-2

Query Match 88.1%; Score 37; DB 5; Length 162;
Best Local Similarity 87.5%; Pred. No. 15;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
DB 149 HOHLSRT 156

RESULT 27
US-10-951-239-2
; Sequence 2, Application US/10951239
; Publication No. US2005009522A1
; GENERAL INFORMATION:
; APPLICANT: Sivakumar, Pallavur
; APPLICANT: Nelson, Andrew
; TITLE OF INVENTION: METHODS OF TREATING AUTOIMMUNE DISEASES
; FILE REFERENCE: 03-09
; CURRENT APPLICATION NUMBER: US/10/951,239
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: 60/505,919
; PRIOR FILING DATE: 2003-09-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-951-239-2

Query Match 88.1%; Score 37; DB 5; Length 162;
Best Local Similarity 87.5%; Pred. No. 15;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
DB 149 HOHLSRT 156

RESULT 28
US-10-775-204-2177
; Sequence 2177, Application US/10775204
; Publication No. US2005018666A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Halseline, William A.
; APPLICANT: Turner, David J.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF564
; CURRENT APPLICATION NUMBER: US/10/775,204
; CURRENT FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/341,811
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/360,000
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/378,950
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/398,008
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/411,355
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/414,984
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/417,611
; PRIOR FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/420,246
; PRIOR FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: 60/423,623
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/351,360
; PRIOR FILING DATE: 2002-01-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2222
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2177
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-775-204-2177

Query Match 88.1%; Score 37; DB 5; Length 162;
Best Local Similarity 87.5%; Pred. No. 15;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
DB 149 HOHLSRT 156

RESULT 29
US-09-923-246-85
; Sequence 85, Application US/09923246
; Patent No. US20020128446A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020128446A1ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALP1A1 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/923,246
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217

;; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
;; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
;; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
;; NUMBER OF SEQ ID NOS: 115
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 85
;; LENGTH: 519
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: MBP-human zalphal1 ligand fusion polypeptide
US-09-923-246-85

Query Match 88.1%; Score 37; DB 3; Length 519;
Best Local Similarity 87.5%; Pred. No. 48;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
Db 506 HOHLSRT 513

RESULT 30
US-10-295-723-85
;; Sequence 85, Application US/10295723
;; Publication No. US20030125524A1
;; GENERAL INFORMATION:
;; APPLICANT: No. US20030125524A1ak, Julia E.
;; APPLICANT: Presnell, Scott R.
;; APPLICANT: Sprecher, Cindy A.
;; APPLICANT: Foster, Donald C.
;; APPLICANT: Holly, Richard D.
;; APPLICANT: Gross, Jane A.
;; APPLICANT: Johnston, Janet V.
;; APPLICANT: Nelson, Andrew J.
;; APPLICANT: Dillon, Stacey R.
;; APPLICANT: Hammond, Angela K.
;; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
;; FILE REFERENCE: 99-16
;; CURRENT APPLICATION NUMBER: US/10/295,723
;; CURRENT FILING DATE: 2002-11-15
;; PRIOR APPLICATION NUMBER: 09/522,217
;; PRIOR FILING DATE: 2000-03-09
;; PRIOR APPLICATION NUMBER: US 60/123,547
;; PRIOR FILING DATE: 1999-03-09
;; PRIOR APPLICATION NUMBER: US 60/123,904
;; PRIOR FILING DATE: 1999-03-11
;; PRIOR APPLICATION NUMBER: US 60/142,013
;; PRIOR FILING DATE: 1999-07-01
;; NUMBER OF SEQ ID NOS: 115
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 85
;; LENGTH: 519
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: MBP-human zalphal1 ligand fusion polypeptide
US-10-295-723-85

Query Match 88.1%; Score 37; DB 4; Length 519;
Best Local Similarity 87.5%; Pred. No. 48;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
Db 506 HOHLSRT 513

RESULT 31
US-10-659-684-85
;; Sequence 85, Application US/10659684

;; Publication No. US20040110932A1
;; GENERAL INFORMATION:
;; APPLICANT: Novak, Julia E.
;; APPLICANT: Presnell, Scott R.
;; APPLICANT: Sprecher, Cindy A.
;; APPLICANT: Foster, Donald C.
;; APPLICANT: Holly, Richard D.
;; APPLICANT: Gross, Jane A.
;; APPLICANT: Johnston, Janet V.
;; APPLICANT: Nelson, Andrew J.
;; APPLICANT: Dillon, Stacey R.
;; APPLICANT: Hammond, Angela K.
;; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
;; FILE REFERENCE: 99-16
;; CURRENT APPLICATION NUMBER: US/10/659,684
;; CURRENT FILING DATE: 2003-09-10
;; PRIOR APPLICATION NUMBER: US/09/522,217
;; PRIOR FILING DATE: 2000-03-09
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,547
;; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
;; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
;; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
;; NUMBER OF SEQ ID NOS: 115
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 85
;; LENGTH: 519
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: MBP-human zalphal1 ligand fusion polypeptide
US-10-659-684-85

Query Match 88.1%; Score 37; DB 4; Length 519;
Best Local Similarity 87.5%; Pred. No. 48;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
Db 506 HOHLSRT 513

RESULT 32
US-10-787-442-85
;; Sequence 85, Application US/10787442
;; Publication No. US2004026065A1
;; GENERAL INFORMATION:
;; APPLICANT: Novak, Julia E.
;; APPLICANT: Presnell, Scott R.
;; APPLICANT: Sprecher, Cindy A.
;; APPLICANT: Foster, Donald C.
;; APPLICANT: Holly, Richard D.
;; APPLICANT: Gross, Jane A.
;; APPLICANT: Johnston, Janet V.
;; APPLICANT: Nelson, Andrew J.
;; APPLICANT: Dillon, Stacey R.
;; APPLICANT: Hammond, Angela K.
;; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
;; FILE REFERENCE: 99-16
;; CURRENT APPLICATION NUMBER: US/10/787,442
;; CURRENT FILING DATE: 2004-02-26
;; PRIOR APPLICATION NUMBER: US/09/522,217
;; PRIOR FILING DATE: 2000-03-09
;; PRIOR APPLICATION NUMBER: US 60/123,547
;; PRIOR FILING DATE: 1999-03-09
;; PRIOR APPLICATION NUMBER: US 60/123,904
;; PRIOR FILING DATE: 1999-03-11
;; PRIOR APPLICATION NUMBER: US 60/142,013
;; PRIOR FILING DATE: 1999-07-01
;; NUMBER OF SEQ ID NOS: 115
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 85

LENGTH: 519
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: MBP-human zalphall Ligand fusion polypeptide
US-10-787-442-85

Query Match 88.1%; Score 37; DB 5; Length 519;
Best Local Similarity 87.5%; Pred. No. 48;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
DB 506 HOYLSRT 513

RESULT 33

US-10-775-204-2167
Sequence 2167, Application US/10775204
Publication No. US2005018666A1
GENERAL INFORMATION:
APPLICANT: Rosen, Craig A.
APPLICANT: Haseltine, William A.
APPLICANT: Balance, David J.
APPLICANT: Turner, Andrew J.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PR564
CURRENT APPLICATION NUMBER: US/10/775,204
CURRENT FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/341,811
PRIOR FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 60/360,000
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: 60/378,950
PRIOR FILING DATE: 2002-05-10
PRIOR APPLICATION NUMBER: 60/358,008
PRIOR FILING DATE: 2002-07-24
PRIOR APPLICATION NUMBER: 60/411,355
PRIOR FILING DATE: 2002-09-18
PRIOR APPLICATION NUMBER: 60/414,984
PRIOR FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: 60/417,611
PRIOR FILING DATE: 2002-10-11
PRIOR APPLICATION NUMBER: 60/420,246
PRIOR FILING DATE: 2002-10-23
PRIOR APPLICATION NUMBER: 60/423,623
PRIOR FILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: 60/351,360
PRIOR FILING DATE: 2002-01-28
Remaining Prior Application data removed - See file Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2222
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2167
LENGTH: 742
TYPE: PRT
ORGANISM: Homo sapiens
US-10-775-204-2167

Query Match 88.1%; Score 37; DB 5; Length 742;
Best Local Similarity 87.5%; Pred. No. 69;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
DB 144 HOYLSRT 151

RESULT 34

US-10-425-115-34136
Sequence 34136, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovacic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 34136
LENGTH: 165
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(165)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_74464C.1.pcp
US-10-425-115-34136

Query Match 85.7%; Score 36; DB 4; Length 165;
Best Local Similarity 75.0%; Pred. No. 24;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
DB 75 HOYLSRT 82

RESULT 35

US-11-013-537-10
Sequence 10, Application US/11013537
Publication No. US20050208048A1
GENERAL INFORMATION:
APPLICANT: McMahon, Catherine J.
APPLICANT: Stepan, Lara Porter
APPLICANT: Laus, Retner
APPLICANT: Vidovic, Danir
TITLE OF INVENTION: HLA-DR-SPECIFIC ANTIBODIES, COMPOSITIONS
FILE REFERENCE: 11311.1005U
CURRENT APPLICATION NUMBER: US/11/013,537
CURRENT FILING DATE: 2004-12-15
NUMBER OF SEQ ID NOS: 70
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 8
TYPE: PRT
ORGANISM: Mouse
US-11-013-537-10

Query Match 83.3%; Score 35; DB 6; Length 8;
Best Local Similarity 87.5%; Pred. No. 1,7e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
DB 1 HOYLSRT 8

RESULT 36

US-10-425-115-318736
Sequence 318736, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovacic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53222)B

```
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 318736
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_53760C.1.pcp
US-10-425-115-318736
```

```
Query Match      83.3%; Score 35; DB 4; Length 58;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 HOYLSSR 7
Db      49 HOYLSSR 55
```

```
RESULT 37
US-10-056-052-10
; Sequence 10, Application US/10056052
; Publication No. US20030099656A1
; GENERAL INFORMATION:
; APPLICANT: PATTI, Joseph M
; APPLICANT: HUTCHINS, Jeff T
; APPLICANT: DOMANSKI, Paul
; APPLICANT: PATEL, Pratiksha
; APPLICANT: HALL, Andrea
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN . . .
; FILE REFERENCE: P07069US04/BAS
; CURRENT APPLICATION NUMBER: US/10/056,052
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/308,116
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/298,413
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/274,611
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/264,072
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-056-052-10
```

```
Query Match      83.3%; Score 35; DB 4; Length 112;
Best Local Similarity 87.5%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 HOYLSSR 8
Db      95 HOYLSSR 102
```

```
RESULT 38
US-10-056-052-14
; Sequence 14, Application US/10056052
; Publication No. US20030099656A1
; GENERAL INFORMATION:
; APPLICANT: PATTI, Joseph M
; APPLICANT: HUTCHINS, Jeff T
; APPLICANT: DOMANSKI, Paul
; APPLICANT: PATEL, Pratiksha
; APPLICANT: HALL, Andrea
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN . . .
; FILE REFERENCE: P07069US04/BAS
; CURRENT APPLICATION NUMBER: US/10/056,052
; CURRENT FILING DATE: 2002-04-19
```

```
; PRIOR APPLICATION NUMBER: 60/308,116
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/298,413
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/274,611
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/264,072
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-056-052-14
```

```
Query Match      83.3%; Score 35; DB 4; Length 112;
Best Local Similarity 87.5%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 HOYLSSR 8
Db      95 HOYLSSR 102
```

```
RESULT 39
US-10-056-052-18
; Sequence 18, Application US/10056052
; Publication No. US20030099656A1
; GENERAL INFORMATION:
; APPLICANT: PATTI, Joseph M
; APPLICANT: HUTCHINS, Jeff T
; APPLICANT: DOMANSKI, Paul
; APPLICANT: PATEL, Pratiksha
; APPLICANT: HALL, Andrea
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN . . .
; FILE REFERENCE: P07069US04/BAS
; CURRENT APPLICATION NUMBER: US/10/056,052
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/308,116
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/298,413
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/274,611
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/264,072
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-056-052-18
```

```
Query Match      83.3%; Score 35; DB 4; Length 112;
Best Local Similarity 87.5%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 HOYLSSR 8
Db      95 HOYLSSR 102
```

```
RESULT 40
US-10-816-938-31
; Sequence 31, Application US/10816938
; Publication No. US20040229301A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Baiyang
; TITLE OF INVENTION: Tissue Factor Antibodies and Uses Thereof
; FILE REFERENCE: 1861.1670002
; CURRENT APPLICATION NUMBER: US/10/816,938
```

CURRENT FILING DATE: 2004-04-05
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patent version 3.2
SEQ ID NO 31
LENGTH: 112
TYPE: PRT
ORGANISM: Mus sp.
US-10-816-938-31

Query Match 83.3%; Score 35; DB 5; Length 112;
Best Local Similarity 87.5%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
DB 95 HOYLSRT 102

RESULT 41
US-11-013-537-2
Sequence 2, Application US/11013537
Publication No. US20050208048A1
GENERAL INFORMATION:
APPLICANT: McMahon, Catherine J.
APPLICANT: Stepan, Lara Porter
APPLICANT: Laus, Reiner
APPLICANT: Vidovic, Damir
TITLE OF INVENTION: HLA-DR-SPECIFIC ANTIBODIES, COMPOSITIONS
FILE REFERENCE: 11311.1005U
CURRENT APPLICATION NUMBER: US/11/013,537
CURRENT FILING DATE: 2004-12-15
NUMBER OF SEQ ID NOS: 70
SOFTWARE: FastsEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 132
TYPE: PRT
ORGANISM: Mouse
US-11-013-537-2

Query Match 83.3%; Score 35; DB 6; Length 132;
Best Local Similarity 87.5%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
DB 115 HOYLSRT 122

RESULT 42
US-11-013-537-1
Sequence 1, Application US/11013537
Publication No. US20050208048A1
GENERAL INFORMATION:
APPLICANT: McMahon, Catherine J.
APPLICANT: Stepan, Lara Porter
APPLICANT: Laus, Reiner
APPLICANT: Vidovic, Damir
TITLE OF INVENTION: HLA-DR-SPECIFIC ANTIBODIES, COMPOSITIONS
FILE REFERENCE: 11311.1005U
CURRENT APPLICATION NUMBER: US/11/013,537
CURRENT FILING DATE: 2004-12-15
NUMBER OF SEQ ID NOS: 70
SOFTWARE: FastsEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 238
TYPE: PRT
ORGANISM: Mouse/Human Chimeric
US-11-013-537-1

Query Match 83.3%; Score 35; DB 6; Length 238;
Best Local Similarity 87.5%; Pred. No. 56;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
DB 115 HOYLSRT 122

RESULT 43
US-10-229-335-4
Sequence 4, Application US/10229335
Publication No. US20030144483A1
GENERAL INFORMATION:
APPLICANT: MEDAREX, INC.
TITLE OF INVENTION: HUMANIZED ANTIBODIES TO FC RECEPTORS FOR IMMUNOBLOBULIN G ON HUMAN MONONUCLEAR PHAGOCYTES
NUMBER OF SEQUENCES: 28
STREET: P.O. Box 953, 1545 Route 22 East
CITY: Annandale
STATE: New Jersey
COUNTRY: USA
ZIP: 08801
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/229,335
FILING DATE: 26-Aug-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/435,516
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MXI-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
MOLECULAR TYPE: linear
FRAGMENT TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-229-335-4

Query Match 81.0%; Score 34; DB 4; Length 112;
Best Local Similarity 87.5%; Pred. No. 42;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
DB 95 HOYLSRT 102

RESULT 44
US-10-229-335-28
Sequence 28, Application US/10229335
Publication No. US20030144483A1
GENERAL INFORMATION:
APPLICANT: MEDAREX, INC.
TITLE OF INVENTION: HUMANIZED ANTIBODIES TO FC RECEPTORS FOR IMMUNOBLOBULIN G ON HUMAN MONONUCLEAR PHAGOCYTES
NUMBER OF SEQUENCES: 28
STREET: P.O. Box 953, 1545 Route 22 East
CITY: Annandale
STATE: New Jersey
COUNTRY: USA
ZIP: 08801

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/229,335
FILING DATE: 26-Aug-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/435,516
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MXI-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-10-229-335-28

Query Match 81.0%; Score 34; DB 4; Length 112;
Best Local Similarity 87.5%; Pred. No. 42;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
Db 95 HOYLSWT 102

RESULT 45
US-09-741-843-2
Sequence 2, Application US/09741843
Patent No. US20020102254A1
GENERAL INFORMATION:
APPLICANT: LEUNG, Shui-on
APPLICANT: HANSEN, Hans
TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED ANTIBODIES SPECIFIC FOR B-CELL LYMPHOMA
FILE REFERENCE: 018733/0996
CURRENT APPLICATION NUMBER: US/09/741,843
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/127,902
PRIOR FILING DATE: 1998-08-03
PRIOR APPLICATION NUMBER: US 08/690,102
PRIOR FILING DATE: 1996-07-06
PRIOR APPLICATION NUMBER: US 08/289,576
PRIOR FILING DATE: 1994-08-12
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 113
TYPE: PRT
ORGANISM: Murinae gen. sp.
US-09-741-843-2

Query Match 81.0%; Score 34; DB 3; Length 113;
Best Local Similarity 87.5%; Pred. No. 42;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
Db 95 HOYLSWT 102

RESULT 46
US-09-741-843-6
Sequence 6, Application US/09741843
Patent No. US20020102254A1
GENERAL INFORMATION:
APPLICANT: LEUNG, Shui-on
APPLICANT: HANSEN, Hans
TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED ANTIBODIES SPECIFIC FOR B-CELL LYMPHOMA
FILE REFERENCE: 018733/0996
CURRENT APPLICATION NUMBER: US/09/741,843
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/127,902
PRIOR FILING DATE: 1998-08-03
PRIOR APPLICATION NUMBER: US 08/690,102
PRIOR FILING DATE: 1996-07-06
PRIOR APPLICATION NUMBER: US 08/289,576
PRIOR FILING DATE: 1994-08-12
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 113
TYPE: PRT
ORGANISM: Homo sapiens
US-09-741-843-6

Query Match 81.0%; Score 34; DB 3; Length 113;
Best Local Similarity 87.5%; Pred. No. 42;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
Db 95 HOYLSWT 102

RESULT 47
US-09-894-839-2
Sequence 2, Application US/09894839
Publication No. US20030035800A1
GENERAL INFORMATION:
APPLICANT: LEUNG, Shui-on
APPLICANT: HANSEN, Hans
TITLE OF INVENTION: GLYCOSYLATED HUMANIZED B-CELL SPECIFIC ANTIBODIES
FILE REFERENCE: 018733/1049
CURRENT APPLICATION NUMBER: US/09/894,839
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 09/155,107
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: US 60/013,709
PRIOR FILING DATE: 1996-03-20
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 113
TYPE: PRT
ORGANISM: Murinae gen. sp.
US-09-894-839-2

Query Match 81.0%; Score 34; DB 3; Length 113;
Best Local Similarity 87.5%; Pred. No. 42;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
Db 95 HOYLSWT 102

RESULT 48
US-09-894-839-6
Sequence 6, Application US/09894839
Publication No. US20030035800A1
GENERAL INFORMATION:

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; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; APPLICANT: OU, Zhengxing
; TITLE OF INVENTION: GLYCOSYLATED HUMANIZED B-CELL SPECIFIC ANTIBODIES
; FILE REFERENCE: 018733/1049
; CURRENT APPLICATION NUMBER: US/09/894,839
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 09/155,107
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: US 60/013,709
; PRIOR FILING DATE: 1996-03-20
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-894-839-6
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Query Match      81.0%; Score 34; DB 3; Length 113;
Best Local Similarity 87.5%; Pred. No. 42;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY      1 HOYLSRT 8
      |||||
Db      95 HOYLSWT 102
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RESULT 49
US-09-894-839-20
; Sequence 20, Application US/09894839
; Publication No. US20030035800A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; APPLICANT: OU, Zhengxing
; TITLE OF INVENTION: GLYCOSYLATED HUMANIZED B-CELL SPECIFIC ANTIBODIES
; FILE REFERENCE: 018733/1049
; CURRENT APPLICATION NUMBER: US/09/894,839
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 09/155,107
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: US 60/013,709
; PRIOR FILING DATE: 1996-03-20
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-894-839-20
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Query Match      81.0%; Score 34; DB 3; Length 113;
Best Local Similarity 87.5%; Pred. No. 42;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      1 HOYLSRT 8
      |||||
Db      95 HOYLSWT 102
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RESULT 50
US-09-988-013A-2
; Sequence 2, Application US/09988013A
; Publication No. US20030103979A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED ANTIBODIES SPECIFIC FOR B-
; FILE REFERENCE: 18733/1082
; CURRENT APPLICATION NUMBER: US/09/988,013A
; CURRENT FILING DATE: 2002-10-29
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; PRIOR APPLICATION NUMBER: US 09/741,843
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/127,902
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 08/590,102
; PRIOR FILING DATE: 1996-07-06
; PRIOR APPLICATION NUMBER: US 08/289,576
; PRIOR FILING DATE: 1994-08-12
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
; US-09-988-013A-2
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Query Match      81.0%; Score 34; DB 3; Length 113;
Best Local Similarity 87.5%; Pred. No. 42;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      1 HOYLSRT 8
      |||||
Db      95 HOYLSWT 102
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OM protein - protein search, using sw model

Run on: May 4, 2006, 13:46:13 ; Search time 9.26984 Seconds
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39.944 Million cell updates/sec

Title: US-10-700-632-6
Perfect score: 42
Sequence: 1 HOYISSRT 8

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Gapop 10.0 , Gapext 0.5

Searched: 235405 seqs, 46284737 residues

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Published Applications_AA_New:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37	88.1	112	11	US-11-136-559-6
2	37	88.1	131	11	US-11-132-947-2
3	37	88.1	160	11	US-11-197-221-1
4	37	88.1	162	8	US-10-511-937-2572
5	37	88.1	162	11	US-11-174-398-2
6	37	88.1	162	11	US-11-174-398-6
7	37	88.1	162	11	US-11-134-489-2
8	37	88.1	162	11	US-11-132-947-9
9	37	88.1	162	11	US-11-197-488-19
10	35	83.3	8	9	US-10-981-356A-20
11	35	83.3	8	11	US-11-096-046-20
12	35	83.3	8	11	US-11-136-559-29
13	35	83.3	112	11	US-11-136-559-10
14	35	83.3	112	11	US-11-136-559-14
15	35	83.3	112	11	US-11-136-559-18
16	35	83.3	112	11	US-11-136-559-22
17	35	83.3	116	9	US-10-981-356A-1
18	35	83.3	116	9	US-10-981-356A-3
19	35	83.3	116	11	US-11-096-046-1
20	35	83.3	116	11	US-11-096-046-3
21	35	83.3	666	9	US-10-981-356A-25

22	35	83.3	666	9	US-10-981-356A-27	Sequence 27, App1
23	35	83.3	666	9	US-10-981-356A-28	Sequence 28, App1
24	35	83.3	666	9	US-10-981-356A-29	Sequence 29, App1
25	35	83.3	666	9	US-10-981-356A-30	Sequence 30, App1
26	35	83.3	666	11	US-11-096-046-27	Sequence 27, App1
27	35	83.3	667	11	US-11-096-046-25	Sequence 25, App1
28	35	83.3	667	11	US-11-096-046-28	Sequence 28, App1
29	35	83.3	667	11	US-11-096-046-29	Sequence 29, App1
30	35	83.3	667	11	US-11-096-046-30	Sequence 30, App1
31	35	83.3	692	9	US-10-981-356A-26	Sequence 26, App1
32	35	83.3	695	11	US-11-096-046-26	Sequence 26, App1
33	31	73.8	252	11	US-11-188-298-19968	Sequence 19968, A
34	31	73.8	1126	11	US-11-110-480-7	Sequence 7, App1
35	31	73.8	1126	11	US-11-110-480-9	Sequence 9, App1
36	31	73.8	1126	11	US-11-110-480-16	Sequence 16, App1
37	31	73.8	1126	11	US-11-110-480-37	Sequence 37, App1
38	31	73.8	1126	11	US-11-110-480-47	Sequence 47, App1
39	31	73.8	1126	11	US-11-110-480-59	Sequence 59, App1
40	31	73.8	1126	11	US-11-110-480-82	Sequence 82, App1
41	31	73.8	1126	11	US-11-110-480-88	Sequence 88, App1
42	31	73.8	1126	11	US-11-110-480-10968	Sequence 10968, A
43	30	71.4	403	11	US-10-821-234-1027	Sequence 1027, App
44	30	71.4	686	9	US-10-453-372-126	Sequence 126, App
45	30	71.4	761	9	US-10-453-372-122	Sequence 122, App
46	30	71.4	823	9	US-10-453-372-124	Sequence 124, App
47	30	71.4	823	9	US-10-453-372-118	Sequence 118, App
48	30	71.4	826	9	US-10-453-372-1156	Sequence 156, App
49	30	71.4	826	9	US-10-453-372-166	Sequence 166, App
50	30	71.4	826	9	US-10-453-372-172	Sequence 172, App
51	30	71.4	826	9	US-10-453-372-174	Sequence 174, App
52	30	71.4	826	9	US-10-453-372-176	Sequence 176, App
53	30	71.4	826	9	US-10-453-372-180	Sequence 180, App
54	30	71.4	832	9	US-10-453-372-120	Sequence 120, App
55	30	71.4	1604	11	US-11-037-424-73	Sequence 73, App
56	30	71.4	2333	9	US-10-453-372-170	Sequence 170, App
57	30	71.4	2662	9	US-10-453-372-114	Sequence 114, App
58	30	71.4	2724	9	US-10-453-372-148	Sequence 148, App
59	30	71.4	2733	9	US-10-453-372-136	Sequence 136, App
60	30	71.4	2733	9	US-10-453-372-142	Sequence 142, App
61	30	71.4	2733	9	US-10-453-372-146	Sequence 146, App
62	30	71.4	2733	9	US-10-453-372-150	Sequence 150, App
63	30	71.4	2733	9	US-10-453-372-154	Sequence 154, App
64	30	71.4	2759	9	US-10-453-372-168	Sequence 168, App
65	29	69.0	2765	9	US-10-453-372-116	Sequence 116, App
66	29	69.0	349	11	US-11-096-568A-12681	Sequence 12681, A
67	29	69.0	307	11	US-11-096-568A-12680	Sequence 12680, A
68	29	69.0	334	11	US-11-188-298-10242	Sequence 10242, A
69	29	69.0	337	11	US-11-098-686-11316	Sequence 11316, A
70	29	69.0	354	11	US-11-096-568A-12679	Sequence 12679, A
71	29	69.0	371	11	US-11-172-740-777	Sequence 777, App
72	29	69.0	450	11	US-11-096-568A-24710	Sequence 24710, A
73	29	69.0	459	11	US-11-188-298-4262	Sequence 4262, App
74	29	69.0	543	11	US-11-106-672A-10	Sequence 10, App1
75	29	69.0	543	11	US-11-057-732-6	Sequence 6, App1
76	29	69.0	543	11	US-11-154-805A-5	Sequence 5, App1
77	29	69.0	592	11	US-11-106-672A-14	Sequence 14, App1
78	29	69.0	632	9	US-10-506-454-719	Sequence 719, App
79	29	69.0	644	11	US-11-096-568A-24709	Sequence 24709, A
80	29	69.0	648	11	US-11-096-568A-24708	Sequence 24708, A
81	29	69.0	2725	11	US-11-113-424-52	Sequence 52, App1
82	29	69.0	2725	11	US-11-100-640-10	Sequence 10, App1
83	29	69.0	2725	11	US-11-100-640-16	Sequence 16, App1
84	29	69.0	2769	11	US-11-113-424-14	Sequence 14, App1
85	28	66.7	8	11	US-11-046-024-1044	Sequence 1044, App
86	28	66.7	9	11	US-11-046-024-1167	Sequence 1167, App
87	28	66.7	9	11	US-11-046-024-11744	Sequence 11744, A
88	28	66.7	10	11	US-11-046-024-5669	Sequence 5669, App
89	28	66.7	11	11	US-11-046-024-1380	Sequence 1380, App
90	28	66.7	15	11	US-11-046-024-13054	Sequence 13054, A
91	28	66.7	15	11	US-11-046-024-13088	Sequence 13088, A
92	28	66.7	26	9	US-10-986-501-236	Sequence 236, App
93	28	66.7	120	11	US-11-096-568A-139	Sequence 139, App
94	28	66.7	122	11	US-11-096-568A-138	Sequence 138, App

95	28	66.7	123	11	US-11-102-512-70	Sequence 70, App1	168	27	64.3	805	11	US-11-074-176-172	Sequence 172, App
96	28	66.7	124	11	US-11-096-568A-137	Sequence 137, App	169	27	64.3	850	11	US-11-037-843-108	Sequence 108, App
97	28	66.7	124	11	US-11-096-568A-140	Sequence 140, App	170	27	64.3	861	11	US-11-038-284-36	Sequence 36, App1
98	28	66.7	124	9	US-10-986-501-231	Sequence 231, App	171	27	64.3	872	9	US-10-467-657-78	Sequence 78, App1
99	28	66.7	133	11	US-11-188-298-11539	Sequence 11539, A	172	27	64.3	886	9	US-10-467-657-454	Sequence 454, App
100	28	66.7	335	9	US-10-520-956-1	Sequence 1, App1	173	27	64.3	894	11	US-11-087-099-11214	Sequence 11214, A
101	28	66.7	345	11	US-11-079-463-7507	Sequence 7507, Ap	174	27	64.3	1342	11	US-11-149-003-24	Sequence 24, App1
102	28	66.7	378	11	US-11-072-512-3698	Sequence 3698, Ap	175	27	64.3	1463	11	US-11-080-991-22	Sequence 22, App1
103	28	66.7	439	11	US-11-188-298-16523	Sequence 16523, A	176	27	64.3	1477	11	US-11-149-003-8	Sequence 8, App1
104	28	66.7	465	9	US-10-967-648A-6	Sequence 6, App1	177	27	64.3	1479	9	US-10-204-639-4	Sequence 4, App1
105	28	66.7	509	11	US-11-188-298-14035	Sequence 14035, A	178	27	64.3	1512	11	US-11-149-003-10	Sequence 10, App1
106	28	66.7	517	11	US-11-037-243-76	Sequence 76, App1	179	27	64.3	1535	11	US-11-149-003-14	Sequence 14, App1
107	28	66.7	575	11	US-11-188-298-13893	Sequence 13893, A	180	27	64.3	1570	11	US-11-149-003-12	Sequence 12, App1
108	28	66.7	739	11	US-11-188-298-3768	Sequence 3768, Ap	181	27	64.3	1593	11	US-11-149-003-2	Sequence 2, App1
109	28	66.7	880	11	US-11-171-701-2	Sequence 2, App1	182	27	64.3	1628	11	US-11-149-003-4	Sequence 4, App1
110	28	66.7	1326	11	US-11-079-463-5820	Sequence 5820, Ap	183	26	61.9	8	11	US-11-045-024-1043	Sequence 1043, Ap
111	27	64.3	85	11	US-11-079-463-8413	Sequence 8413, Ap	184	26	61.9	9	11	US-11-045-024-1166	Sequence 1166, Ap
112	27	64.3	130	11	US-11-090-331-4	Sequence 4, App1	185	26	61.9	9	11	US-11-045-024-13690	Sequence 13690, Ap
113	27	64.3	138	11	US-11-090-331-8	Sequence 8, App1	186	26	61.9	10	11	US-11-045-024-5668	Sequence 5668, Ap
114	27	64.3	175	9	US-10-793-626-1874	Sequence 1874, Ap	187	26	61.9	10	11	US-11-045-024-1282	Sequence 1282, Ap
115	27	64.3	203	11	US-11-038-284-21	Sequence 21, App1	188	26	61.9	11	11	US-11-045-024-1377	Sequence 1377, Ap
116	27	64.3	213	11	US-11-038-284-22	Sequence 22, App1	189	26	61.9	11	11	US-11-045-024-1378	Sequence 1378, Ap
117	27	64.3	215	11	US-11-102-621-141	Sequence 141, App	190	26	61.9	11	11	US-11-045-024-1379	Sequence 1379, Ap
118	27	64.3	215	11	US-11-166-906-2	Sequence 2, App1	191	26	61.9	11	11	US-11-045-024-4187	Sequence 4187, Ap
119	27	64.3	222	9	US-10-453-372-844	Sequence 844, App1	192	26	61.9	13	11	US-11-220-372-80	Sequence 80, App1
120	27	64.3	228	9	US-11-096-568A-3221	Sequence 3221, Ap	193	26	61.9	15	9	US-10-530-061-2186	Sequence 2186, Ap
121	27	64.3	245	9	US-10-115-609-2	Sequence 2, App1	194	26	61.9	15	11	US-11-022-562-35	Sequence 35, App1
122	27	64.3	245	11	US-11-264-096-762	Sequence 762, App	195	26	61.9	15	11	US-11-022-562-36	Sequence 36, App1
123	27	64.3	251	11	US-11-096-568A-1257	Sequence 1257, Ap	196	26	61.9	15	11	US-11-045-024-13024	Sequence 13024, A
124	27	64.3	251	11	US-11-096-568A-1259	Sequence 1259, Ap	197	26	61.9	15	11	US-11-045-024-13033	Sequence 13033, A
125	27	64.3	280	11	US-11-096-568A-1256	Sequence 1256, Ap	198	26	61.9	15	11	US-11-045-024-13034	Sequence 13034, A
126	27	64.3	280	9	US-10-453-372-850	Sequence 850, App	199	26	61.9	15	11	US-11-045-024-14210	Sequence 14210, A
127	27	64.3	290	9	US-10-453-372-836	Sequence 836, App	200	26	61.9	15	11	US-11-045-024-14400	Sequence 14400, A
128	27	64.3	290	9	US-10-453-372-842	Sequence 842, App	201	26	61.9	15	11	US-11-045-024-14417	Sequence 14417, A
129	27	64.3	290	9	US-10-453-372-848	Sequence 848, App	202	26	61.9	15	11	US-11-045-024-14477	Sequence 14477, A
130	27	64.3	290	9	US-10-115-609-4	Sequence 4, App1	203	26	61.9	20	9	US-10-530-061-1611	Sequence 1611, Ap
131	27	64.3	290	11	US-11-113-424-77	Sequence 77, App1	204	26	61.9	20	11	US-11-022-562-288	Sequence 288, App
132	27	64.3	290	11	US-11-245-713-1	Sequence 1, App1	205	26	61.9	20	11	US-11-022-562-289	Sequence 289, App
133	27	64.3	290	11	US-11-264-096-763	Sequence 763, App	206	26	61.9	35	11	US-11-096-568A-725-24	Sequence 24, App1
134	27	64.3	295	9	US-10-453-372-840	Sequence 840, App	207	26	61.9	36	9	US-10-973-977-39	Sequence 39, App1
135	27	64.3	303	11	US-11-072-512-3897	Sequence 3897, Ap	208	26	61.9	36	9	US-10-973-977-104	Sequence 104, App
136	27	64.3	331	11	US-11-096-568A-16394	Sequence 16394, A	209	26	61.9	95	11	US-11-096-568A-4963	Sequence 4963, Ap
137	27	64.3	348	9	US-10-467-657-6602	Sequence 6602, Ap	210	26	61.9	111	11	US-11-049-536-90	Sequence 90, App1
138	27	64.3	348	9	US-10-467-657-7662	Sequence 7662, Ap	211	26	61.9	111	11	US-11-199-739-90	Sequence 90, App1
139	27	64.3	352	9	US-10-627-633-6	Sequence 6, App1	212	26	61.9	121	11	US-11-045-004-1672	Sequence 1672, Ap
140	27	64.3	358	11	US-11-096-568A-16393	Sequence 16393, A	213	26	61.9	128	9	US-10-821-234-1315	Sequence 1315, Ap
141	27	64.3	375	11	US-11-172-740-778	Sequence 778, App	214	26	61.9	174	11	US-11-079-463-10145	Sequence 10145, A
142	27	64.3	383	11	US-11-087-099-8378	Sequence 8378, Ap	215	26	61.9	178	11	US-11-079-463-6828	Sequence 6828, Ap
143	27	64.3	397	11	US-11-096-568A-3220	Sequence 3222, Ap	216	26	61.9	180	7	US-09-578-360A-633	Sequence 633, App
144	27	64.3	398	9	US-11-096-568A-3222	Sequence 311, App	217	26	61.9	189	9	US-10-793-626-2572	Sequence 2572, App
145	27	64.3	409	9	US-10-627-633-4	Sequence 4, App1	218	26	61.9	215	11	US-11-087-099-2630	Sequence 2630, Ap
146	27	64.3	410	11	US-11-096-568A-5681	Sequence 5681, Ap	219	26	61.9	215	11	US-11-188-298-13539	Sequence 13539, A
147	27	64.3	412	11	US-11-096-568A-3219	Sequence 3219, Ap	220	26	61.9	217	11	US-11-079-463-10365	Sequence 10365, A
148	27	64.3	413	11	US-11-188-298-14323	Sequence 14323, A	221	26	61.9	225	11	US-11-188-298-14560	Sequence 14560, A
149	27	64.3	415	11	US-11-079-463-5547	Sequence 5547, Ap	222	26	61.9	224	11	US-11-087-099-9532	Sequence 9232, Ap
150	27	64.3	452	11	US-11-188-298-4557	Sequence 4557, Ap	223	26	61.9	244	11	US-11-188-298-15258	Sequence 15258, A
151	27	64.3	454	11	US-11-188-298-3971	Sequence 3971, Ap	224	26	61.9	246	9	US-10-510-941-22	Sequence 22, App1
152	27	64.3	471	11	US-11-096-568A-5680	Sequence 5680, Ap	225	26	61.9	250	11	US-11-188-298-17748	Sequence 17748, A
153	27	64.3	472	11	US-11-188-298-10453	Sequence 10453, A	226	26	61.9	255	11	US-11-100-183-23	Sequence 23, App1
154	27	64.3	480	11	US-11-096-568A-5689	Sequence 5679, Ap	227	26	61.9	274	11	US-11-096-568A-1420	Sequence 1420, Ap
155	27	64.3	513	11	US-11-129-442-46	Sequence 447, App	228	26	61.9	287	7	US-09-978-360A-427	Sequence 427, App
156	27	64.3	513	11	US-11-087-099-447	Sequence 447, App	229	26	61.9	287	11	US-11-188-298-8207	Sequence 8207, Ap
157	27	64.3	599	11	US-11-079-463-10057	Sequence 10057, A	230	26	61.9	300	11	US-11-079-463-6693	Sequence 6693, Ap
158	27	64.3	611	11	US-11-079-463-5321	Sequence 5321, Ap	231	26	61.9	301	11	US-11-188-298-16621	Sequence 16621, A
159	27	64.3	640	11	US-11-079-463-5321	Sequence 6814, Ap	232	26	61.9	302	11	US-11-165-226-137	Sequence 127, App
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161	27	64.3	749	11	US-11-096-568A-24600	Sequence 24599, A	234	26	61.9	305	9	US-10-821-334-1518	Sequence 1518, App
162	27	64.3	768	11	US-11-096-568A-24599	Sequence 24599, A	235	26	61.9	305	9	US-10-973-1158-264	Sequence 264, App
163	27	64.3	769	9	US-10-485-517-401	Sequence 401, App	236	26	61.9	305	9	US-10-137-873A-264	Sequence 264, App
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165	27	64.3	785	11	US-11-096-568A-24598	Sequence 348, App	238	26	61.9	305	11	US-11-290-153-264	Sequence 264, App
166	27	64.3	799	11	US-11-074-176-348	Sequence 71, App1	239	26	61.9	309	11	US-11-096-568A-27939	Sequence 27939, A
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242	26	61.9	329	11	US-11-172-740-1387	Sequence 1387, Ap	315	26	61.9	858	9	US-10-613-744-6	Sequence 6, App1
243	26	61.9	332	11	US-11-156-084-293	Sequence 293, App	316	26	61.9	873	11	US-11-096-568A-28140	Sequence 28140, A
244	26	61.9	333	11	US-11-188-298-17696	Sequence 17696, A	317	26	61.9	882	11	US-11-151-601-20	Sequence 20, App1
245	26	61.9	340	11	US-11-188-298-9660	Sequence 9660, Ap	318	26	61.9	1303	11	US-11-087-099-10526	Sequence 10526, A
246	26	61.9	347	11	US-11-096-568A-26732	Sequence 26732, A	319	26	61.9	3343	11	US-11-122-396-7	Sequence 7, App1
247	26	61.9	363	11	US-11-014-842A-41	Sequence 41, App1	320	26	61.9	4051	8	US-10-501-834-6	Sequence 6, App1
248	26	61.9	375	11	US-11-188-298-358	Sequence 358, App	321	26	61.9	4059	8	US-10-501-834-6	Sequence 2, App1
249	26	61.9	377	11	US-11-079-463-5276	Sequence 5276, Ap	322	26	61.9	4074	8	US-10-501-834-2	Sequence 3191, Ap
250	26	61.9	378	11	US-11-096-568A-27938	Sequence 27938, A	323	25.5	60.7	498	11	US-11-072-512-13191	Sequence 794, App
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253	26	61.9	398	11	US-11-072-512-2010	Sequence 2010, Ap	326	25	59.5	96	11	US-11-053-076-64	Sequence 7339, Ap
254	26	61.9	398	11	US-11-079-463-6004	Sequence 6004, Ap	327	25	59.5	102	11	US-11-079-463-7339	Sequence 1994, Ap
255	26	61.9	404	11	US-11-079-463-8858	Sequence 8858, Ap	328	25	59.5	116	9	US-10-467-657-1994	Sequence 10311, A
256	26	61.9	410	9	US-10-467-657-2312	Sequence 2312, Ap	329	25	59.5	127	11	US-11-087-099-10311	Sequence 731, App
257	26	61.9	424	11	US-11-098-686-10445	Sequence 10445, A	330	25	59.5	129	11	US-11-264-096-731	Sequence 7147, Ap
258	26	61.9	432	11	US-11-188-298-6788	Sequence 6788, Ap	331	25	59.5	142	11	US-11-079-463-7147	Sequence 1622, Ap
259	26	61.9	440	11	US-11-096-568A-27937	Sequence 27937, A	332	25	59.5	148	11	US-11-188-298-1622	Sequence 205, App
260	26	61.9	443	11	US-11-188-298-1015	Sequence 1015, Ap	333	25	59.5	149	11	US-11-226-657-205	Sequence 204, App
261	26	61.9	445	11	US-11-079-463-9167	Sequence 9167, Ap	334	25	59.5	166	11	US-11-226-657-204	Sequence 132, App
262	26	61.9	447	9	US-10-821-234-1584	Sequence 1584, Ap	335	25	59.5	167	9	US-10-793-626-132	Sequence 10366, A
263	26	61.9	447	9	US-10-784-004-378	Sequence 378, App	336	25	59.5	175	11	US-11-098-686-10396	Sequence 430, App
264	26	61.9	447	9	US-10-784-004-698	Sequence 698, App	337	25	59.5	176	9	US-10-194-487-430	Sequence 430, App
265	26	61.9	447	9	US-10-784-004-932	Sequence 932, App	338	25	59.5	176	9	US-10-195-883-430	Sequence 430, App
266	26	61.9	447	9	US-10-784-004-1077	Sequence 1077, Ap	339	25	59.5	176	9	US-10-195-889-430	Sequence 430, App
267	26	61.9	448	11	US-11-119-569-4	Sequence 4, App1	340	25	59.5	176	9	US-10-195-889-430	Sequence 463, App
268	26	61.9	449	11	US-11-096-568A-24583	Sequence 24583, A	341	25	59.5	180	7	US-09-978-360A-463	Sequence 1248, Ap
269	26	61.9	450	11	US-11-119-569-21	Sequence 21, App1	342	25	59.5	184	11	US-11-264-096-1249	Sequence 1248, Ap
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271	26	61.9	482	11	US-11-087-099-390	Sequence 390, App	344	25	59.5	194	11	US-11-096-568A-15483	Sequence 20, App1
272	26	61.9	500	9	US-10-519-531-3	Sequence 3, App1	345	25	59.5	198	11	US-11-210-756-20	Sequence 4, App1
273	26	61.9	500	9	US-10-507-928-4	Sequence 4, App1	346	25	59.5	203	11	US-11-165-141-4	Sequence 5605, Ap
274	26	61.9	500	9	US-10-524-647-20	Sequence 20, App1	347	25	59.5	205	11	US-11-087-099-5605	Sequence 388, App
275	26	61.9	500	9	US-10-524-972-20	Sequence 20, App1	348	25	59.5	207	11	US-11-264-096-388	Sequence 45, App1
276	26	61.9	500	9	US-10-853-807A-11	Sequence 11, App1	349	25	59.5	216	11	US-11-170-653-45	Sequence 45, App1
277	26	61.9	500	9	US-10-541-513-8	Sequence 8, App1	350	25	59.5	218	11	US-11-072-512-2212	Sequence 2212, Ap
278	26	61.9	500	11	US-11-042-988-11	Sequence 11, App1	351	25	59.5	223	11	US-11-087-099-7197	Sequence 7197, Ap
279	26	61.9	500	11	US-11-022-562-339	Sequence 339, App	352	25	59.5	229	9	US-10-793-626-2818	Sequence 2818, Ap
280	26	61.9	500	11	US-11-029-465-4	Sequence 4, App1	353	25	59.5	235	11	US-11-096-568A-8666	Sequence 8666, Ap
281	26	61.9	500	11	US-11-033-039-978	Sequence 978, App	354	25	59.5	241	9	US-10-821-234-1602	Sequence 1602, Ap
282	26	61.9	500	11	US-11-129-442-44	Sequence 44, App1	355	25	59.5	241	9	US-10-330-773-221	Sequence 221, App
283	26	61.9	500	11	US-11-204-755-3	Sequence 3, App1	356	25	59.5	244	11	US-11-184-339-10	Sequence 10, App1
284	26	61.9	500	11	US-11-204-755-5	Sequence 5, App1	357	25	59.5	245	11	US-11-018-868-44	Sequence 44, App1
285	26	61.9	501	11	US-11-129-442-23	Sequence 23, App1	358	25	59.5	245	11	US-11-018-868-44	Sequence 8665, Ap
286	26	61.9	501	11	US-11-079-463-5432	Sequence 5432, Ap	359	25	59.5	252	9	US-10-506-454-660	Sequence 660, App
287	26	61.9	504	9	US-10-507-928-6	Sequence 6, App1	360	25	59.5	256	11	US-11-087-099-9614	Sequence 9614, Ap
288	26	61.9	504	11	US-11-029-465-6	Sequence 6, App1	361	25	59.5	260	9	US-10-793-626-224	Sequence 224, App
289	26	61.9	505	9	US-10-507-928-8	Sequence 8, App1	362	25	59.5	262	11	US-11-264-096-2220	Sequence 2220, Ap
290	26	61.9	505	11	US-11-029-465-8	Sequence 8, App1	363	25	59.5	265	9	US-10-330-773-218	Sequence 218, App
291	26	61.9	505	11	US-11-096-568A-26731	Sequence 26731, A	364	25	59.5	272	11	US-11-087-099-9074	Sequence 9074, Ap
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293	26	61.9	512	9	US-10-519-531-4	Sequence 4, App1	366	25	59.5	273	11	US-11-096-568A-9305	Sequence 9305, Ap
294	26	61.9	512	11	US-11-009-063-25	Sequence 25, App1	367	25	59.5	277	9	US-10-793-626-94	Sequence 94, App1
295	26	61.9	512	11	US-11-009-063-30	Sequence 30, App1	368	25	59.5	279	11	US-11-087-099-2110	Sequence 2110, Ap
296	26	61.9	519	11	US-11-087-099-759	Sequence 759, App	369	25	59.5	286	11	US-11-087-099-421	Sequence 421, App
297	26	61.9	519	11	US-11-188-298-11752	Sequence 11752, A	370	25	59.5	286	11	US-11-172-740-776	Sequence 776, App
298	26	61.9	519	11	US-11-188-298-11752	Sequence 11752, A	371	25	59.5	290	11	US-11-096-568A-18388	Sequence 18388, A
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302	26	61.9	616	11	US-11-087-099-5968	Sequence 5968, Ap	375	25	59.5	300	11	US-11-096-568A-18358	Sequence 18358, A
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305	26	61.9	688	11	US-11-079-463-7941	Sequence 7941, Ap	378	25	59.5	319	11	US-11-096-568A-6065	Sequence 6065, Ap
306	26	61.9	704	11	US-11-096-568A-28142	Sequence 28142, A	379	25	59.5	321	9	US-10-329-2458-18	Sequence 18, App1
307	26	61.9	710	11	US-11-096-568A-28141	Sequence 28141, A	380	25	59.5	326	11	US-11-188-298-15268	Sequence 15268, A
308	26	61.9	716	11	US-11-264-096-833	Sequence 833, App	381	25	59.5	333	11	US-11-096-568A-18356	Sequence 18356, A
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310	26	61.9	744	9	US-10-455-772-974	Sequence 974, App	383	25	59.5	338	11	US-11-045-004-2666	Sequence 2666, Ap
311	26	61.9	768	11	US-11-144-630-12	Sequence 12, App1	384	25	59.5	339	9	US-10-485-517-367	Sequence 367, App
312	26	61.9	800	11	US-11-045-004-2544	Sequence 2544, Ap	385	25	59.5	340	11	US-11-096-568A-10225	Sequence 10225, A
313	26	61.9	836	9	US-10-455-772-970	Sequence 970, App	386	25	59.5	341	11	US-11-096-568A-6064	Sequence 6064, Ap

387	25	59.5	345	11	US-11-096-568A-26752	Sequence 26752, A	460	25	59.5	636	11	US-11-072-512-2449	Sequence 2449, Ap
388	25	59.5	347	11	US-11-188-298-4925	Sequence 4925, Ap	461	25	59.5	639	11	US-11-124-367A-379	Sequence 379, App
389	25	59.5	347	11	US-11-188-298-11437	Sequence 11437, A	462	25	59.5	656	9	US-10-330-773-118	Sequence 118, App
390	25	59.5	350	11	US-11-096-568A-26751	Sequence 26751, A	463	25	59.5	667	11	US-11-206-416-13	Sequence 13, App1
391	25	59.5	356	11	US-10-506-454-372	Sequence 372, App	464	25	59.5	669	11	US-11-072-511-2373	Sequence 2373, Ap
392	25	59.5	359	11	US-11-096-568A-26750	Sequence 26750, A	465	25	59.5	716	11	US-11-188-298-6358	Sequence 6358, Ap
393	25	59.5	364	11	US-11-098-686-10327	Sequence 10327, A	466	25	59.5	724	11	US-11-096-568A-28968	Sequence 28968, A
394	25	59.5	365	11	US-11-188-298-2929	Sequence 2929, Ap	467	25	59.5	725	11	US-11-096-568A-28967	Sequence 28967, A
395	25	59.5	366	9	US-10-510-386-42	Sequence 42, App1	468	25	59.5	726	11	US-11-051-720-1604	Sequence 1604, Ap
396	25	59.5	378	11	US-11-188-298-7858	Sequence 7858, Ap	469	25	59.5	742	11	US-11-072-512-2807	Sequence 2807, Ap
397	25	59.5	381	8	US-10-505-828-73	Sequence 73, App1	470	25	59.5	745	9	US-10-532-153-15	Sequence 15, App1
398	25	59.5	381	9	US-10-784-004-727	Sequence 727, App	471	25	59.5	747	11	US-11-051-720-1605	Sequence 1605, Ap
399	25	59.5	381	9	US-10-784-004-1087	Sequence 1087, Ap	472	25	59.5	749	9	US-10-793-626-138	Sequence 138, App
400	25	59.5	381	11	US-11-185-859-6	Sequence 6, App1	473	25	59.5	759	9	US-10-467-657-4166	Sequence 4166, Ap
401	25	59.5	389	11	US-11-096-568A-30068	Sequence 30068, A	474	25	59.5	766	9	US-10-821-234-1691	Sequence 1691, Ap
402	25	59.5	397	11	US-11-188-298-12112	Sequence 12112, A	475	25	59.5	779	11	US-11-096-568A-28966	Sequence 28966, A
403	25	59.5	401	11	US-11-079-463-6477	Sequence 6477, Ap	476	25	59.5	779	11	US-11-124-367A-380	Sequence 380, App
404	25	59.5	403	11	US-11-096-568A-8100	Sequence 8100, Ap	477	25	59.5	782	11	US-11-096-568A-28967	Sequence 28967, A
405	25	59.5	414	11	US-11-096-568A-10224	Sequence 10224, A	478	25	59.5	789	11	US-11-188-298-1224	Sequence 12, App1
406	25	59.5	416	11	US-11-079-463-5969	Sequence 5969, Ap	479	25	59.5	795	9	US-10-532-153-12	Sequence 21, App1
407	25	59.5	417	11	US-11-096-568A-6229	Sequence 6229, Ap	480	25	59.5	799	11	US-11-124-367A-378	Sequence 378, App
408	25	59.5	421	11	US-11-087-099-4040	Sequence 4040, Ap	481	25	59.5	801	9	US-10-532-153-18	Sequence 18, App1
409	25	59.5	425	11	US-11-096-568A-6228	Sequence 6228, Ap	482	25	59.5	808	9	US-10-532-153-3	Sequence 3, App1
410	25	59.5	435	9	US-10-467-657-5694	Sequence 5694, Ap	483	25	59.5	808	9	US-10-532-153-6	Sequence 6, App1
411	25	59.5	435	11	US-11-264-096-390	Sequence 390, App	484	25	59.5	808	9	US-10-532-153-24	Sequence 24, App1
412	25	59.5	437	9	US-10-967-648A-2	Sequence 2, App1	485	25	59.5	816	11	US-11-057-058-10	Sequence 10, App1
413	25	59.5	437	11	US-11-233-510-14	Sequence 14, App1	486	25	59.5	839	11	US-11-124-367A-377	Sequence 377, App
414	25	59.5	447	11	US-11-079-463-9897	Sequence 9897, Ap	487	25	59.5	865	11	US-11-087-099-196	Sequence 196, Ap
415	25	59.5	451	11	US-10-770-726-79	Sequence 79, App1	488	25	59.5	883	9	US-10-506-448A-13	Sequence 13, App1
416	25	59.5	464	11	US-11-096-568A-10223	Sequence 10223, A	489	25	59.5	937	11	US-11-057-058-55	Sequence 55, App1
417	25	59.5	469	11	US-11-072-512-2744	Sequence 2744, Ap	490	25	59.5	950	9	US-10-981-267-24	Sequence 24, App1
418	25	59.5	473	11	US-11-165-141-23	Sequence 23, App1	491	25	59.5	952	9	US-10-821-234-1557	Sequence 1557, Ap
419	25	59.5	481	11	US-11-096-568A-30067	Sequence 30067, A	492	25	59.5	962	11	US-11-057-058-54	Sequence 54, App1
420	25	59.5	489	11	US-11-188-298-3607	Sequence 3607, Ap	493	25	59.5	982	11	US-11-055-497A-6	Sequence 6, App1
421	25	59.5	491	11	US-11-098-662-14	Sequence 14, App1	494	25	59.5	983	11	US-11-057-058-53	Sequence 53, App1
422	25	59.5	491	11	US-11-165-141-2	Sequence 2, App1	495	25	59.5	993	11	US-11-057-058-56	Sequence 56, App1
423	25	59.5	491	11	US-11-266-626-24	Sequence 24, App1	496	25	59.5	993	11	US-11-057-058-57	Sequence 57, App1
424	25	59.5	504	11	US-11-096-568A-24727	Sequence 24727, A	497	25	59.5	957	11	US-11-264-096-2012	Sequence 2012, Ap
425	25	59.5	508	9	US-10-330-773-113	Sequence 113, App	498	25	59.5	997	11	US-11-057-058-33	Sequence 33, App1
426	25	59.5	516	9	US-10-467-657-4870	Sequence 4870, Ap	499	25	59.5	1011	11	US-11-057-058-31	Sequence 31, App1
427	25	59.5	516	11	US-11-051-720-1606	Sequence 1606, Ap	500	25	59.5	1107	11	US-11-057-058-41	Sequence 41, App1
428	25	59.5	516	11	US-11-096-568A-16324	Sequence 16324, A	501	25	59.5	1228	11	US-11-202-566-7	Sequence 7, App1
429	25	59.5	520	11	US-11-098-662-12	Sequence 12, App1	502	25	59.5	1246	9	US-10-873-528-109	Sequence 109, App
430	25	59.5	520	11	US-11-165-141-19	Sequence 19, App1	503	25	59.5	1256	11	US-11-288-720-17	Sequence 17, App1
431	25	59.5	520	11	US-11-193-955-11	Sequence 11, App1	504	25	59.5	1745	11	US-11-264-096-2222	Sequence 2222, Ap
432	25	59.5	520	11	US-11-266-626-27	Sequence 27, App1	505	25	59.5	1771	11	US-11-195-009-2	Sequence 2, App1
433	25	59.5	522	11	US-11-184-399-8	Sequence 8, App1	506	25	59.5	1771	11	US-11-195-009-4	Sequence 4, App1
434	25	59.5	525	9	US-10-194-487-436	Sequence 436, App	507	25	59.5	1771	11	US-11-195-009-9	Sequence 9, App1
435	25	59.5	525	9	US-10-195-883-436	Sequence 436, App	508	25	59.5	1771	11	US-11-195-009-11	Sequence 11, App1
436	25	59.5	525	9	US-10-195-888-436	Sequence 436, App	509	25	59.5	1892	10	US-11-131-901-6	Sequence 6, App1
437	25	59.5	525	9	US-10-195-889-436	Sequence 436, App	510	25	59.5	1892	11	US-11-195-009-13	Sequence 13, App1
438	25	59.5	525	9	US-10-218-784-154	Sequence 154, App	511	25	59.5	1911	11	US-11-195-009-17	Sequence 17, App1
439	25	59.5	525	9	US-10-219-061-154	Sequence 154, App	512	25	59.5	1921	11	US-11-195-009-19	Sequence 19, App1
440	25	59.5	525	9	US-10-219-062-154	Sequence 154, App	513	25	59.5	1944	11	US-11-195-009-15	Sequence 15, App1
441	25	59.5	525	9	US-10-219-064-154	Sequence 154, App	514	25	59.5	2671	8	US-10-505-928-784	Sequence 784, App
442	25	59.5	525	9	US-10-233-134-154	Sequence 154, App	515	25	59.5	2671	9	US-10-876-787-8	Sequence 6, App1
443	25	59.5	525	9	US-10-216-161A-301	Sequence 301, App	516	25	59.5	3011	9	US-10-985-205-3	Sequence 3, App1
444	25	59.5	560	11	US-11-040-218-7	Sequence 7, App1	517	25	59.5	6738	9	US-10-922-2328-56	Sequence 56, App1
445	25	59.5	565	11	US-11-188-298-17212	Sequence 17212, A	518	24	57.1	9	10	US-11-300-563-6	Sequence 6, App1
446	25	59.5	566	11	US-11-096-568A-30066	Sequence 30066, A	519	24	57.1	10	9	US-10-530-061-663	Sequence 663, App
447	25	59.5	566	11	US-11-079-463-7770	Sequence 7770, Ap	520	24	57.1	15	9	US-10-530-061-1717	Sequence 1717, Ap
448	25	59.5	576	11	US-11-040-218-9	Sequence 9, App1	521	24	57.1	23	11	US-11-043-806-467	Sequence 467, App
449	25	59.5	589	11	US-11-040-218-5	Sequence 5, App1	522	24	57.1	26	11	US-11-226-657-216	Sequence 216, App
450	25	59.5	590	9	US-10-218-784-70	Sequence 70, App1	523	24	57.1	28	11	US-11-142-397-4	Sequence 4, App1
451	25	59.5	590	9	US-10-219-061-70	Sequence 70, App1	524	24	57.1	28	11	US-11-189-817-8	Sequence 8, App1
452	25	59.5	590	9	US-10-219-062-70	Sequence 70, App1	525	24	57.1	41	11	US-11-189-817-10	Sequence 10, App1
453	25	59.5	590	9	US-10-219-064-70	Sequence 70, App1	526	24	57.1	64	11	US-10-467-657-8933	Sequence 8933, Ap
454	25	59.5	590	9	US-10-233-134-70	Sequence 70, App1	527	24	57.1	64	11	US-11-142-392-1	Sequence 1, App1
455	25	59.5	590	11	US-11-040-218-11	Sequence 11, App1	528	24	57.1	69	9	US-10-467-657-5932	Sequence 5932, Ap
456	25	59.5	593	9	US-10-330-773-116	Sequence 116, App1	529	24	57.1	78	11	US-11-120-308-50	Sequence 50, App1
457	25	59.5	599	11	US-11-165-141-33	Sequence 33, App1	530	24	57.1	78	11	US-11-079-463-9870	Sequence 9870, Ap
458	25	59.5	611	11	US-11-188-298-14425	Sequence 14425, A	531	24	57.1	83	11	US-11-096-568A-32448	Sequence 32448, A
459	25	59.5	632	11	US-11-188-298-978	Sequence 978, App	532	24	57.1	88	11	US-11-096-568A-32447	Sequence 32447, A

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534	24	57.1	90	9	US-10-948-571-79	Sequence 79, Appl	607	24	57.1	247	11	US-11-096-568A-28475	Sequence 28475, A
535	24	57.1	91	11	US-11-188-298-1734	Sequence 1734, Ap	608	24	57.1	248	9	US-10-517-939-228	Sequence 228, Ap
536	24	57.1	97	9	US-10-980-388-82	Sequence 82, Appl	609	24	57.1	249	11	US-11-096-568A-14903	Sequence 14903, A
537	24	57.1	105	9	US-10-530-253-27	Sequence 27, Appl	610	24	57.1	259	9	US-10-510-386-52	Sequence 52, Appl
538	24	57.1	110	10	US-11-300-563-16	Sequence 16, Appl	611	24	57.1	266	9	US-10-793-626-1974	Sequence 1974, Ap
539	24	57.1	117	11	US-11-096-568A-20483	Sequence 20483, A	612	24	57.1	269	11	US-11-096-568A-26635	Sequence 26635, A
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541	24	57.1	130	11	US-11-096-568A-17927	Sequence 17927, A	614	24	57.1	270	11	US-11-172-740-1584	Sequence 1584, Ap
542	24	57.1	111	11	US-11-098-686-77	Sequence 77, Appl	615	24	57.1	272	11	US-11-172-740-1585	Sequence 1585, Ap
543	24	57.1	111	11	US-11-096-568A-17926	Sequence 17926, A	616	24	57.1	273	11	US-11-079-463-7506	Sequence 7506, Ap
544	24	57.1	112	11	US-11-073-605-15	Sequence 15, Appl	617	24	57.1	277	9	US-10-467-657-2152	Sequence 2152, Ap
545	24	57.1	132	11	US-11-064-774A-151	Sequence 151, Appl	618	24	57.1	277	11	US-11-096-568A-18044	Sequence 18044, A
546	24	57.1	132	11	US-11-075-400-22	Sequence 22, Appl	619	24	57.1	283	11	US-11-188-298-5627	Sequence 5627, Ap
547	24	57.1	132	11	US-11-075-047A-93	Sequence 93, Appl	620	24	57.1	287	11	US-11-096-568A-5135	Sequence 5135, Ap
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549	24	57.1	133	11	US-11-096-568A-20481	Sequence 20481, A	622	24	57.1	293	11	US-11-096-568A-1146	Sequence 1146, Ap
550	24	57.1	144	11	US-11-188-298-21604	Sequence 21604, A	623	24	57.1	295	9	US-10-467-657-1604	Sequence 1604, Ap
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552	24	57.1	142	11	US-11-096-568A-1325	Sequence 1325, Ap	625	24	57.1	301	11	US-11-098-686-11244	Sequence 11244, A
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554	24	57.1	143	9	US-11-120-308-56	Sequence 56, Appl	627	24	57.1	309	11	US-11-124-368A-197	Sequence 197, Appl
555	24	57.1	146	11	US-11-226-657-212	Sequence 212, Appl	628	24	57.1	311	11	US-11-096-568A-11284	Sequence 11284, A
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557	24	57.1	149	9	US-10-467-657-3668	Sequence 3668, Ap	630	24	57.1	311	11	US-11-188-298-6834	Sequence 6834, Ap
558	24	57.1	150	11	US-11-188-298-21854	Sequence 21854, A	631	24	57.1	312	9	US-10-467-657-8834	Sequence 8834, Ap
559	24	57.1	152	9	US-10-467-657-5262	Sequence 5262, Ap	632	24	57.1	318	9	US-10-467-657-6416	Sequence 6416, Ap
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561	24	57.1	160	11	US-11-188-298-13327	Sequence 13327, A	634	24	57.1	322	11	US-11-045-004-260	Sequence 260, Appl
562	24	57.1	162	11	US-11-188-298-8839	Sequence 8839, Ap	635	24	57.1	323	11	US-11-188-298-18020	Sequence 18020, A
563	24	57.1	164	11	US-11-045-004-2113	Sequence 2113, Ap	636	24	57.1	324	11	US-11-098-686-10760	Sequence 10760, A
564	24	57.1	167	9	US-10-821-234-1589	Sequence 1589, Ap	637	24	57.1	325	11	US-11-166-412-65	Sequence 65, Appl
565	24	57.1	168	11	US-11-096-568A-23106	Sequence 23106, A	638	24	57.1	326	11	US-11-096-568A-25585	Sequence 25585, A
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568	24	57.1	177	11	US-11-079-463-6747	Sequence 6747, Ap	641	24	57.1	328	11	US-11-096-568A-5609	Sequence 5609, Ap
569	24	57.1	181	11	US-11-096-568A-25375	Sequence 25375, A	642	24	57.1	329	11	US-11-096-568A-28474	Sequence 28474, A
570	24	57.1	182	11	US-11-096-568A-3775	Sequence 3775, Ap	643	24	57.1	330	11	US-11-096-568A-21644	Sequence 21644, A
571	24	57.1	182	11	US-11-096-568A-26637	Sequence 26637, A	644	24	57.1	332	11	US-11-096-568A-51133	Sequence 51133, A
572	24	57.1	183	11	US-11-096-568A-3774	Sequence 3774, Ap	645	24	57.1	332	11	US-11-172-740-1388	Sequence 1388, Ap
573	24	57.1	184	11	US-11-096-568A-15640	Sequence 15640, A	646	24	57.1	333	11	US-11-127-877-57	Sequence 57, Appl
574	24	57.1	185	11	US-11-096-568A-26636	Sequence 26636, A	647	24	57.1	334	11	US-11-096-568A-18043	Sequence 18043, A
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576	24	57.1	189	11	US-11-188-298-10147	Sequence 10147, A	649	24	57.1	337	11	US-11-096-568A-14901	Sequence 14901, A
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579	24	57.1	192	11	US-11-087-099-12035	Sequence 12035, A	652	24	57.1	340	11	US-11-096-568A-28473	Sequence 28473, A
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581	24	57.1	197	11	US-11-079-463-6484	Sequence 6484, Ap	654	24	57.1	342	11	US-11-096-568A-21643	Sequence 21643, A
582	24	57.1	199	9	US-10-793-626-2546	Sequence 2546, Appl	655	24	57.1	342	9	US-11-079-463-7307	Sequence 7307, Ap
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584	24	57.1	206	11	US-11-079-463-5898	Sequence 5898, Ap	657	24	57.1	344	11	US-11-008-570-44	Sequence 44, Appl
585	24	57.1	209	11	US-11-079-463-7585	Sequence 7585, Ap	658	24	57.1	348	11	US-11-188-298-310	Sequence 310, Appl
586	24	57.1	213	9	US-10-714-887-136	Sequence 136, Appl	659	24	57.1	350	11	US-11-096-568A-21642	Sequence 21642, A
587	24	57.1	216	11	US-11-045-004-2686	Sequence 2686, Ap	660	24	57.1	351	11	US-11-172-740-2270	Sequence 2270, Ap
588	24	57.1	216	11	US-11-098-686-10129	Sequence 10129, A	661	24	57.1	351	11	US-11-172-740-15982	Sequence 15982, A
589	24	57.1	217	11	US-11-079-463-7603	Sequence 7603, Ap	662	24	57.1	352	9	US-10-455-772-1020	Sequence 1020, Ap
590	24	57.1	217	11	US-11-170-653-48	Sequence 48, Appl	663	24	57.1	352	9	US-10-455-772-1022	Sequence 1022, Ap
591	24	57.1	220	11	US-11-188-298-1593	Sequence 1593, Ap	664	24	57.1	354	11	US-11-189-817-2	Sequence 2, Appl
592	24	57.1	222	9	US-10-517-939-168	Sequence 168, Appl	665	24	57.1	355	9	US-10-517-939-206	Sequence 206, Appl
593	24	57.1	222	11	US-11-087-099-5018	Sequence 5018, Ap	666	24	57.1	356	9	US-10-455-772-1008	Sequence 1008, Ap
594	24	57.1	225	9	US-10-517-939-172	Sequence 172, Appl	667	24	57.1	356	9	US-10-455-772-1010	Sequence 1010, Ap
595	24	57.1	226	11	US-11-188-298-2715	Sequence 2715, Ap	668	24	57.1	356	9	US-10-455-772-1012	Sequence 1012, Ap
596	24	57.1	228	9	US-10-793-626-970	Sequence 970, Appl	669	24	57.1	356	9	US-10-455-772-1028	Sequence 1028, Ap
597	24	57.1	228	9	US-10-517-939-204	Sequence 204, Appl	670	24	57.1	361	9	US-10-517-939-212	Sequence 212, Appl
598	24	57.1	228	11	US-11-072-512-2483	Sequence 2483, Ap	671	24	57.1	363	11	US-11-087-099-8290	Sequence 8290, Ap
599	24	57.1	232	11	US-11-098-686-10962	Sequence 10962, A	672	24	57.1	366	11	US-11-188-298-4763	Sequence 4763, Ap
600	24	57.1	233	11	US-11-087-099-3263	Sequence 3263, Ap	673	24	57.1	367	11	US-11-087-099-4088	Sequence 4088, Ap
601	24	57.1	234	11	US-11-096-568A-18045	Sequence 18045, A	674	24	57.1	372	11	US-11-096-568A-14936	Sequence 14936, A
602	24	57.1	237	9	US-10-714-887-104	Sequence 104, Appl	675	24	57.1	372	11	US-11-294-997-33	Sequence 33, Appl
603	24	57.1	237	11	US-11-188-298-10392	Sequence 10392, A	676	24	57.1	379	11	US-11-079-463-7981	Sequence 7981, Ap
604	24	57.1	242	11	US-11-098-686-10770	Sequence 10770, A	677	24	57.1	379	11	US-11-264-096-1365	Sequence 1365, Ap
605	24	57.1	242	11	US-11-096-568A-25373	Sequence 25373, A	678	24	57.1	382	11	US-11-120-308-66	Sequence 66, Appl

679	24	\$7.1	382	11	US-11-096-568A-5608	Sequence 5608, Ap	752	24	57.1	474	11	US-11-087-099-4488	Sequence 4488, Ap
680	24	\$7.1	383	11	US-11-096-568A-28110	Sequence 28110, A	753	24	57.1	474	11	US-11-188-298-4160	Sequence 4160, Ap
681	24	\$7.1	385	11	US-11-096-568A-8487	Sequence 8487, Ap	754	24	57.1	477	11	US-11-198-975-45	Sequence 27, Appl
682	24	\$7.1	385	11	US-11-096-568A-16118	Sequence 16118, A	755	24	57.1	477	11	US-11-128-354-27	Sequence 27, Appl
683	24	\$7.1	385	11	US-11-079-463-5941	Sequence 5941, Ap	756	24	57.1	479	11	US-11-188-298-19109	Sequence 19109, A
684	24	\$7.1	386	11	US-11-079-463-7036	Sequence 7036, Ap	757	24	57.1	485	11	US-11-098-666-11130	Sequence 11130, A
685	24	\$7.1	388	11	US-11-072-512-3454	Sequence 3454, Ap	758	24	57.1	487	11	US-11-124-368A-198	Sequence 198, Appl
686	24	\$7.1	388	11	US-11-096-568A-5607	Sequence 5607, Ap	759	24	57.1	490	11	US-11-133-949-20	Sequence 20, Appl
687	24	\$7.1	388	11	US-11-096-568A-9638	Sequence 9638, Ap	760	24	57.1	490	11	US-11-096-568A-21871	Sequence 21871, A
688	24	\$7.1	388	11	US-11-096-568A-28109	Sequence 28109, A	761	24	57.1	493	11	US-11-188-298-3254	Sequence 3254, Ap
689	24	\$7.1	390	11	US-11-188-298-6017	Sequence 6017, Ap	762	24	57.1	494	11	US-11-188-298-526	Sequence 526, Appl
690	24	\$7.1	392	9	US-10-498-026-90	Sequence 90, Appl	763	24	57.1	495	11	US-11-129-076-8	Sequence 8, Appl1
691	24	\$7.1	392	11	US-11-087-099-9117	Sequence 9117, Ap	764	24	57.1	495	11	US-11-096-568A-7940	Sequence 7940, Ap
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693	24	\$7.1	392	11	US-11-096-568A-9637	Sequence 9637, A	766	24	57.1	496	11	US-11-067-121-12	Sequence 12, Appl
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696	24	\$7.1	393	9	US-10-506-454-100	Sequence 100, Appl	769	24	57.1	497	11	US-11-287-235-3	Sequence 3, Appl1
697	24	\$7.1	395	11	US-11-096-568A-16117	Sequence 16117, A	770	24	57.1	497	11	US-11-287-235-10	Sequence 10, Appl
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707	24	\$7.1	408	11	US-11-096-568A-22953	Sequence 22953, A	780	24	57.1	514	11	US-11-188-298-17783	Sequence 17783, Ap
708	24	\$7.1	411	11	US-11-096-568A-7144	Sequence 7144, Ap	781	24	57.1	517	11	US-11-188-298-8963	Sequence 8963, Ap
709	24	\$7.1	414	11	US-11-096-568A-13745	Sequence 13745, A	782	24	57.1	518	11	US-11-188-298-16472	Sequence 16472, A
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714	24	\$7.1	419	11	US-11-096-568A-8485	Sequence 8485, Ap	787	24	57.1	531	11	US-11-072-512-2775	Sequence 2775, Appl
715	24	\$7.1	419	11	US-11-096-568A-9636	Sequence 9636, Ap	788	24	57.1	532	11	US-11-120-308-72	Sequence 72, Appl
716	24	\$7.1	420	11	US-11-124-368A-194	Sequence 194, Appl	789	24	57.1	533	11	US-11-230-995-3	Sequence 3, Appl1
717	24	\$7.1	421	11	US-11-120-308-64	Sequence 64, Appl	790	24	57.1	534	11	US-11-057-733-2	Sequence 2, Appl1
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721	24	\$7.1	424	11	US-11-096-568A-14935	Sequence 14935, A	794	24	57.1	536	11	US-11-233-510-24	Sequence 24, Appl
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723	24	\$7.1	426	11	US-11-079-463-9085	Sequence 9085, Ap	796	24	57.1	545	11	US-11-188-298-21733	Sequence 21733, A
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729	24	\$7.1	432	11	US-11-188-298-20229	Sequence 20229, A	802	24	57.1	559	9	US-10-793-626-1376	Sequence 1376, Ap
730	24	\$7.1	435	11	US-11-087-099-6985	Sequence 6985, Ap	803	24	57.1	561	11	US-11-124-368A-195	Sequence 195, Appl
731	24	\$7.1	435	11	US-11-188-298-9097	Sequence 9097, Ap	804	24	57.1	564	11	US-11-096-568A-2541	Sequence 2541, Ap
732	24	\$7.1	435	11	US-11-188-298-17434	Sequence 17434, A	805	24	57.1	570	11	US-11-124-368A-196	Sequence 196, Appl
733	24	\$7.1	439	11	US-11-188-298-6960	Sequence 6960, Ap	806	24	57.1	570	11	US-11-072-512-2109	Sequence 2109, Ap
734	24	\$7.1	439	11	US-11-188-298-8028	Sequence 8028, Ap	807	24	57.1	572	11	US-11-087-099-5680	Sequence 5680, Ap
735	24	\$7.1	440	11	US-11-188-298-760	Sequence 760, Appl	808	24	57.1	577	11	US-11-079-463-7370	Sequence 7370, Ap
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737	24	\$7.1	441	11	US-11-087-099-2892	Sequence 2892, Ap	810	24	57.1	588	11	US-11-096-568A-24586	Sequence 24586, A
738	24	\$7.1	441	11	US-11-188-298-13775	Sequence 13775, A	811	24	57.1	593	11	US-11-120-808-54	Sequence 54, Appl
739	24	\$7.1	445	9	US-10-517-939-368	Sequence 368, Appl	812	24	57.1	593	11	US-11-188-298-21880	Sequence 21880, A
740	24	\$7.1	445	11	US-11-096-568A-2542	Sequence 2542, Ap	813	24	57.1	602	11	US-11-096-568A-2540	Sequence 2540, Ap
741	24	\$7.1	447	11	US-11-072-512-3437	Sequence 3437, Ap	814	24	57.1	602	9	US-10-455-772-528	Sequence 528, Appl
742	24	\$7.1	449	11	US-11-096-568A-22952	Sequence 22952, A	815	24	57.1	607	11	US-11-096-051-14	Sequence 14, Appl
743	24	\$7.1	454	11	US-11-188-298-22040	Sequence 22040, A	816	24	57.1	611	9	US-10-455-772-508	Sequence 508, Appl
744	24	\$7.1	457	11	US-11-194-246-326	Sequence 326, Appl	817	24	57.1	611	9	US-10-455-772-510	Sequence 510, Appl
745	24	\$7.1	463	11	US-11-024-959-395	Sequence 395, Appl	818	24	57.1	611	9	US-10-455-772-512	Sequence 512, Appl
746	24	\$7.1	463	11	US-11-087-099-7935	Sequence 7935, Ap	819	24	57.1	611	9	US-10-455-772-514	Sequence 514, Appl
747	24	\$7.1	463	11	US-11-188-298-18358	Sequence 18358, A	820	24	57.1	611	9	US-10-455-772-516	Sequence 516, Appl
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749	24	\$7.1	466	11	US-11-096-568A-7942	Sequence 7942, Ap	822	24	57.1	613	11	US-11-052-554A-44	Sequence 44, Appl
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827	24	57.1	623	11	US-11-188-298-14730	Sequence 14730, A	900	24	57.1	858	9	US-10-995-561-874	Sequence 874, App
828	24	57.1	623	11	US-11-285-818-2	Sequence 2, App1	901	24	57.1	858	9	US-10-995-561-875	Sequence 875, App
829	24	57.1	626	11	US-11-098-686-10124	Sequence 10124, A	902	24	57.1	858	11	US-11-077-550-22	Sequence 22, App1
830	24	57.1	628	11	US-11-080-991-108	Sequence 108, App	903	24	57.1	860	11	US-11-077-550-175	Sequence 175, App
831	24	57.1	629	11	US-11-072-512-3405	Sequence 3405, A	904	24	57.1	862	11	US-11-077-550-94	Sequence 94, App1
832	24	57.1	635	11	US-11-096-568A-28634	Sequence 28634, App	905	24	57.1	862	11	US-11-077-550-171	Sequence 171, App1
833	24	57.1	639	9	US-10-506-454-1306	Sequence 1306, App	906	24	57.1	862	11	US-11-096-051-20	Sequence 20, App1
834	24	57.1	651	11	US-11-128-660-1	Sequence 1, App1	907	24	57.1	862	11	US-11-077-550-102	Sequence 102, App
835	24	57.1	654	11	US-11-120-308-52	Sequence 52, App1	908	24	57.1	864	11	US-11-188-298-19464	Sequence 19464, A
836	24	57.1	676	11	US-11-096-568A-30396	Sequence 30396, A	909	24	57.1	865	11	US-11-077-550-100	Sequence 100, App
837	24	57.1	683	11	US-11-124-368A-243	Sequence 243, App	910	24	57.1	865	11	US-11-077-550-88	Sequence 88, App1
838	24	57.1	686	11	US-11-096-568A-30395	Sequence 30395, A	911	24	57.1	866	11	US-11-077-550-104	Sequence 104, App1
839	24	57.1	690	11	US-11-079-463-6647	Sequence 6647, App	912	24	57.1	867	11	US-11-077-550-80	Sequence 80, App1
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841	24	57.1	708	11	US-11-096-568A-27412	Sequence 27412, A	914	24	57.1	867	11	US-11-077-550-98	Sequence 98, App1
842	24	57.1	709	9	US-10-745-586-5	Sequence 5, App1	915	24	57.1	867	11	US-11-077-550-92	Sequence 92, App1
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847	24	57.1	727	9	US-10-793-626-2862	Sequence 2862, App	920	24	57.1	873	11	US-11-057-058-58	Sequence 58, App1
848	24	57.1	732	11	US-11-124-368A-248	Sequence 248, App	921	24	57.1	876	11	US-11-077-550-82	Sequence 82, App1
849	24	57.1	742	11	US-11-188-298-15750	Sequence 15750, A	922	24	57.1	876	11	US-11-077-550-106	Sequence 106, App
850	24	57.1	748	9	US-10-455-772-300	Sequence 300, App	923	24	57.1	876	11	US-11-077-550-108	Sequence 108, App
851	24	57.1	749	11	US-11-188-298-10526	Sequence 10526, A	924	24	57.1	876	11	US-11-096-568A-31320	Sequence 31320, A
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853	24	57.1	750	11	US-11-124-368A-249	Sequence 249, App	926	24	57.1	880	9	US-10-516-100-2	Sequence 2, App1
854	24	57.1	754	9	US-10-455-772-294	Sequence 294, App	927	24	57.1	883	9	US-10-770-346-57	Sequence 57, App1
855	24	57.1	754	11	US-10-455-772-298	Sequence 298, App	928	24	57.1	883	9	US-10-877-146-37	Sequence 37, App1
856	24	57.1	754	11	US-11-096-568A-30394	Sequence 30394, A	929	24	57.1	888	11	US-11-077-550-112	Sequence 112, App
857	24	57.1	755	9	US-10-455-772-302	Sequence 302, App	930	24	57.1	888	11	US-11-096-568A-30756	Sequence 30756, A
858	24	57.1	755	9	US-10-455-772-304	Sequence 304, App	931	24	57.1	891	11	US-11-096-568A-28841	Sequence 28841, A
859	24	57.1	755	9	US-10-501-841-35	Sequence 35, App1	932	24	57.1	897	11	US-11-096-568A-30755	Sequence 30755, A
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861	24	57.1	766	11	US-11-264-096-2229	Sequence 2229, App	934	24	57.1	901	11	US-11-188-298-15338	Sequence 15338, A
862	24	57.1	777	11	US-10-455-772-938	Sequence 938, App	935	24	57.1	912	11	US-11-096-568A-28840	Sequence 28840, A
863	24	57.1	777	11	US-11-124-368A-238	Sequence 238, App	936	24	57.1	917	11	US-11-096-568A-14780	Sequence 14780, A
864	24	57.1	777	11	US-10-455-772-292	Sequence 292, App	937	24	57.1	925	11	US-10-453-172-1124	Sequence 1124, App
865	24	57.1	778	11	US-11-124-368A-240	Sequence 240, App	938	24	57.1	925	11	US-11-096-568A-30755	Sequence 30755, A
866	24	57.1	778	11	US-11-124-368A-240	Sequence 240, App	939	24	57.1	931	11	US-11-1230-145-2	Sequence 2, App1
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869	24	57.1	791	11	US-11-124-368A-245	Sequence 245, App	942	24	57.1	937	11	US-11-096-568A-31319	Sequence 31319, A
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871	24	57.1	802	9	US-10-194-487-312	Sequence 312, App	944	24	57.1	940	11	US-11-096-568A-27411	Sequence 27411, A
872	24	57.1	802	9	US-10-195-883-312	Sequence 312, App	945	24	57.1	942	11	US-11-096-568A-27410	Sequence 27410, A
873	24	57.1	802	9	US-10-195-888-312	Sequence 312, App	946	24	57.1	942	11	US-10-853-8078-51	Sequence 51, App1
874	24	57.1	802	11	US-10-195-889-312	Sequence 312, App	947	24	57.1	966	9	US-10-877-146-32	Sequence 32, App1
875	24	57.1	803	11	US-11-124-368A-241	Sequence 241, App	948	24	57.1	966	9	US-10-877-146-32	Sequence 32, App1
876	24	57.1	803	11	US-11-124-368A-242	Sequence 242, App	949	24	57.1	972	9	US-10-453-372-1128	Sequence 1128, App
877	24	57.1	811	8	US-10-511-937-2584	Sequence 2584, App	950	24	57.1	980	11	US-11-188-298-9632	Sequence 9632, App
878	24	57.1	812	11	US-11-072-512-2027	Sequence 2027, App	951	24	57.1	990	11	US-11-188-298-12671	Sequence 12671, A
879	24	57.1	816	9	US-10-455-772-490	Sequence 490, App	952	24	57.1	1003	11	US-11-096-568A-311774	Sequence 311774, A
880	24	57.1	821	9	US-10-455-772-518	Sequence 518, App	953	24	57.1	1006	8	US-10-511-937-2425	Sequence 2425, App
881	24	57.1	821	9	US-10-455-772-534	Sequence 534, App	954	24	57.1	1006	11	US-11-203-251A-30	Sequence 30, App1
882	24	57.1	821	9	US-11-096-051-6	Sequence 6, App1	955	24	57.1	1017	11	US-11-072-512-2312	Sequence 2312, App
883	24	57.1	826	11	US-11-087-099-6618	Sequence 6618, App	956	24	57.1	1033	11	US-11-096-568A-311773	Sequence 311773, A
884	24	57.1	827	9	US-10-455-772-520	Sequence 520, App	957	24	57.1	1036	11	US-11-072-512-2509	Sequence 2509, App
885	24	57.1	827	9	US-10-455-772-532	Sequence 532, App	958	24	57.1	1050	8	US-10-505-928-347	Sequence 347, App
886	24	57.1	827	9	US-10-455-772-536	Sequence 536, App	959	24	57.1	1050	9	US-10-523-477-12	Sequence 12, App1
887	24	57.1	828	11	US-11-096-568A-14781	Sequence 14781, A	960	24	57.1	1050	9	US-10-770-1726-47	Sequence 47, App1
888	24	57.1	828	11	US-11-043-806-455	Sequence 455, App	961	24	57.1	1054	11	US-11-096-568A-311772	Sequence 311772, A
889	24	57.1	833	9	US-10-455-772-496	Sequence 496, App	962	24	57.1	1055	11	US-11-188-298-17762	Sequence 17762, A
890	24	57.1	834	11	US-11-188-298-10387	Sequence 10387, A	963	24	57.1	1060	11	US-11-188-298-9146	Sequence 9146, App
891	24	57.1	836	11	US-11-124-368A-246	Sequence 246, App	964	24	57.1	1070	11	US-11-062	Sequence 4, App1
892	24	57.1	838	9	US-10-455-772-492	Sequence 492, App	965	24	57.1	1095	11	US-11-099-855-2	Sequence 2, App1
893	24	57.1	838	9	US-10-455-772-538	Sequence 538, App	966	24	57.1	1104	11	US-11-099-855-11	Sequence 11, App1
894	24	57.1	838	11	US-11-079-463-8537	Sequence 8537, App	967	24	57.1	1104	11	US-11-099-855-12	Sequence 12, App1
895	24	57.1	841	11	US-11-216-333-2	Sequence 2, App1	968	24	57.1	1104	11	US-11-099-855-13	Sequence 13, App1
896	24	57.1	841	11	US-11-216-333-6	Sequence 6, App1	969	24	57.1	1104	11	US-11-099-855-13	Sequence 13, App1
897	24	57.1	845	9	US-10-455-772-494	Sequence 494, App	970	24	57.1	1169	11	US-11-077-550-20	Sequence 20, App1

971 24 57.1 1278 9 US-10-995-561-952 Sequence 952, App
972 24 57.1 1286 9 US-10-877-346-38 Sequence 38, Appl
973 24 57.1 1420 11 US-11-077-550-110 Sequence 110, Appl
974 24 57.1 1420 11 US-11-098-686-10577 Sequence 10577, A
975 24 57.1 1510 11 US-11-055-822-72 Sequence 72, Appl
976 24 57.1 1565 11 US-11-188-298-7537 Sequence 7537, Ap
977 24 57.1 1574 9 US-10-455-772-1026 Sequence 1026, Ap
978 24 57.1 1576 9 US-10-455-772-1014 Sequence 1014, Ap
979 24 57.1 1576 9 US-10-455-772-1016 Sequence 1016, Ap
980 24 57.1 1593 9 US-10-455-772-1006 Sequence 1006, Ap
981 24 57.1 1637 9 US-10-821-234-1204 Sequence 1204, Ap
982 24 57.1 1854 11 US-11-180-074-4 Sequence 4, Appl
983 24 57.1 1900 9 US-10-513-786-3 Sequence 3, Appl
984 24 57.1 1912 8 US-10-511-937-2561 Sequence 2561, Ap
985 24 57.1 1924 8 US-10-512-386-56 Sequence 56, Appl
986 24 57.1 1924 9 US-10-469-469-250 Sequence 250, Appl
987 24 57.1 2004 9 US-10-469-469-250 Sequence 250, Appl
988 24 57.1 2011 11 US-11-080-991-56 Sequence 56, Appl
989 24 57.1 2053 9 US-10-877-346-11 Sequence 11, Appl
990 24 57.1 2066 9 US-10-877-346-9 Sequence 9, Appl
991 24 57.1 2376 11 US-11-096-051-4 Sequence 4, Appl
992 24 57.1 2613 9 US-10-455-772-530 Sequence 530, Appl
993 24 57.1 2628 9 US-10-455-772-502 Sequence 502, Appl
994 24 57.1 2715 11 US-11-096-051-2 Sequence 2, Appl
995 24 57.1 2715 11 US-11-113-424-51 Sequence 51, Appl
996 24 57.1 2721 9 US-10-455-772-522 Sequence 522, Appl
997 24 57.1 2721 11 US-11-096-051-10 Sequence 10, Appl
998 24 57.1 2725 9 US-10-455-772-486 Sequence 486, Appl
999 24 57.1 2725 9 US-10-455-772-526 Sequence 526, Appl
1000 24 57.1 2725 9 US-10-455-772-544 Sequence 544, Appl
Sequence 546, Appl

ALIGNMENTS

RESULT 1
US-11-136-559-6
; Sequence 6, Application US/11136559
; Publication No. US2005028716A1
; GENERAL INFORMATION:
; APPLICANT: PATTI, Joseph M
; APPLICANT: HUTCHINS, Jeff T
; APPLICANT: DOMANSKI, Paul
; APPLICANT: PATEL, Pratishtha
; APPLICANT: HALL, Andrea
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN . . .
; FILE REFERENCE: P07069US04/BAS
; CURRENT APPLICATION NUMBER: US/11/136,559
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US/10/056,052
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: 60/308,116
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/298,413
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/274,611
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/264,072
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-11-136-559-6

Query Match 88.1%; Score 37; DB 11; Length 112;
Best Local Similarity 87.5%; Pred. No. 0.64;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 HOYLSRT 8
|||||

Db 95 HOYLSRT 102
RESULT 2
US-11-132-947-2
; Sequence 2, Application US/11132947
; Publication No. US20060024268A1
; GENERAL INFORMATION:
; APPLICANT: Kasai, Marion
; APPLICANT: Wood, Nancy L.
; APPLICANT: Donaldson, Debra D.
; APPLICANT: Collins, Mary
; TITLE OF INVENTION: MODULATION OF IMMUNOGLOBULIN PRODUCTION AND APOPTIC DISORDERS
; FILE REFERENCE: 16158-016001
; CURRENT APPLICATION NUMBER: US/11/132,947
; CURRENT FILING DATE: 2005-05-19
; PRIOR APPLICATION NUMBER: US 60/572,407
; PRIOR FILING DATE: 2004-05-19
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-132-947-2
Query Match 88.1%; Score 37; DB 11; Length 131;
Best Local Similarity 87.5%; Pred. No. 0.75;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 HOYLSRT 8
|||||

Db 118 HOYLSRT 125
RESULT 3
US-11-197-221-1
; Sequence 1, Application US/11197221
; Publication No. US20060057123A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; APPLICANT: represented by the Secretary of the Department of Health and
; APPLICANT: Human Services
; APPLICANT: Leonard, Warren J.
; APPLICANT: Lipsky, Peter
; APPLICANT: Morse, Herbert C.
; APPLICANT: Bettinger, Catherine Rachel
; APPLICANT: Spolski, Rosanne
; TITLE OF INVENTION: METHOD OF INDUCING MEMORY B CELL DEVELOPMENT AND TERMINAL
; FILE REFERENCE: 4239-66179-03
; CURRENT APPLICATION NUMBER: US/11/197,221
; CURRENT FILING DATE: 2005-08-03
; PRIOR APPLICATION NUMBER: 60/523,754
; PRIOR FILING DATE: 2003-11-19
; PRIOR APPLICATION NUMBER: PCT/US2004/039135
; PRIOR FILING DATE: 2004-11-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-197-221-1

Query Match 88.1%; Score 37; DB 11; Length 160;
Best Local Similarity 87.5%; Pred. No. 0.93;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 HOYLSRT 8
|||||

Db 149 HOYLSRT 156

RESULT 4

US-10-511-937-2572
; Sequence 2572, Application US/10511937
; Publication No. US2006008836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, Macdonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 50661200104
; CURRENT APPLICATION NUMBER: US/10/511,937
; PRIOR FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2572
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2572

Query Match 88.1%; Score 37; DB 8; Length 162;
Best Local Similarity 87.5%; Pred. No. 0.94;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
DB 149 HOHLSRT 156

RESULT 5

US-11-174-398-2
; Sequence 2, Application US/11174398
; Publication No. US20050244930A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: West, James W.
; APPLICANT: Novak, Julia E.
; TITLE OF INVENTION: ZALPHA1 LIGAND ANTAGONISTS
; FILE REFERENCE: 01-37
; CURRENT APPLICATION NUMBER: US/11/174,398
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US/10/282,622
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 60/337,586
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-174-398-2

Query Match 88.1%; Score 37; DB 11; Length 162;
Best Local Similarity 87.5%; Pred. No. 0.94;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
DB 149 HOHLSRT 156

RESULT 6

US-11-174-398-6
; Sequence 6, Application US/11174398
; Publication No. US20050244930A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: West, James W.
; APPLICANT: Novak, Julia E.
; TITLE OF INVENTION: ZALPHA1 LIGAND ANTAGONISTS
; FILE REFERENCE: 01-37
; CURRENT APPLICATION NUMBER: US/11/174,398
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US/10/282,622
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 60/337,586
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: zalpahl1 ligand Q153D/1156D
US-11-174-398-6

Query Match 88.1%; Score 37; DB 11; Length 162;
Best Local Similarity 87.5%; Pred. No. 0.94;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
DB 149 HOHLSRT 156

RESULT 7

US-11-134-489-2
; Sequence 2, Application US/11134489
; Publication No. US20050265966A1
; GENERAL INFORMATION:
; APPLICANT: Kindsvogel, Wayne R.
; APPLICANT: Hughes, Steven D.
; APPLICANT: Holly, Richard D.
; APPLICANT: Clegg, Christopher H.
; APPLICANT: Foster, Donald C.
; APPLICANT: Johnson, Rebecca A.
; APPLICANT: Heipel, Mark D.
; APPLICANT: Siva Kumar, Pallavur V.
; TITLE OF INVENTION: METHODS OF TREATING CANCER USING IL-21 AND MONOCLONAL ANTIBODY TH
; FILE REFERENCE: 04-03
; CURRENT APPLICATION NUMBER: US/11/134,489
; CURRENT FILING DATE: 2005-05-20
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-134-489-2

Query Match 88.1%; Score 37; DB 11; Length 162;
Best Local Similarity 87.5%; Pred. No. 0.94;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
DB 149 HOHLSRT 156

RESULT 8
US-11-132-947-9

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; Sequence 9, Application US/11132947
; Publication No. US20060024268A1
; GENERAL INFORMATION:
; APPLICANT: Kasalan, Marion
; APPLICANT: Wood, Nancy L.
; APPLICANT: Donaldson, Debra D.
; APPLICANT: Collins, Mary
; TITLE OF INVENTION: MODULATION OF IMMUNOGLOBULIN PRODUCTION AND ATOPIC DISORDERS
; FILE REFERENCE: 16158-016001
; CURRENT APPLICATION NUMBER: US/11/132,947
; CURRENT FILING DATE: 2005-05-19
; PRIOR APPLICATION NUMBER: US 60/572,407
; PRIOR FILING DATE: 2004-05-19
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-132-947-9
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Query Match      88.1%; Score 37; DB 11; Length 162;
Best Local Similarity 87.5%; Pred. No. 0.94;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
OY      1 HOYLSRT 8
Db      149 HOHLSRT 156
```

```
RESULT 9
US-11-197-488-19
; Sequence 19, Application US/11197488
; Publication No. US2006003902A1
; GENERAL INFORMATION:
; APPLICANT: Young, Deborah A.
; APPLICANT: Collins, Mary
; APPLICANT: Dunnsel-Joannopoulos, Kyriaki
; APPLICANT: O'Hara, Richard Michael, Jr.
; APPLICANT: Kasalan, Marion T.
; APPLICANT: Mathew J. Whiteers
; TITLE OF INVENTION: Antagonizing Interleukin-21 Receptor Activity
; FILE REFERENCE: 01997.043400
; CURRENT APPLICATION NUMBER: US/11/197,488
; CURRENT FILING DATE: 2005-08-05
; PRIOR APPLICATION NUMBER: US 60/599,086
; PRIOR FILING DATE: 2004-08-05
; PRIOR APPLICATION NUMBER: US 60/639,176
; PRIOR FILING DATE: 2004-12-23
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Human
US-11-197-488-19
```

```
Query Match      88.1%; Score 37; DB 11; Length 162;
Best Local Similarity 87.5%; Pred. No. 0.94;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
OY      1 HOYLSRT 8
Db      149 HOHLSRT 156
```

```
RESULT 10
US-10-981-356A-20
; Sequence 20, Application US/10981356A
; Publication No. US20060015952A1
; GENERAL INFORMATION:
; APPLICANT: FILVAROFF, ELLEN H.
; TITLE OF INVENTION: SCREENING ASSAYS AND METHODS OF TUMOR TREATMENT
```

```
; FILE REFERENCE: P2068R1
; CURRENT APPLICATION NUMBER: US/10/981,356A
; CURRENT FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: US 60/520,398
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/557,951
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 45
; SEQ ID NO 20
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-10-981-356A-20
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Query Match      83.3%; Score 35; DB 9; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.9e+05;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
OY      1 HOYLSRT 8
Db      1 HOYLSRT 8
```

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RESULT 11
US-11-096-046-20
; Sequence 20, Application US/11096046
; Publication No. US20050276802A1
; GENERAL INFORMATION:
; APPLICANT: ADAMS, CAMELLIA W.
; APPLICANT: FERRARA, NAPOLEONE
; APPLICANT: FILVAROFF, ELLEN H.
; APPLICANT: MAO, WEIGUANG
; APPLICANT: PRESTA, LEONARD G.
; APPLICANT: TEJADA, MAX L.
; TITLE OF INVENTION: Humanized Anti-TGF-Beta Antibodies
; FILE REFERENCE: P1954RIUS
; CURRENT APPLICATION NUMBER: US/11/096,046
; CURRENT FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: US 60/558,290
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 20
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-096-046-20
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```
Query Match      83.3%; Score 35; DB 11; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.9e+05;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      1 HOYLSRT 8
Db      1 HOYLSRT 8
```

```
RESULT 12
US-11-136-559-29
; Sequence 29, Application US/11136559
; Publication No. US20050287164A1
; GENERAL INFORMATION:
; APPLICANT: PATTI, Joseph M
; APPLICANT: HUTCHINS, Jeff T
; APPLICANT: DOMANSKI, Paul
; APPLICANT: PATEL, Pratiksha
; APPLICANT: HALL, Andrea
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLPA PROTEIN . . .
; FILE REFERENCE: P07069US04/BAS
; CURRENT APPLICATION NUMBER: US/11/136,559
```

;; CURRENT FILING DATE: 2005-05-25
;; PRIOR APPLICATION NUMBER: US/10/056,052
;; PRIOR FILING DATE: 2002-01-18
;; PRIOR APPLICATION NUMBER: 60/308,116
;; PRIOR FILING DATE: 2001-07-30
;; PRIOR APPLICATION NUMBER: 60/298,413
;; PRIOR FILING DATE: 2001-06-18
;; PRIOR APPLICATION NUMBER: 60/274,611
;; PRIOR FILING DATE: 2001-03-12
;; PRIOR APPLICATION NUMBER: 60/264,072
;; PRIOR FILING DATE: 2001-01-26
;; NUMBER OF SEQ ID NOS: 29
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 29
;; LENGTH: 8
;; TYPE: PRT
;; ORGANISM: Staphylococcus aureus
US-11-136-559-29

Query Match 83.3%; Score 35; DB 11; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.9e+05;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
Db 1 HOYLSRT 8

RESULT 13
US-11-136-559-10
;; Sequence 10, Application US/11136559
;; Publication No. US20050287164A1
;; GENERAL INFORMATION:
;; APPLICANT: PATTI, Joseph M
;; APPLICANT: HUTCHINS, Jeff T
;; APPLICANT: DOMANSKI, Paul
;; APPLICANT: PATEL, Pratiksha
;; APPLICANT: HALL, Andrea
;; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLPA PROTEIN . . .
;; FILE REFERENCE: P07069US04/BAS
;; CURRENT APPLICATION NUMBER: US/11/136,559
;; CURRENT FILING DATE: 2005-05-25
;; PRIOR APPLICATION NUMBER: US/10/056,052
;; PRIOR FILING DATE: 2002-01-18
;; PRIOR APPLICATION NUMBER: 60/308,116
;; PRIOR FILING DATE: 2001-07-30
;; PRIOR APPLICATION NUMBER: 60/298,413
;; PRIOR FILING DATE: 2001-06-18
;; PRIOR APPLICATION NUMBER: 60/274,611
;; PRIOR FILING DATE: 2001-03-12
;; PRIOR APPLICATION NUMBER: 60/264,072
;; PRIOR FILING DATE: 2001-01-26
;; NUMBER OF SEQ ID NOS: 29
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 10
;; LENGTH: 112
;; TYPE: PRT
;; ORGANISM: Staphylococcus aureus
US-11-136-559-10

Query Match 83.3%; Score 35; DB 11; Length 112;
Best Local Similarity 87.5%; Pred. No. 1.7;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
Db 95 HOYLSRT 102

RESULT 14
US-11-136-559-14
;; Sequence 14, Application US/11136559
;; Publication No. US20050287164A1

;; GENERAL INFORMATION:
;; APPLICANT: PATTI, Joseph M
;; APPLICANT: HUTCHINS, Jeff T
;; APPLICANT: DOMANSKI, Paul
;; APPLICANT: PATEL, Pratiksha
;; APPLICANT: HALL, Andrea
;; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLPA PROTEIN . . .
;; FILE REFERENCE: P07069US04/BAS
;; CURRENT APPLICATION NUMBER: US/11/136,559
;; CURRENT FILING DATE: 2005-05-25
;; PRIOR APPLICATION NUMBER: US/10/056,052
;; PRIOR FILING DATE: 2002-01-18
;; PRIOR APPLICATION NUMBER: 60/308,116
;; PRIOR FILING DATE: 2001-07-30
;; PRIOR APPLICATION NUMBER: 60/298,413
;; PRIOR FILING DATE: 2001-06-18
;; PRIOR APPLICATION NUMBER: 60/274,611
;; PRIOR FILING DATE: 2001-03-12
;; PRIOR APPLICATION NUMBER: 60/264,072
;; PRIOR FILING DATE: 2001-01-26
;; NUMBER OF SEQ ID NOS: 29
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 14
;; LENGTH: 112
;; TYPE: PRT
;; ORGANISM: Staphylococcus aureus
US-11-136-559-14

Query Match 83.3%; Score 35; DB 11; Length 112;
Best Local Similarity 87.5%; Pred. No. 1.7;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
Db 95 HOYLSRT 102

RESULT 15
US-11-136-559-18
;; Sequence 18, Application US/11136559
;; Publication No. US20050287164A1
;; GENERAL INFORMATION:
;; APPLICANT: PATTI, Joseph M
;; APPLICANT: HUTCHINS, Jeff T
;; APPLICANT: DOMANSKI, Paul
;; APPLICANT: PATEL, Pratiksha
;; APPLICANT: HALL, Andrea
;; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLPA PROTEIN . . .
;; FILE REFERENCE: P07069US04/BAS
;; CURRENT APPLICATION NUMBER: US/11/136,559
;; CURRENT FILING DATE: 2005-05-25
;; PRIOR APPLICATION NUMBER: US/10/056,052
;; PRIOR FILING DATE: 2002-01-18
;; PRIOR APPLICATION NUMBER: 60/308,116
;; PRIOR FILING DATE: 2001-07-30
;; PRIOR APPLICATION NUMBER: 60/298,413
;; PRIOR FILING DATE: 2001-06-18
;; PRIOR APPLICATION NUMBER: 60/274,611
;; PRIOR FILING DATE: 2001-03-12
;; PRIOR APPLICATION NUMBER: 60/264,072
;; PRIOR FILING DATE: 2001-01-26
;; NUMBER OF SEQ ID NOS: 29
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 18
;; LENGTH: 112
;; TYPE: PRT
;; ORGANISM: Staphylococcus aureus
US-11-136-559-18

Query Match 83.3%; Score 35; DB 11; Length 112;
Best Local Similarity 87.5%; Pred. No. 1.7;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
| | | | |
Db 95 HOYLSRT 102

RESULT 16
US-11-136-559-22
; Sequence 22, Application US/11136559
; Publication No. US20050287164A1
; GENERAL INFORMATION:
; APPLICANT: PATTI, Joseph M
; APPLICANT: HUTCHINS, Jeff T
; APPLICANT: DOMANSKI, Paul
; APPLICANT: PATEL, Pratishtha
; APPLICANT: HALL, Andrea
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN . . .
; FILE REFERENCE: P07069US04/BAS
; CURRENT FILING DATE: US/11/136,559
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US/10/056,052
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: 60/308,116
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/298,413
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/274,611
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/264,072
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-11-136-559-22

Query Match 83.3%; Score 35; DB 11; Length 112;
Best Local Similarity 87.5%; Pred. No. 1.7;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
| | | | |
Db 95 HOYLSRT 102

RESULT 17
US-10-981-356A-1
; Sequence 1, Application US/10981356A
; Publication No. US20060015952A1
; GENERAL INFORMATION:
; APPLICANT: FILVAROFF, ELLEN H.
; TITLE OF INVENTION: SCREENING ASSAYS AND METHODS OF TUMOR TREATMENT
; FILE REFERENCE: P2068R1
; CURRENT APPLICATION NUMBER: US/10/981,356A
; CURRENT FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: US 60/520,398
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/557,951
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 45
; SEQ ID NO 1
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-981-356A-1

Query Match 83.3%; Score 35; DB 9; Length 116;
Best Local Similarity 87.5%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
| | | | |

Db 95 HOYLSRT 102

RESULT 18
US-10-981-356A-3
; Sequence 3, Application US/10981356A
; Publication No. US20060015952A1
; GENERAL INFORMATION:
; APPLICANT: FILVAROFF, ELLEN H.
; TITLE OF INVENTION: SCREENING ASSAYS AND METHODS OF TUMOR TREATMENT
; FILE REFERENCE: P2068R1
; CURRENT APPLICATION NUMBER: US/10/981,356A
; CURRENT FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: US 60/520,398
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/557,951
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 45
; SEQ ID NO 3
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-10-981-356A-3

Query Match 83.3%; Score 35; DB 9; Length 116;
Best Local Similarity 87.5%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
| | | | |
Db 95 HOYLSRT 102

RESULT 19
US-11-096-046-1
; Sequence 1, Application US/11096046
; Publication No. US20050276802A1
; GENERAL INFORMATION:
; APPLICANT: ADAMS, CAMELIA W.
; APPLICANT: FERRARA, NAPOLEONE
; APPLICANT: FILVAROFF, ELLEN H.
; APPLICANT: MAO, WEIGUANG
; APPLICANT: PRESTA, LEONARD G.
; APPLICANT: TEJADA, MAX L.
; TITLE OF INVENTION: Humanized Anti-TGF-Beta Antibodies
; FILE REFERENCE: P1954R1US
; CURRENT APPLICATION NUMBER: US/11/096,046
; CURRENT FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: US 60/558,290
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 1
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-096-046-1

Query Match 83.3%; Score 35; DB 11; Length 116;
Best Local Similarity 87.5%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
| | | | |
Db 95 HOYLSRT 102

RESULT 20
US-11-096-046-3
; Sequence 3, Application US/11096046
; Publication No. US20050276802A1
; GENERAL INFORMATION:

APPLICANT: ADAMS, CAMELLIA W.
APPLICANT: FERRARA, NAPOLEONE
APPLICANT: FILVAROFF, ELLEN H.
APPLICANT: MAO, WEIGUANG
APPLICANT: PRESTA, LEONARD G.
APPLICANT: TRADA, MAX L.
TITLE OF INVENTION: Humanized Anti-TGF-Beta Antibodies
FILE REFERENCE: P1954R1US
CURRENT APPLICATION NUMBER: US/11/096,046
CURRENT FILING DATE: 2005-03-31
PRIOR APPLICATION NUMBER: US 60/558,290
PRIOR FILING DATE: 2004-03-31
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 3
LENGTH: 116
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: sequence is synthesized
US-11-096-046-3

Query Match 83.3%; Score 35; DB 11; Length 116;
Best Local Similarity 87.5%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
Db 95 HOYLSRT 102

RESULT 21
US-10-981-356A-25
Sequence 25, Application US/10981356A
Publication No. US20060015952A1
GENERAL INFORMATION:
APPLICANT: FILVAROFF, ELLEN H.
TITLE OF INVENTION: SCREENING ASSAYS AND METHODS OF TUMOR TREATMENT
FILE REFERENCE: P2068R1
CURRENT APPLICATION NUMBER: US/10/981,356A
CURRENT FILING DATE: 2004-11-04
PRIOR APPLICATION NUMBER: US 60/520,398
PRIOR FILING DATE: 2003-11-13
PRIOR APPLICATION NUMBER: US 60/557,951
PRIOR FILING DATE: 2004-03-31
NUMBER OF SEQ ID NOS: 45
SEQ ID NO 25
LENGTH: 666
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Sequence is synthesized
US-10-981-356A-25

Query Match 83.3%; Score 35; DB 9; Length 666;
Best Local Similarity 87.5%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
Db 95 HOYLSRT 102

RESULT 22
US-10-981-356A-27
Sequence 27, Application US/10981356A
Publication No. US20060015952A1
GENERAL INFORMATION:
APPLICANT: FILVAROFF, ELLEN H.
TITLE OF INVENTION: SCREENING ASSAYS AND METHODS OF TUMOR TREATMENT
FILE REFERENCE: P2068R1
CURRENT APPLICATION NUMBER: US/10/981,356A
CURRENT FILING DATE: 2004-11-04
PRIOR APPLICATION NUMBER: US 60/520,398

PRIOR FILING DATE: 2003-11-13
PRIOR APPLICATION NUMBER: US 60/557,951
PRIOR FILING DATE: 2004-03-31
NUMBER OF SEQ ID NOS: 45
SEQ ID NO 27
LENGTH: 666
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Sequence is synthesized
US-10-981-356A-27

Query Match 83.3%; Score 35; DB 9; Length 666;
Best Local Similarity 87.5%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
Db 95 HOYLSRT 102

RESULT 23
US-10-981-356A-28
Sequence 28, Application US/10981356A
Publication No. US20060015952A1
GENERAL INFORMATION:
APPLICANT: FILVAROFF, ELLEN H.
TITLE OF INVENTION: SCREENING ASSAYS AND METHODS OF TUMOR TREATMENT
FILE REFERENCE: P2068R1
CURRENT APPLICATION NUMBER: US/10/981,356A
CURRENT FILING DATE: 2004-11-04
PRIOR APPLICATION NUMBER: US 60/520,398
PRIOR FILING DATE: 2003-11-13
PRIOR APPLICATION NUMBER: US 60/557,951
PRIOR FILING DATE: 2004-03-31
NUMBER OF SEQ ID NOS: 45
SEQ ID NO 28
LENGTH: 666
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Sequence is synthesized
US-10-981-356A-28

Query Match 83.3%; Score 35; DB 9; Length 666;
Best Local Similarity 87.5%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
Db 95 HOYLSRT 102

RESULT 24
US-10-981-356A-29
Sequence 29, Application US/10981356A
Publication No. US20060015952A1
GENERAL INFORMATION:
APPLICANT: FILVAROFF, ELLEN H.
TITLE OF INVENTION: SCREENING ASSAYS AND METHODS OF TUMOR TREATMENT
FILE REFERENCE: P2068R1
CURRENT APPLICATION NUMBER: US/10/981,356A
CURRENT FILING DATE: 2004-11-04
PRIOR APPLICATION NUMBER: US 60/520,398
PRIOR FILING DATE: 2003-11-13
PRIOR APPLICATION NUMBER: US 60/557,951
PRIOR FILING DATE: 2004-03-31
NUMBER OF SEQ ID NOS: 45
SEQ ID NO 29
LENGTH: 666
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:

OTHER INFORMATION: Sequence is synthesized
US-10-981-356A-29.

Query Match 83.3%; Score 35; DB 9; Length 666;
Best Local Similarity 87.5%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
Db 95 HOYLSRT 102

RESULT 25

US-10-981-356A-30
; Sequence 30, Application US/10981356A
; Publication No. US20060015952A1
; GENERAL INFORMATION:
; APPLICANT: FILVAROFF, ELLEN H.
; TITLE OF INVENTION: SCREENING ASSAYS AND METHODS OF TUMOR TREATMENT
; FILE REFERENCE: P2068R1
; CURRENT APPLICATION NUMBER: US/10/981.356A
; PRIOR FILING DATE: 2004-11-04, 2003, 11-13
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/557,951
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 45
; SEQ ID NO 30
; LENGTH: 666
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-10-981-356A-30

Query Match 83.3%; Score 35; DB 9; Length 666;
Best Local Similarity 87.5%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
Db 95 HOYLSRT 102

RESULT 26

US-11-096-046-27
; Sequence 27, Application US/11096046
; Publication No. US20050276802A1
; GENERAL INFORMATION:
; APPLICANT: ADAMS, CAMELLIA W.
; APPLICANT: FERRARA, NAPOLEONE
; APPLICANT: FILVAROFF, ELLEN H.
; APPLICANT: MAO, WEIGUANG
; APPLICANT: PRESTA, LEONARD G.
; APPLICANT: TEJADA, MAX L.
; TITLE OF INVENTION: Humanized Anti-TGF-Beta Antibodies
; FILE REFERENCE: P1954R1US
; CURRENT APPLICATION NUMBER: US/11/096,046
; PRIOR FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: US 60/558,290
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 27
; LENGTH: 666
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-096-046-27

Query Match 83.3%; Score 35; DB 11; Length 666;
Best Local Similarity 87.5%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
Db 95 HOYLSRT 102

RESULT 27

US-11-096-046-25
; Sequence 25, Application US/11096046
; Publication No. US20050276802A1
; GENERAL INFORMATION:
; APPLICANT: ADAMS, CAMELLIA W.
; APPLICANT: FERRARA, NAPOLEONE
; APPLICANT: FILVAROFF, ELLEN H.
; APPLICANT: MAO, WEIGUANG
; APPLICANT: PRESTA, LEONARD G.
; APPLICANT: TEJADA, MAX L.
; TITLE OF INVENTION: Humanized Anti-TGF-Beta Antibodies
; FILE REFERENCE: P1954R1US
; CURRENT APPLICATION NUMBER: US/11/096,046
; PRIOR FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: US 60/558,290
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 25
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
; NAME/KEY: Unsure
; LOCATION: 220
; OTHER INFORMATION: Unknown amino acid
US-11-096-046-25

Query Match 83.3%; Score 35; DB 11; Length 667;
Best Local Similarity 87.5%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSRT 8
Db 95 HOYLSRT 102

RESULT 28

US-11-096-046-28
; Sequence 28, Application US/11096046
; Publication No. US20050276802A1
; GENERAL INFORMATION:
; APPLICANT: ADAMS, CAMELLIA W.
; APPLICANT: FERRARA, NAPOLEONE
; APPLICANT: FILVAROFF, ELLEN H.
; APPLICANT: MAO, WEIGUANG
; APPLICANT: PRESTA, LEONARD G.
; APPLICANT: TEJADA, MAX L.
; TITLE OF INVENTION: Humanized Anti-TGF-Beta Antibodies
; FILE REFERENCE: P1954R1US
; CURRENT APPLICATION NUMBER: US/11/096,046
; PRIOR FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: US 60/558,290
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 28
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-096-046-28

Query Match 83.3%; Score 35; DB 11; Length 667;
Best Local Similarity 87.5%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

US-11-096-046-28

Query Match 83.3%; Score 35; DB 11; Length 667;
Best Local Similarity 87.5%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSRT 8

Db 95 HOYLSRT 102

RESULT 29

US-11-096-046-29
; Sequence 29, Application US/11096046
; Publication No. US20050276802A1
; GENERAL INFORMATION:
; APPLICANT: ADAMS, CAMELIA W.
; APPLICANT: FERRARA, NAPOLEONE
; APPLICANT: FILVAROFF, ELLEN H.
; APPLICANT: MAO, WEIGUANG
; APPLICANT: PRESTA, LEONARD G.
; APPLICANT: TEJADA, MAX L.
; TITLE OF INVENTION: Humanized Anti-TGF-Beta Antibodies
; FILE REFERENCE: P1954RIUS
; CURRENT APPLICATION NUMBER: US/11/096,046
; CURRENT FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: US 60/558,290
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 29
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
; NAME/KEY: Unsure
; LOCATION: 220
; OTHER INFORMATION: Unknown amino acid
US-11-096-046-29

Query Match 83.3%; Score 35; DB 11; Length 667;
Best Local Similarity 87.5%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSRT 8

Db 95 HOYLSRT 102

RESULT 30

US-11-096-046-30
; Sequence 30, Application US/11096046
; Publication No. US20050276802A1
; GENERAL INFORMATION:
; APPLICANT: ADAMS, CAMELIA W.
; APPLICANT: FERRARA, NAPOLEONE
; APPLICANT: FILVAROFF, ELLEN H.
; APPLICANT: MAO, WEIGUANG
; APPLICANT: PRESTA, LEONARD G.
; APPLICANT: TEJADA, MAX L.
; TITLE OF INVENTION: Humanized Anti-TGF-Beta Antibodies
; FILE REFERENCE: P1954RIUS
; CURRENT APPLICATION NUMBER: US/11/096,046
; CURRENT FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: US 60/558,290
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 30
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:

OTHER INFORMATION: sequence is synthesized
; FEATURE:
; NAME/KEY: Unsure
; LOCATION: 220
; OTHER INFORMATION: Unknown amino acid
US-11-096-046-30

Query Match 83.3%; Score 35; DB 11; Length 667;
Best Local Similarity 87.5%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSRT 8

Db 95 HOYLSRT 102

RESULT 31

US-10-981-356A-26
; Sequence 26, Application US/10981356A
; Publication No. US20060015952A1
; GENERAL INFORMATION:
; APPLICANT: FILVAROFF, ELLEN H.
; TITLE OF INVENTION: SCREENING ASSAYS AND METHODS OF TUMOR TREATMENT
; FILE REFERENCE: P2068RI
; CURRENT APPLICATION NUMBER: US/10/981,356A
; CURRENT FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: US 60/520,398
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/557,951
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 45
; SEQ ID NO 26
; LENGTH: 692
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-10-981-356A-26

Query Match 83.3%; Score 35; DB 9; Length 692;
Best Local Similarity 87.5%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSRT 8

Db 95 HOYLSRT 102

RESULT 32

US-11-096-046-26
; Sequence 26, Application US/11096046
; Publication No. US20050276802A1
; GENERAL INFORMATION:
; APPLICANT: ADAMS, CAMELIA W.
; APPLICANT: FERRARA, NAPOLEONE
; APPLICANT: FILVAROFF, ELLEN H.
; APPLICANT: MAO, WEIGUANG
; APPLICANT: PRESTA, LEONARD G.
; APPLICANT: TEJADA, MAX L.
; TITLE OF INVENTION: Humanized Anti-TGF-Beta Antibodies
; FILE REFERENCE: P1954RIUS
; CURRENT APPLICATION NUMBER: US/11/096,046
; CURRENT FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: US 60/558,290
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 26
; LENGTH: 695
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized

NAME/KEY: Unsure
LOCATION: 220; 668, 673
OTHER INFORMATION: Unknown amino acid
US-11-096-046-26

Query Match 83.3%; Score 35; DB 11; Length 695;
Best Local Similarity 87.5%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HOYLSRT 8
Db 95 HOYLSRT 102

RESULT 33
US-11-188-298-19968
Sequence 19968, Application US/11188298
Publication No. US20060075522A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-21 (53452)B
CURRENT FILING DATE: 2005-07-22
PRIOR APPLICATION NUMBER: 60/592,978
PRIOR FILING DATE: 2004-07-31
NUMBER OF SEQ ID NOS: 22569
SEQ ID NO 19968
LENGTH: 252
TYPE: PRT
ORGANISM: Buchnera aphidicola str. Bp (Baizongia pistaciae)
US-11-188-298-19968

Query Match 73.8%; Score 31; DB 11; Length 252;
Best Local Similarity 62.5%; Pred. No. 30;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HOYLSRT 8
Db 135 HEVLSRT 142

RESULT 34
US-11-110-480-7
Sequence 7, Application US/11110480
Publication No. US20050287672A1
GENERAL INFORMATION:
APPLICANT: NORDGREN, ROBERT
APPLICANT: LOOSMORE, SHEENA MAY
APPLICANT: AUDONNET, JEAN-CHRISTOPHE FRANCIS
APPLICANT: GRUBMAN, MARVIN, J.
TITLE OF INVENTION: AVIROX RECOMBINANTS EXPRESSING FOOT AND MOUTH DISEASE
FILE REFERENCE: 574313-3235
CURRENT FILING DATE: 2005-04-20
PRIOR APPLICATION NUMBER: 60/563,786
PRIOR FILING DATE: 2004-04-20
NUMBER OF SEQ ID NOS: 88
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 7
LENGTH: 1126
TYPE: PRT
ORGANISM: Foot-and-mouth disease virus
US-11-110-480-7

Query Match 73.8%; Score 31; DB 11; Length 1126;
Best Local Similarity 62.5%; Pred. No. 1.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HOYLSRT 8
Db 231 HOYLSRT 238

RESULT 35
US-11-110-480-9
Sequence 9, Application US/11110480
Publication No. US20050287672A1
GENERAL INFORMATION:
APPLICANT: NORDGREN, ROBERT
APPLICANT: LOOSMORE, SHEENA MAY
APPLICANT: AUDONNET, JEAN-CHRISTOPHE FRANCIS
APPLICANT: GRUBMAN, MARVIN, J.
TITLE OF INVENTION: AVIROX RECOMBINANTS EXPRESSING FOOT AND MOUTH DISEASE
FILE REFERENCE: 574313-3235
CURRENT FILING DATE: 2005-04-20
PRIOR APPLICATION NUMBER: 60/563,786
PRIOR FILING DATE: 2004-04-20
NUMBER OF SEQ ID NOS: 88
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 9
LENGTH: 1126
TYPE: PRT
ORGANISM: Foot-and-mouth disease virus
US-11-110-480-9

Query Match 73.8%; Score 31; DB 11; Length 1126;
Best Local Similarity 62.5%; Pred. No. 1.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HOYLSRT 8
Db 231 HOYLSRT 238

RESULT 36
US-11-110-480-16
Sequence 16, Application US/11110480
Publication No. US20050287672A1
GENERAL INFORMATION:
APPLICANT: NORDGREN, ROBERT
APPLICANT: LOOSMORE, SHEENA MAY
APPLICANT: AUDONNET, JEAN-CHRISTOPHE FRANCIS
APPLICANT: GRUBMAN, MARVIN, J.
TITLE OF INVENTION: AVIROX RECOMBINANTS EXPRESSING FOOT AND MOUTH DISEASE
FILE REFERENCE: 574313-3235
CURRENT FILING DATE: 2005-04-20
PRIOR APPLICATION NUMBER: 60/563,786
PRIOR FILING DATE: 2004-04-20
NUMBER OF SEQ ID NOS: 88
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 16
LENGTH: 1126
TYPE: PRT
ORGANISM: Foot-and-mouth disease virus
US-11-110-480-16

Query Match 73.8%; Score 31; DB 11; Length 1126;
Best Local Similarity 62.5%; Pred. No. 1.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HOYLSRT 8
Db 231 HOYLSRT 238

RESULT 37
US-11-110-480-27
Sequence 27, Application US/11110480
Publication No. US20050287672A1
GENERAL INFORMATION:

```

; APPLICANT: NORDGREN, ROBERT
; APPLICANT: LOOSMORE, SHEENA MAY
; APPLICANT: AUDONNET, JEAN-CHRISTOPHE FRANCIS
; APPLICANT: GRUBMAN, MARVIN, J.
; TITLE OF INVENTION: AVIPOX RECOMBINANTS EXPRESSING FOOT AND MOUTH DISEASE
; FILE REFERENCE: 574313-3235
; CURRENT APPLICATION NUMBER: US/11/110,480
; PRIOR FILING DATE: 2005-04-20
; PRIOR APPLICATION NUMBER: 60/563,786
; PRIOR FILING DATE: 2004-04-20
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: Patentln Ver. 3.3
; SEQ ID NO 27
; LENGTH: 1126
; TYPE: PRT
; ORGANISM: Foot-and-mouth disease virus
; US-11-110-480-27

```

```

Query Match      73.8%; Score 31; DB 11; Length 1126;
Best Local Similarity 62.5%; Pred. No. 1.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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QY      1 HOYLSRT 8
Db      231 HOFSRPT 238

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RESULT 38
US-11-110-480-37
; Sequence 37, Application US/11110480
; Publication No. US20050287672A1
; GENERAL INFORMATION:
; APPLICANT: NORDGREN, ROBERT
; APPLICANT: LOOSMORE, SHEENA MAY
; APPLICANT: AUDONNET, JEAN-CHRISTOPHE FRANCIS
; APPLICANT: GRUBMAN, MARVIN, J.
; TITLE OF INVENTION: AVIPOX RECOMBINANTS EXPRESSING FOOT AND MOUTH DISEASE
; FILE REFERENCE: 574313-3235
; CURRENT APPLICATION NUMBER: US/11/110,480
; CURRENT FILING DATE: 2005-04-20
; PRIOR APPLICATION NUMBER: 60/563,786
; PRIOR FILING DATE: 2004-04-20
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: Patentln Ver. 3.3
; SEQ ID NO 37
; LENGTH: 1126
; TYPE: PRT
; ORGANISM: Foot-and-mouth disease virus
; US-11-110-480-37

```

```

Query Match      73.8%; Score 31; DB 11; Length 1126;
Best Local Similarity 62.5%; Pred. No. 1.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```
QY      1 HOYLSRT 8
Db      231 HOFSRPT 238

```

```

RESULT 39
US-11-110-480-47
; Sequence 47, Application US/11110480
; Publication No. US20050287672A1
; GENERAL INFORMATION:
; APPLICANT: NORDGREN, ROBERT
; APPLICANT: LOOSMORE, SHEENA MAY
; APPLICANT: AUDONNET, JEAN-CHRISTOPHE FRANCIS
; APPLICANT: GRUBMAN, MARVIN, J.
; TITLE OF INVENTION: AVIPOX RECOMBINANTS EXPRESSING FOOT AND MOUTH DISEASE
; FILE REFERENCE: 574313-3235

```

```

; CURRENT APPLICATION NUMBER: US/11/110,480
; CURRENT FILING DATE: 2005-04-20
; PRIOR APPLICATION NUMBER: 60/563,786
; PRIOR FILING DATE: 2004-04-20
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: Patentln Ver. 3.3
; SEQ ID NO 47
; LENGTH: 1126
; TYPE: PRT
; ORGANISM: Foot-and-mouth disease virus
; US-11-110-480-47

```

```

Query Match      73.8%; Score 31; DB 11; Length 1126;
Best Local Similarity 62.5%; Pred. No. 1.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```
QY      1 HOYLSRT 8
Db      231 HOFSRPT 238

```

```

RESULT 40
US-11-110-480-59
; Sequence 59, Application US/11110480
; Publication No. US20050287672A1
; GENERAL INFORMATION:
; APPLICANT: NORDGREN, ROBERT
; APPLICANT: LOOSMORE, SHEENA MAY
; APPLICANT: AUDONNET, JEAN-CHRISTOPHE FRANCIS
; APPLICANT: GRUBMAN, MARVIN, J.
; TITLE OF INVENTION: AVIPOX RECOMBINANTS EXPRESSING FOOT AND MOUTH DISEASE
; FILE REFERENCE: 574313-3235
; CURRENT APPLICATION NUMBER: US/11/110,480
; CURRENT FILING DATE: 2005-04-20
; PRIOR APPLICATION NUMBER: 60/563,786
; PRIOR FILING DATE: 2004-04-20
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: Patentln Ver. 3.3
; SEQ ID NO 59
; LENGTH: 1126
; TYPE: PRT
; ORGANISM: Foot-and-mouth disease virus
; US-11-110-480-59

```

```

Query Match      73.8%; Score 31; DB 11; Length 1126;
Best Local Similarity 62.5%; Pred. No. 1.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```
QY      1 HOYLSRT 8
Db      231 HOFSRPT 238

```

```

RESULT 41
US-11-110-480-82
; Sequence 82, Application US/11110480
; Publication No. US20050287672A1
; GENERAL INFORMATION:
; APPLICANT: NORDGREN, ROBERT
; APPLICANT: LOOSMORE, SHEENA MAY
; APPLICANT: AUDONNET, JEAN-CHRISTOPHE FRANCIS
; APPLICANT: GRUBMAN, MARVIN, J.
; TITLE OF INVENTION: AVIPOX RECOMBINANTS EXPRESSING FOOT AND MOUTH DISEASE
; FILE REFERENCE: 574313-3235
; CURRENT APPLICATION NUMBER: US/11/110,480
; CURRENT FILING DATE: 2005-04-20
; PRIOR APPLICATION NUMBER: 60/563,786
; PRIOR FILING DATE: 2004-04-20
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: Patentln Ver. 3.3
; SEQ ID NO 82

```

LENGTH: 1126
TYPE: PRT
ORGANISM: Foot-and-mouth disease virus
US-11-110-480-82

Query Match 73.8%; Score 31; DB 11; Length 1126;
Best Local Similarity 62.5%; Pred. No. 1.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HOYLSRT 8
Db 231 HOFSRPT 238

RESULT 42
US-11-110-480-88
Sequence 88, Application US/11110480
Publication No. US20050287672A1
GENERAL INFORMATION:
APPLICANT: NORDGREN, ROBERT
APPLICANT: LOOSMORE, SHEENA MAY
APPLICANT: AUDONNET, JEAN-CHRISTOPHE FRANCIS
APPLICANT: GRUBMAN, MARVIN, J.
TITLE OF INVENTION: AVIPOX RECOMBINANTS EXPRESSING FOOT AND MOUTH DISEASE
TITLE OF INVENTION: VIRUS GENES
FILE REFERENCE: 574313-3235
CURRENT APPLICATION NUMBER: US/11/110,480
CURRENT FILING DATE: 2005-04-20
PRIOR APPLICATION NUMBER: 60/563,786
PRIOR FILING DATE: 2004-04-20
NUMBER OF SEQ ID NOS: 88
SOFTWARE: Patent In Ver. 3.3
SEQ ID NO 88
LENGTH: 1126
TYPE: PRT
ORGANISM: Foot-and-mouth disease virus
US-11-110-480-88

Query Match 73.8%; Score 31; DB 11; Length 1126;
Best Local Similarity 62.5%; Pred. No. 1.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HOYLSRT 8
Db 231 HOFSRPT 238

RESULT 43
US-11-098-686-10968
Sequence 10968, Application US/11098686
Publication No. US20060024696A1
GENERAL INFORMATION:
APPLICANT: Kapur, Vivek and Gebhart, Connie J.
TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
FILE REFERENCE: 09531-128001
CURRENT APPLICATION NUMBER: US/11/098,686
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US03/31318
PRIOR FILING DATE: 2003-10-01
PRIOR APPLICATION NUMBER: US 60/416,395
PRIOR FILING DATE: 2002-10-04
NUMBER OF SEQ ID NOS: 11433
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10968
LENGTH: 403
TYPE: PRT
ORGANISM: Lawsonia intracellularis
US-11-098-686-10968

Query Match 71.4%; Score 30; DB 11; Length 403;
Best Local Similarity 71.4%; Pred. No. 81;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HOYLSR 7
Db 81 HOYLSRK 87

RESULT 44
US-10-821-234-1027
Sequence 1027, Application US/10821234
Publication No. US20050255114A1
GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmati, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: PC_SEQ_genes Version 1.0
SEQ ID NO 1027
LENGTH: 686
TYPE: PRT
ORGANISM: Homo sapiens
US-10-821-234-1027

Query Match 71.4%; Score 30; DB 9; Length 686;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QYLSRT 8
Db 331 RYLSRT 337

RESULT 45
US-10-453-372-126
Sequence 126, Application US/10453372
Publication No. US20060003323A1
GENERAL INFORMATION:
APPLICANT: Alsobrook, et al.
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
FILE REFERENCE: 21402-589 A
CURRENT APPLICATION NUMBER: US/10/453,372
CURRENT FILING DATE: 2003-06-03
PRIOR APPLICATION NUMBER: 09/789390
PRIOR FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 60/185967
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 09/823187
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/195792
PRIOR FILING DATE: 2000-03-10
PRIOR APPLICATION NUMBER: 09/839446
PRIOR FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 60/199476
PRIOR FILING DATE: 2000-03-25
PRIOR APPLICATION NUMBER: 09/863776
PRIOR FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: 60/208263
PRIOR FILING DATE: 2000-05-31
PRIOR APPLICATION NUMBER: 09/939398
PRIOR FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: 60/227800
PRIOR FILING DATE: 2000-08-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1609
SOFTWARE: CuiSeqdist Version 0.1
SEQ ID NO 126
LENGTH: 761

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-453-372-126
Query Match      71.4%; Score 30; DB 9; Length 761;
Best Local Similarity 85.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 QYLSRT 8
Db      561 RYLSRT 567

RESULT 46
US-10-453-372-122
; Sequence 122, Application US/10453372
; Publication No. US2006003323A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-589 A
; CURRENT APPLICATION NUMBER: US/10/453,372
; PENDING FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 09/789390
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/823187
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195792
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/839446
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/199476
; PRIOR FILING DATE: 2000-03-25
; PRIOR APPLICATION NUMBER: 09/863776
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/208263
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/939398
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/227800
; REMAINING PRIOR APPLICATION data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1609
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 122
; LENGTH: 823
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-453-372-122
Query Match      71.4%; Score 30; DB 9; Length 823;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 QYLSRT 8
Db      623 RYLSRT 629

RESULT 47
US-10-453-372-124
; Sequence 124, Application US/10453372
; Publication No. US2006003323A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-589 A
; CURRENT APPLICATION NUMBER: US/10/453,372
; PENDING FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 09/789390
; PRIOR FILING DATE: 2001-02-23
```

```

; PRIOR APPLICATION NUMBER: 60/185967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/823187
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195792
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/839446
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/199476
; PRIOR FILING DATE: 2000-03-25
; PRIOR APPLICATION NUMBER: 09/863776
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/208263
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/939398
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/227800
; REMAINING PRIOR APPLICATION data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1609
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 124
; LENGTH: 823
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-453-372-124
Query Match      71.4%; Score 30; DB 9; Length 823;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 QYLSRT 8
Db      623 RYLSRT 629

RESULT 48
US-10-453-372-118
; Sequence 118, Application US/10453372
; Publication No. US2006003323A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-589 A
; CURRENT APPLICATION NUMBER: US/10/453,372
; PENDING FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 09/789390
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/823187
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195792
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/839446
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/199476
; PRIOR FILING DATE: 2000-03-25
; PRIOR APPLICATION NUMBER: 09/863776
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/208263
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/939398
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/227800
; REMAINING PRIOR APPLICATION data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1609
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 118
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-10-453-372-118

Query Match 71.4%; Score 30; DB 9; Length 826;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYLSRT 8
:|||||
Db 629 RYLSRT 635

RESULT 49

US-10-453-372-156
; Sequence 156, Application US/10453372
; Publication No. US2006003323A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-589 A
; CURRENT APPLICATION NUMBER: US/10/453,372
; PRIORITY FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 09/789390
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/823187
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195792
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/839446
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/199476
; PRIOR FILING DATE: 2000-03-25
; PRIOR APPLICATION NUMBER: 09/863776
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/208263
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/939398
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/227800
; PRIOR FILING DATE: 2000-08-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1609
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 156
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-453-372-156

Query Match 71.4%; Score 30; DB 9; Length 826;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYLSRT 8
:|||||
Db 629 RYLSRT 635

RESULT 50

US-10-453-372-166
; Sequence 166, Application US/10453372
; Publication No. US2006003323A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-589 A
; CURRENT APPLICATION NUMBER: US/10/453,372
; PRIORITY FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 09/789390
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185967
; PRIOR FILING DATE: 2000-03-01

; PRIOR APPLICATION NUMBER: 09/823187
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195792
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/839446
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/199476
; PRIOR FILING DATE: 2000-03-25
; PRIOR APPLICATION NUMBER: 09/863776
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/208263
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/939398
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/227800
; PRIOR FILING DATE: 2000-08-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1609
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 166
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-453-372-166

Query Match 71.4%; Score 30; DB 9; Length 826;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYLSRT 8
:|||||
Db 629 RYLSRT 635

Search completed: May 4, 2006, 13:53:55
Job time: 21.2698 secs